

Result No.	Score	Query		Length	DB	ID	Description
		Match					
1	2752	100.0	2752	6	AX449572	6	AX449572 Sequence
2	2687.4	97.7	2697	6	AX451652	6	AX451652 Sequence
3	2676.4	97.3	2881	6	AX527916	6	AX527916 Sequence
4	2435.4	88.5	2784	6	CQ730306	6	CQ730306 Sequence
5	2356	85.6	3580	6	AX367094	6	AX367094 Sequence
6	2323.2	84.4	3392	10	MMU487852	10	MMU487852 Mus musculus
7	2259	82.1	3014	6	BD057524	6	BD057524 Netrin re
8	2252.2	81.8	2697	6	AX368596	6	AX368596 Sequence
9	2252.2	81.8	2697	10	RNU87305	10	RNU87305 Rattus nor
10	1983.6	72.1	3844	10	BC058084	10	BC058084 Mus muscu
11	1635.4	59.4	2688	9	BC009333	9	BC009333 Homo sapi
12	1562.4	56.8	1787	6	BD057525	6	BD057525 Netrin re
13	1304.2	47.4	9700	6	AX054976	6	AX054976 Sequence
14	992	36.0	9299	10	MMU72634	10	MMU72634 Mus muscul
15	991	36.0	2962	5	AY187310	5	AY187310 Gallus ga
16	986	35.8	9328	10	AB118026	10	AB118026 Rattus n
17	970	35.2	3646	6	CQ881060	6	CQ881060 Sequence
18	970	35.2	3646	9	AF055634	9	AF055634 Homo sapi
19	943.8	34.3	3770	9	AY126637	9	AY126637 Homo sapi

[illegible]

Db	13261	CCCGCTCAGCATCAAGCCCGACCAAGGACAGACAACCCCCATCTGCTCAACATCCAGCCGGAC	13260
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Db	13321	CTCAGCACCAACCACACCACTACAGGCGAGTCTGTGTCGCCGCGAGGATGGGCCCCAGC	13380
Qy	13381	CCCAAGTTTCAGCTTCACAAATGGGCACTGTCTAGCCCCCTGGGTGGCGCGGCCACACA	14440
Db	13381	CCCAAGTTTCAGCTTCACAAATGGGCACTGTCTAGCCCCCTGGGTGGCGCGGCCACACA	14440
Qy	14441	CTGCACCAACAGCTCTCCCACTCTGAGGCGAGGAGTTCTCTCCGCTCTCCACCCAG	15000
Db	14441	CTGCACCAACAGCTCTCCCACTCTGAGGCGAGGAGTTCTCTCCGCTCTCCACCCAG	15000
Qy	1501	AACTACTTCGCTCCCTGCCCGAGGACACAGCAATGACCTATGGGACCTTTCAACTTC	15600
Db	1501	AACTACTTCGCTCCCTGCCCGAGGACACAGCAATGACCTATGGGACCTTTCAACTTC	15600
Qy	1561	CTGGGGGCGGCTGATGATCCCTAATACAGGTATCAGCTCTCATCTCCGCCAGATGCC	16200
Db	1561	CTGGGGGCGGCTGATGATCCCTAATACAGGTATCAGCTCTCATCTCCGCCAGATGCC	16200
Qy	1621	ATACCCCGAGGAGATCTATGAGATCTACTCTCAGCTGCACAAGCCGGAAGACGTGAGG	16800
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Qy	1681	TTGGCCCTAGTGTGCTGCAGACCTCTGTAGTGCCCATCGTTAGCTGTGACACCCCTGGC	17400
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Qy	1741	GTCTGTCTCACCCGGCCAGTCACTCTGGCTATGGAACCACTGTGGGAGCCAGCCCTGAC	18000
Db	1741	GTCTGTCTCACCCGGCCAGTCACTCTGGCTATGGAACCACTGTGGGAGCCAGCCCTGAC	18000
Qy	1801	AGCTGAGCCTGTGCGCTCAAAAAGCACTGTGCGAGGCGAGCTGGGAGGATGTCTGCAC	18600
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Qy	1861	CTGGGCGAGAGGGCCCTCCCACTCTACTCTGCAGCTGGAGGCCAGTGCCTGCTAC	19200
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Qy	1921	GTCTTCCAGGACGTGGGCGGCTTTGCCCTGTGGGAGAGGCCCTCAGCTGGCTGCC	19800
Db	1921	GTCTTCCAGGACGTGGGCGGCTTTGCCCTGTGGGAGAGGCCCTCAGCTGGCTGCC	19800
Qy	1981	GCGAAGCGCTCAAGCTGCTTCTGTTTGGCGCGGTGGCTGCACCTCCCTCGAGTACAAC	20400
Db	1981	GCGAAGCGCTCAAGCTGCTTCTGTTTGGCGCGGTGGCTGCACCTCCCTCGAGTACAAC	20400
Qy	2041	ATCCGGGTCTACTGCGCTGCATGACACCCACGATGCACTCAAGGAGGTGGTGCAGCTGGAG	21000
Db	2041	ATCCGGGTCTACTGCGCTGCATGACACCCACGATGCACTCAAGGAGGTGGTGCAGCTGGAG	21000
Qy	2101	AAGCAGCTGGGGGACAGCTGATCCAGGAGCCACGGGTCTCTGCACCTTCAAGGACAGTTAC	21600
Db	2101	AAGCAGCTGGGGGACAGCTGATCCAGGAGCCACGGGTCTCTGCACCTTCAAGGACAGTTAC	21600
Qy	2161	CACAACTGGGCGCTATCCATCCAGATGTGCCAGCTCCCTGTGGAAAGAGTAAGCTCCTT	22200
Db	2161	CACAACTGGGCGCTATCCATCCAGATGTGCCAGCTCCCTGTGGAAAGAGTAAGCTCCTT	22200
Qy	2221	GTACGCTACAGGAGATCCCTTTTATCACATCTGGAAATGGCACGACGGGTACTTGCAC	22800
Db	2221	GTACGCTACAGGAGATCCCTTTTATCACATCTGGAAATGGCACGACGGGTACTTGCAC	22800
Qy	2281	TGCACCTTCACTCTGGAGCGTGTGAGGCCAGACACTAGTCACTTGGCTCTGCAAGCTGTGG	23400
Db	2281	TGCACCTTCACTCTGGAGCGTGTGAGGCCAGACACTAGTCACTTGGCTCTGCAAGCTGTGG	23400
Qy	2341	GTGTGGCAGGTGGAGGGCGAGCGGCGAGAGCTTCAGCATCAACTTCAACATCAACAGGAC	24000
Db	2341	GTGTGGCAGGTGGAGGGCGAGCGGCGAGAGCTTCAGCATCAACTTCAACATCAACAGGAC	24000

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Qy |||||
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Db |||||
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Db |||||
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Qy |||||
2701 CCAGAGCTGGCTTTCACAGTGTGGAGGCTGAGTCTGAGGCCGCCAG 2752
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RESULT 2
LOCUS AX451652 2697 bp DNA linear PAT 03-JUL-2002
DEFINITION Sequence 1 from Patent WO0233080.
ACCESSION AX451652
VERSION AX451652.1 GI:21698587
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Koehler, R. H.
TITLE Regulation of human netrin binding membrane receptor unc5h-1
JOURNAL Patent: WO 0233080-A 1 25-APR-2002;
Bayer Aktiengesellschaft (DE)
FEATURES
source location/Qualifiers
1..2697 /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 97.7%; Score 2687.4; DB 6; Length 2697;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2691; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 46 ATGCGCGTCCGCGCGGCTGTGGCAGCTCTCTGGGCAATAGTCTCGCGCTTGCTC 105
Db 1 ATGCGCGTCCGCGCGGCTGTGGCAGCTCTCTGGGCAATAGTCTCTCGCGCTTGCTC 60
Qy 106 CGCGGCTCGGTCGCCAGAGTGCACCGTGGCCCAACCCAGTGCCTGTGGCCAAACCCG 165
Db 61 CGCGGCTCGGTCGCCAGAGTGCACCGTGGCCCAACCCAGTGCCTGTGGCCAAACCCG 120
Qy 166 GACCTGCTTCCCACTTCTCTGGTGGAGCCCGAGGATGTATCATCGTCAAGAAAGGCCA 225
Db 121 GACCTGCTTCCCACTTCTCTGGTGGAGCCCGAGGATGTATCATCGTCAAGAAAGGCCA 180
Qy 226 GTGCTGCTTGTGTGAAGCGCTGCCCGCCACGAGATCTTTCAAGTGAACCGGGAG 285
Db 181 GTGCTGCTTGTGTGAAGCGCTGCCCGCCACGAGATCTTTCAAGTGAACCGGGAG 240
Qy 286 TGCGTGGCCAGGTGGACCACTGATCGAGCGGAGCAGACGCGGAGCAGTGGGCTGCC 345
Db 241 TGGGTGGCCAGGTGGACCACTGATCGAGCGGAGCAGACGCGGAGCAGTGGGCTGCC 300

Qy 346 ACCATGAGGTCCGCATTAATGTCTCAAGGCGAGAGTGTGAGAAAGTGTCTCGGGCTGGAG 405
Db |||||
301 ACCATGAGGTCCGCATTAATGTCTCAAGGCGAGAGTGTGAGAAAGTGTCTCGGGCTGGAG 360
Qy |||||
406 GAATATCTGGTCCAGTGTGGCATTGGAGTCTCTCGGGCACCAACAGAGTCAAGAGGCC 465
Db |||||
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Qy |||||
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Db |||||
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Db |||||
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Qy |||||
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Db |||||
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Qy |||||
1126 CTCTATGTGGGCTCTATGCGCGTGGCGCTGTGCTGTGCTGTGCTGTGCTCTCATC 1185
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Qy 1546 GGGACCTTTCAACTTCTCGGGGGCGGCTGATGATCCCTAATACAGTATCAGCCTCCTC 1605
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Qy 1846 GAGGATGTGTGACCTGGGCGAGGCGCCCTCCACCTCTACTACTGCGAGCTGGAG 1905
Db 1801 GAGGATGTGTGACCTGGGCGAGGCGCCCTCCACCTCTACTACTGCGAGCTGGAG 1860
Qy 1906 GCCAGTGGCTGCTAGCTTTTACCGAGCAGTGGGCGCTTTGCTGCTGGTGGAGAGGCC 1965
Db 1861 GCCAGTGGCTGCTAGCTTTTACCGAGCAGTGGGCGCTTTGCTGCTGGTGGAGAGGCC 1920
Qy 1966 CTGAGCTGGCTGGCGCAAGCGCTCAAGCTGCTTCTGTTTGGCGGCTGGCTGCACC 2025
Db 1921 CTGAGCTGGCTGGCGCAAGCGCTCAAGCTGCTTCTGTTTGGCGGCTGGCTGCACC 1980
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Db 1981 TCCCTCGAGTACAAATCCCGGCTTACTGCTGATGACACCCACGATGCACTCAAGGAG 2040
Qy 2086 GTGCTGAGCTGGAGAGCAGCTGGGGGACAGCTGATCAGAGCCACCGGCTCTGCAC 2145
Db 2041 GTGCTGAGCTGGAGAGCAGCTGGGGGACAGCTGATCAGAGAGCCACCGGCTCTGCAC 2100
Qy 2146 TTCAAGGACAGTTTACCAACCTCGCGCTATCCATCCACGATGTGCCAGCTCCCTGTGG 2205
Db 2101 TTCAAGGACAGTTTACCAACCTCGCGCTATCCATCCACGATGTGCCAGCTCCCTGTGG 2160
Qy 2206 AAGAGTAAAGCTCTTGTGCTAGTACCAAGAGATCCCTTTTATCACAATCTGGAATGGCAG 2265
Db 2161 AAGAGTAAAGCTCTTGTGCTAGTACCAAGAGATCCCTTTTATCACAATCTGGAATGGCAG 2220
Qy 2266 CAGCGGTACTGTGACTGCACCTTACCCCTGAGGGGTGTCAGCCCCAGCACTAGTGAACCTG 2325
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Db 2401 CCAGCCCTGTGGGCCCCAGTCCCTTCAAGATCCCTTCTCATTCGGGCGAGAGATAATT 2460
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Qy 2686 GCTGGACTGGGCCAGCAGCAGCTGGCTCTTCCACAGTTCGAGAGCTGAGTCTGA 2742
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RESULT 3
AX527916 2881 bp DNA linear PAT 21-NOV-2002
LOCUS
DEFINITION Sequence 1 from Patent WO0229036.
ACCESSION AX527916
VERSION AX527916.1 GI:25172359
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Herrmann, J.L., Rastelli, L. and Shinkets, R.A.
TITLE Novel proteins and nucleic acids encoding same and antibodies
directed against these proteins
JOURNAL Patent: WO 0229038-A 1 11-APR-2002;
Curagen Corporation (US)
FEATURES
source
1. .2881
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ORIGIN

Query Match 97.3%; Score 2676.4; DB 6; Length 2881;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2728; Conservative 0; Mismatches 21; Indels 9; Gaps 3;

Qy 1 CCGCGGGGGCCCCCGCGCGCGCGCTGCGCGCTGCGCGCGCGCCATGGCGCTCGGCCCC 60
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Qy 61 GGCTGTGGCAGCGCTCCTGGGCATAGTCTCCTCGCGCTTGGCTCGCGCGCTCGGGTGCC 120
Db 102 GGCTGTGGCAGCGCTCCTGGGCATAGTCTCCTCGCGCTTGGCTCGCGCGCTCGGGTGCC 161
Qy 121 CAGCAGAGTGCCACCGTGGCCAAACCCAGTGCCTGGTGCCAAACCCGACCTGCTTCCCCAC 180
Db 162 CAGCAGAGTGCCACCGTGGCCAAACCCAGTGCCTGGTGCCAAACCCGACCTGCTTCCCCAC 221
Qy 181 TTCTGTGGAGCGCGGAGATGTATCATGTCAGACAGCAGTGTCTGTGTGTC 240
Db 222 TTCTGTGGAGCGCGGAGATGTATCATGTCAGACAGCAGTGTCTGTGTGTC 281
Qy 241 AAGCGCTGTGCCCGCCACCGAGATCTTCTTCAAGTGAACCGGGAGTGGGTGCGCCAGGTG 300
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Qy 301 GACACAGTATCAGCGCAGACACAGCGGAGCAGTGGGTGCGCCACCATGAGAGTCCGC 360
Db 342 GACACAGTATCAGCGCAGACACAGCGGAGCAGTGGGTGAGCCGACCATGAGAGTCCGC 401
Qy 361 ATTAATGTCTCAAGGAGCAGGTCGAGAGGTGCTGGGCTGGAGGAATACTGGTCCAG 420
Db 402 ATTAATGTCTCAAGGAGCAGGTCGAGAGGTGCTGGGCTGGAGGAATACTGGTCCAG 461
Qy 421 TGGCTGGCATGAGAGCTCTCTCGGCGACCCACCAAGAGTCAAGAGGCCTACATCCCGCATAGCC 480
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Db 1816 GACCACTGTGGGAGCCAGCCCTGACAGCTGAGAGCTTGGCCCTCAAAAAGCAGTGTGTC 1875
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QY 1894 TGCCAGCTGGAGGCGCAGTCTGTCTTCAACCGAGCAGCTGGGCGCTTTGCCCTG 1953
Db 1936 TGCCAGCTGGAGGCGCAGTCTGTCTTCAACCGAGCAGCTGGGCGCTTTGCCCTG 1995
QY 1954 GTGGGAGGCGCCTCAGGCTGGCTGCGCCGAAGCGCCTCAGCTGCTTCTGTTGGCGG 2013
Db 1996 GTGGGAGGCGCCTCAGGCTGGCTGCGCCGAAGCGCCTCAGCTGCTTCTGTTGGCGG 2055
QY 2014 GTGGCTGTGCACCTCCCTCGAGTACAAATCCGGGTCTACTCCCTGCATGACACCCACGAT 2073
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Db 2536 CAGAAGATATTTCCAGCTGGACCCACCTGTAGGCGGGGTGCCGACTGGCGACTCTG 2595
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QY 2614 GCCATGATCTCAACCTGTGGGAGCGCGGCACTTCCCAACCGGCAACCTCAGCCAGCTG 2673
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QY 2734 GAGTGTCTGA 2742
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RESULT 5
AX367094
LOCUS AX367094 3580 bp DNA linear PAT 16-FEB-2002
DEFINITION Sequence 13 from Patent WO0198354.
ACCESSION AX367094
VERSION AX367094.1 GI:18855296
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Griffin,J.A., Kallick,D.A., Tribouley,C.M., Yue,H., Nguyen,D.B.,
Tang,Y.T., Lal,P., Policky,J.L., Azimzai,Y., Lu,D.A., Graul,R.,
Yao,M.G., Burford,N., Hafalia,A.J., Baughn,M.R., Bandman,O.,
Patterson,C., Yang,J., Xu,Y., Warren,B.A., Ding,L. and
Sanjanwala,M.S.
RECEPTORS
Patent: WO 0198354-A 13 27-DEC-2001;
Incyte Genomics, Inc. (US)
FEATURES
Location/Qualifiers
source 1..3580
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ORIGIN

Query Match 85.6%; Score 2356; DB 6; Length 3580;
Best Local Similarity 93.6%; Pred. No. 0;
Matches 2537; Conservative 0; Mismatches 5; Indels 168; Gaps 1;

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REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE

AUTHORS Engelkamp,D.
 TITLE Cloning of three mouse Unc5 genes and their expression patterns at mid-gestation
 JOURNAL Mech. Dev. 118 (1-2), 191-197 (2002)
 MEDLINE 2239710
 PUBMED 12351186
 REFERENCE 2 (bases 1 to 3992)
 AUTHORS Engelkamp,D.
 TITLE Direct Submission
 JOURNAL Submitted (15-MAY-2002) Neuroanatomy, Max Planck Institute for Brain Research, Deutscherordenstrasse 46, Frankfurt 60528, GERMANY

FEATURES

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DEFINITION Sequence 15 from Patent WO0175440.
ACCESSION AX268596
VERSION AX268596.1 GI:16541710
KEYWORDS
SOURCE Rattus sp.
ORGANISM Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Rattus.

REFERENCE 1
AUTHORS Cochran,S.W., Paterson,G.Y., Ohashi,Y.W., Morris,B.Y. and
Pratt,J.Y.
TITLE Schizophrenia related genes
JOURNAL Patent: WO 0175440-A 15 11-OCT-2001;
WELFIDE CORPORATION (JP)
FEATURES
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Query Match 81.8%; Score 2252.2; DB 6; Length 2697;
Best Local Similarity 89.7%; Pred. No. 0;
Matches 2419; Conservative 0; Mismatches 278; Indels 0; Gaps 0;

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ACCESSION U87305
VERSION U87305.1 GI:2055391
KEYWORDS Rattus norvegicus (Norway rat)
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus
REFERENCE 1 (bases 1 to 2697)
AUTHORS Leonardo, E.D., Hinc, L., Masu, M., Keino-Masu, K., Ackerman, S.L. and Tessier-Lavigne, M.
TITLE Vertebrate homologues of C. elegans UNC-5 are candidate netrin receptors
JOURNAL Nature 386 (6627), 833-838 (1997)
MEDLINE 97271897
PUBMED 9126742
REFERENCE 2 (bases 1 to 2697)
AUTHORS Leonardo, E.D., Hinc, L., Masu, M., Keino-Masu, K. and Tessier-Lavigne, M.
TITLE Direct Submission
JOURNAL Submitted (28-JAN-1997) Anatomy, UCSF, 513 Parnassus, San Francisco, CA 94143-0452, USA
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ORIGIN

Query Match 81.8%; Score 2252.2; DB 10; Length 2697;
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RESULT 10
BC058084
LOCUS BC058084 3844 bp mRNA linear ROD 21-OCT-2003
DEFINITION Mus musculus unc-5 homolog A (C. elegans), mRNA (cdna clone
MGC:66671 IMAGE:6813463), complete cds.
ACCESSION BC058084
VERSION BC058084.1 GI:34784158
KEYWORDS MGC.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 3844)
REFERENCE Strausberg, R.L., Feingold, B.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusik, K., Farmer, A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Ustin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinaki, M.I., Skalek, U., Smalus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
12477932
2 (bases 1 to 3844)
Strausberg, R.
Direct Submission
Submitted (08-SEP-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library Preparation: M. Bento Soares, University of Iowa
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Leticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Nees, Pawan Pandoh, Anna-Lisea Prabhu, Parvaneh Saeedi, Jacqueline
Schein, Duane Smalus, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAC Plate: 126 Row: b Column: 11
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 23346570.
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SLBQGLVPCRPPEGIPPAEVEWRLNEDLDVPSLDPNVYITRHSILVVRQARLADTN
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Db 2019 ACCAAGCGCTCAGGCTCTCTGTGTTGGCCCTGTGGCTGTAGCTCTCTCGAGTACAAC 2078
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Db 2079 ATCCGAGTGTACTGCTGCAGACACCCACCATGCTCTCAAGGAGGTTGTCAGCTGGAG 2138
Qy 2101 AAGCAGCTGGGGGACAGCTGATCAGGAGCAGCGGTCTGCACTTCAAGGACAGTTAC 2160
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RESULT 11
BC009333
LOCUS
DEFINITION Homo sapiens unc-5 homolog A (C. elegans), mRNA (cdna clone IMAGE:4126760), partial cds.
ACCESSION BC009333
VERSION BC009333.2
KEYWORDS GI:40226527
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
MAMMALIA; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 2688)
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heish, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Ustin, T.B., Toshiki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahy, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butlerfield, Y.S., Krzywinski, M.I., Skalek, U., Smal, D.E., Scherch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 2688)
Strausberg, R.
Direct Submission
Submitted (12-JUN-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
NTH-MGC Project URL: <http://mgc.nci.nih.gov>
On Dec 19, 2003 this sequence version replaced gi:14424611.
Contact: MGC help desk
Email: cgapbs-x@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc.mgc@nih.gov
Akhtar, N., Ayale, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., McDowell, J., Masello, C., Maekeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W., Tauregon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at: <http://image.llnl.gov>
Series: IRAL Plate: 26 Row: g Column: 22.
FEATURES
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Qy 2747 GGCCAG 2752
Db 1675 GGCCAG 1680

RESULT 13
AX054976
LOCUS AX054976 9700 bp DNA linear PAT 13-JAN-2001
DEFINITION Sequence 91 from Patent WO0073328.
ACCESSION AX054976
VERSION AX054976.1 GI:12228344

KEYWORDS synthetic construct
SOURCE other sequences; artificial sequences.
ORGANISM 1
REFERENCE 1
AUTHORS van Criekeing, W., Roelens, I., Bogaert, T. and Verwaerde, P.
TITLE Unc-5 constructs and screening methods
JOURNAL Patent: WO 0073328-A 91 07-DEC-2000;
Devgen NV (BB)

FEATURES
source location/Qualifiers
1..9700
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="plasmid pGc1037"

ORIGIN

Query Match 47.4%; Score 1304.2; DB 6; Length 9700;
Best Local Similarity 99.8%; Pred. No. 6.8e-209;
Matches 1306; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1437 CAGCTGCACACAGCTCTCCACCTCTGAGGCCGAGAGTTCGTCTCCGCTCTCCAC 1496
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DEFINITION Mus musculus rostral cerebellar malformation protein (rcm) mRNA,
complete cds.
ACCESSION U72634
VERSION U72634.1 GI:2088526

MMU72634 9299 bp mRNA linear ROD 13-MAY-1997
Mus musculus rostral cerebellar malformation protein (rcm) mRNA,
complete cds.
U72634
U72634.1 GI:2088526

KEYWORDS	Mus musculus (house mouse)
SOURCE	Mus musculus
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE	1 (bases 1 to 9299)
AUTHORS	Ackerman, S.L., Kozak, L.P., Przyborski, S.A., Rund, L.A., Boyer, B.B. and Knowles, B.
TITLE	The mouse rostral cerebellar malformation gene encodes an UNC-5-like protein
JOURNAL	Nature 386 (6627), 838-842 (1997)
MEDLINE	97271898
PUBMED	9126743
REFERENCE	2 (bases 1 to 9299)
AUTHORS	Ackerman, S.L., Kozak, L.P., Rund, L.A. and Knowles, B.B.
TITLE	Direct Submission
JOURNAL	Submitted (25-SEP-1996) The Jackson Laboratory, 600 Main Street, Bar Harbor, ME 04609, USA
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VERSION	AV187310.1	GI:31442350	
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	1 (bases 1 to 2962)		
AUTHORS	Guan,W. and Condic,M.L.		
TITLE	Characterization of Netrin-1, Neogenin and cUNC-5H3 expression		
JOURNAL	during chick dorsal root ganglia development		
REFERENCE	Gene Expr. Patterns 3, 369-373 (2003)		
AUTHORS	2 (bases 1 to 2962)		
TITLE	Guan,W. and Condic,M.L.		
JOURNAL	Direct Submission		
FEATURES	Submitted (26-NOV-2002) Neurobiology & Anatomy, University of Utah,		
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Query Match 36.0%; Score 991; DB 5; Length 2962;

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 7, 2005, 05:11:16 ; Search time 2192 Seconds
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Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
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8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2752	100.0	2752	6	ABK37922
2	2752	100.0	2752	12	ADH71617
3	2687.4	97.7	2697	6	ABK52891
4	2676.4	97.3	2881	6	ABK49422
5	2676.4	97.3	2881	12	ADH71609
6	2674.8	97.2	2881	12	ADH71649
7	2674.8	97.2	2881	12	ADH71635
8	2674.8	97.2	2881	12	ADH71637
9	2674.8	97.2	2881	12	ADH71641
10	2674.8	97.2	2881	12	ADH71629
11	2674.8	97.2	2881	12	ADH71631
12	2674.8	97.2	2881	12	ADH71645
13	2674.8	97.2	2881	12	ADH71627
14	2674.8	97.2	2881	12	ADH71639
15	2674.8	97.2	2881	12	ADH71643
16	2674.8	97.2	2881	12	ADH71625
17	2674.8	97.2	2881	12	ADH71647
18	2673.2	97.1	2881	10	ADG42568
19	2662.8	96.8	2880	12	ADH71633
20	2368.6	86.1	2907	4	AAK52261

21	2356	85.6	3561	12	ADL06497
22	2356	85.6	3580	6	ABK15169
23	2328	84.6	2575	12	ADH71621
24	2266.2	82.3	2463	12	ADH71623
25	2259	82.1	3014	2	AAV52940
26	2252.2	81.8	2697	6	AAV52940
27	1635.4	59.4	2635	11	ADN95100
28	1562.4	56.8	1787	2	AAV52941
29	1304.2	47.4	9700	4	AAV52941
30	1266.6	43.8	1321	4	AAV52941
31	987.6	35.9	1002	12	ADH71619
32	985.6	35.8	1009	12	ADH71613
33	970	35.2	3646	5	AAV52941
34	970	35.2	3646	13	ADN95257
35	968.8	35.2	2795	10	AAV52941
36	943.4	34.3	993	12	ADH71611
37	936.2	34.0	2860	6	ABT06279
38	936.2	34.0	2860	6	ABT06280
39	913.6	33.2	2895	6	ABQ93898
40	905.6	32.9	3933	13	ADN07892
41	904.2	32.9	2985	13	ADN95249
42	902.4	32.8	3884	4	AAV52941
43	902.4	32.8	3884	8	AAV52941
44	902.4	32.8	3884	8	ABX89213
45	902.4	32.8	3884	8	ACD41867

ALIGNMENTS

RESULT 1
ABK37922
ID ABK37922 standard; cDNA; 2752 BP.

XX AC ABK37922;

XX DT 21-MAY-2002 (first entry)

XX DE cDNA encoding Human protein NOV1.

XX KW Human; NOVX; ss; gene; cardiomyopathy; atherosclerosis; diabetes;
cell signal processing disorder; metabolic disorder; obesity; infection;
anorexia; cancer-associated cachexia; cancer; neurodegenerative disorder;
Alzheimer's disease; Parkinson's disease; immune disorder;
haematopoietic disorders; dyslipidaemia; pain; asthma; hypertension;
osteoporosis; Crohn's disease; multiple sclerosis; benign prostatic hypertrophy;
myocardial infarction; ulcer; allergy; benign prostatic hypertrophy;
psychosis; neurological disorder; anxiety; schizophrenia;
manic depression; dementia; dyskinesia; Huntington's disease;
Gilles de la Tourette's syndrome; gene therapy.

XX OS Homo sapiens.

XX WO200210216-A2.

XX PD 07-FEB-2002.

XX PF 30-JUL-2001; 2001WO-US024225.

XX PR 28-JUL-2000; 2000US-0221409P.

XX PR 04-AUG-2000; 2000US-0222840P.

XX PR 04-AUG-2000; 2000US-0223752P.

XX PR 04-AUG-2000; 2000US-0223762P.

XX PR 04-AUG-2000; 2000US-0223769P.

XX PR 04-AUG-2000; 2000US-0223770P.

XX PR 14-AUG-2000; 2000US-0225146P.

XX PR 15-AUG-2000; 2000US-0225392P.

XX PR 16-AUG-2000; 2000US-0225470P.

XX PR 01-FEB-2001; 2001US-0263662P.

XX PR 05-APR-2001; 2001US-0281645P.

XX PA (CURA-) CURAGEN CORP.

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RESULT 2
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ID ADH71617 standard; DNA; 2752 BP.
XX
AC ADH71617;
XX
DT 25-MAR-2004 (first entry)
XX
Human gene of the invention NOV21e SEQ ID NO:513.
ds; gene; human; cytotatic; immunomodulator; neuroprotective; nootropic;
anorectic; antidiabetic; antimicrobial; antilipemic; gene therapy;
vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
obesity; diabetes; infectious disease; metabolic syndrome X;
dyslipidaemia.
XX
Homo sapiens.
XX
PN WO2003102155-A2.
XX
PD 11-DEC-2003.
XX
PF 03-JUN-2003; 2003WO-US017430.
XX
PR 03-JUN-2002; 2002US-0385120P.
PR 04-JUN-2002; 2002US-0385784P.
PR 05-JUN-2002; 2002US-0386041P.
PR 05-JUN-2002; 2002US-0386047P.
PR 06-JUN-2002; 2002US-0386376P.
PR 06-JUN-2002; 2002US-0386453P.
PR 06-JUN-2002; 2002US-0386864P.
PR 06-JUN-2002; 2002US-0387016P.
PR 07-JUN-2002; 2002US-0386796P.
PR 07-JUN-2002; 2002US-0386816P.
PR 07-JUN-2002; 2002US-0386931P.
PR 07-JUN-2002; 2002US-0386942P.
PR 07-JUN-2002; 2002US-0386971P.
PR 07-JUN-2002; 2002US-0387262P.
PR 08-JUN-2002; 2002US-0296960P.
PR 10-JUN-2002; 2002US-0387400P.
PR 10-JUN-2002; 2002US-0387535P.
PR 11-JUN-2002; 2002US-0387610P.
PR 11-JUN-2002; 2002US-0387625P.
PR 11-JUN-2002; 2002US-0387634P.
PR 11-JUN-2002; 2002US-0387668P.
PR 11-JUN-2002; 2002US-0387696P.
PR 11-JUN-2002; 2002US-0387702P.
PR 11-JUN-2002; 2002US-0387836P.
PR 11-JUN-2002; 2002US-0387859P.
PR 12-JUN-2002; 2002US-0387933P.
PR 12-JUN-2002; 2002US-0387934P.
PR 12-JUN-2002; 2002US-0387960P.
PR 12-JUN-2002; 2002US-0388022P.
PR 12-JUN-2002; 2002US-0388096P.
PR 13-JUN-2002; 2002US-0389123P.
PR 14-JUN-2002; 2002US-0389118P.
PR 14-JUN-2002; 2002US-0389120P.
PR 14-JUN-2002; 2002US-0389144P.
PR 14-JUN-2002; 2002US-0389146P.
PR 17-JUN-2002; 2002US-0389729P.
PR 17-JUN-2002; 2002US-0389742P.
PR 18-JUN-2002; 2002US-0389884P.
PR 19-JUN-2002; 2002US-0390006P.


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RESULT 3

ABK52891

ID ABK52891 standard; DNA; 2697 BP.

XX

AC ABK52891;

XX

DT 27-AUG-2002 (first entry)

XX

Human netrin binding membrane receptor UNC5H-1 DNA sequence #1.

DE

XX

KW Netrin binding membrane receptor; receptor; UNC5H-1; gene; ds; human;

KW neurotrophic; neuroprotective; cytosolic; antiparkinsonian;

KW cerebroprotective; cancer; central nervous system; CNS; stroke;

KW Parkinson's disease; multiple sclerosis; Alzheimer's disease.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

CDS 1..2697

FT /*tag= a

FT /product= "Netrin binding membrane receptor UNC5H-1"

XX WO200233080-A2.

XX

PD 25-APR-2002.

XX

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PF 15-OCT-2001; 2001WO-EP011891.
XX
PR 16-OCT-2000; 2000US-0240061P.
XX
XX (PARB ) BAYER AG.
XX
XX Koehler RH;
XX
XX WPI; 2002-463314/49.
XX
XX P-PSDB; AAU97899.
XX
XX Novel human netrin binding membrane receptor polypeptide and
PT polynucleotides for identifying modulating agents useful in treating
PT diseases e.g. Parkinson's disease, multiple sclerosis, stroke,
PT Alzheimer's disease.
XX
XX Claim 1; Fig 1; 94pp; English.
XX
XX This invention relates to the DNA and protein sequences of a novel
CC purified human netrin binding membrane receptor, UNC5H-1. The DNA
CC sequence of the invention is useful as a probe for detecting a nucleic
CC acid encoding the UNC5H-1 protein in a biological sample. The sequences
CC of the invention are useful to screen for agents which decrease the
CC activity of the UNC5H-1 protein. The sequences are also useful for
CC screening agents which regulate (modulate) the activity of the protein of
CC the invention. A pharmaceutical composition containing the protein of the
CC invention or a reagent that modulates the activity of the UNC5H-1 protein
CC may be useful for treating a UNC5H-1 dysfunction related disease such as
CC cancer or a central nervous system (CNS) disorders (e.g. Parkinson's
CC disease, multiple sclerosis, stroke and Alzheimer's disease). Fusion
CC proteins comprising the UNC5H-1 protein are useful for generating
CC antibodies and for in various assay systems, and the protein can be used
CC as a bait protein in a two-hybrid assay or three-hybrid assay. The method
CC of the invention is useful for detecting a coding sequence for the UNC5H-
CC 1 protein. The present sequence represents a DNA sequence encoding the
CC human netrin binding membrane receptor UNC5H-1 protein of the invention
XX
XX
SQ Sequence 2697 BP; 503 A; 906 C; 807 G; 481 T; 0 U; 0 Other;

Query Match 97.7%; Score 2687.4; DB 6; Length 2697;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2691; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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DB |||||
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QY 406 GAATACCTGGTCCAGTGGGTGGATGGAGTCTCTCGGGCACCACCAAGAGTCAGAGGCC 465
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Db 2161 AAGAGTAACTCTTGTGAGTACAGAGAGATCCCTTTTATCATCTGGAATGGCAGC 2220
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Db 2281 GCCTGCAAGCTGTGGGTGTGAGGTGAGGCGGACCGGCGAGAGCTTTCAGCATCAACTTC 2340
Qy 2386 AACATCAACAGGACACAAAGTTTGTGAGCTGTGCTGTGGAGTGAAGCGGGGTC 2445
Db 2341 AACATCAACAGGACACAAAGTTTGTGAGCTGTGCTGTGGAGTGAAGCGGGGTC 2400
Qy 2446 CCAGCCTGTGGTGGGCGGCGGCTTCAAGATCCCTTCTCATCTGCGGAGAGATTAAT 2505
Db 2401 CCAGCCTGTGGTGGGCGGCGGCTTCAAGATCCCTTCTCATCTGCGGAGAGATTAAT 2460
Qy 2506 TCCAGCTTGGACCCACCTGTAGGCGGGTGGCGGAGCTCTGGCCCGCAAAACTC 2565
Db 2461 TCCAGCTTGGACCCACCTGTAGGCGGGTGGCGGAGCTCTGGCCCGCAAAACTC 2520
Qy 2566 CACTTGAACAGCCATCTCAGCTTCTTGTCTTCAAGCCCGGCGGCGGCGGCGGCTCCTC 2625
Db 2521 CACTTGAACAGCCATCTCAGCTTCTTGTCTTCAAGCCCGGCGGCGGCGGCGGCTCCTC 2580
Qy 2626 AACTTGTGGAGGCGGCGGCTTCCCCCAAGGCACTTCCAGCAGCTGGCTGCGAGCAGTG 2685
Db 2581 AACTTGTGGAGGCGGCGGCTTCCCCCAAGGCACTTCCAGCAGCTGGCTGCGAGCAGTG 2640
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Qy 2686 GCTGAGCTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2742
Db 2641 GCTGAGCTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2697

RESULT 4
ID ABK49422 standard; DNA; 2881 BP.
XX
AC ABK49422;
XX DT 15-JUL-2002 (first entry)
XX DNA encoding human UNC5-like protein NOV1.
XX
KW Human; NOVX polypeptide; cardiomyopathy; atherosclerosis; cancer;
cell signal processing; metabolic pathway modulation; cancerous tissue;
KW antibody; diabetes; transgenic animal; UNC5-like protein; NOV1;
KW chromosome 13; gene; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
CDS 87..2786
FT /*tag= a
FT /product= "Human UNC5-like protein NOV1"
XX
PN W0200229038-A2.
XX
PD 11-APR-2002.
XX
PF 04-OCT-2001; 2001WO-US031377.
XX
PR 04-OCT-2000; 2000US-0237862P.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Herrmann JL, Rastelli L, Shimkets RA;
XX WPI; 2002-340104/37.
XX P-PSDB; AAU79939.
XX
PT Novel isolated NOVX polypeptide, and encoded polynucleotide, useful for
treating cardiomyopathy, atherosclerosis, and cancer.
XX
PS Claim 8; Page 7-8; 180pp; English.
XX
CC The present invention relates to a new NOVX polypeptide having a 900
(NOV1), 4349 (NOV2), 940 (NOV3), 798 (NOV4), 865 (NOV5), or 331 (NOV6)
residue amino acid sequence, as given in the specification. The novel
polypeptide, and its encoding polynucleotide, are used to treat
cardiomyopathy, atherosclerosis, cancer or a disease related to cell
signal processing and metabolic pathway modulation, in a human. Detecting
the polypeptide or polynucleotide is useful for identifying cancerous
tissue. The antibody can be used to treat diabetes or cancer. The host
cells can be used to produce non-human transgenic animals useful in drug
screening. The present nucleic acid sequence is that of the human UNC5-
like NOV1 gene located on chromosome 13. This sequence encodes the human
UNC5-like protein NOV1 of the invention
XX
SQ Sequence 2881 BP; 526 A; 985 C; 868 G; 502 T; 0 U; 0 Other;

Query Match 97.3%; Score 2676.4; DB 6; Length 2881;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2728; Conservative 0; Mismatches 21; Indels 9; Gaps 3;

Qy 1 CCGCGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 60
Db 42 CCGCGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 101
Qy 61 GGCGCTGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 120
Db 102 GGCGCTGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 161
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Qy	121	CAGCAGATGTCACCGTGGCCCAACCCAGTGCCTGGTGCCCAACCCGGGACCTGCTTCCCCAC	180
Db	162	CAGCAGATGTCACCGTGGCCCAACCCAGTGCCTGGTGCCCAACCCGGGACCTGCTTCCCCAC	221
Qy	181	TTCTGTGTGAGCCCGGAGGATGTGTACATCGTCAAGAACCAAGCCAGTGCCTGTGTGTGC	240
Db	222	TTCTGTGTGAGCCCGGAGGATGTGTACATCGTCAAGAACCAAGCCAGTGCCTGTGTGTGC	281
Qy	241	AAGGCCGTGGCCCGCACCGCAGATCTTCTTCAAGTGCACACGGGGAGTGGGTGCGCCAGGTG	300
Db	282	AAGGCCGTGGCCCGCACCGCAGATCTTCTTCAAGTGCACACGGGGAGTGGGTGCGCCAGGTG	341
Qy	301	GACACATGATTCGAGCGCAGCAGACAGCGGAGCAGTGGGTGCCCAACATGAGAGTCCGC	360
Db	342	GACACATGATTCGAGCGCAGCAGACAGCGGAGCAGTGGGTGCCCAACATGAGAGTCCGC	401
Qy	361	ATTAAATGTCTCAAGSCAGCAGTGCAGNAGGTGTTCCGGCTGGAGGAATACTGGTGCCAG	420
Db	402	ATTAAATGTCTCAAGSCAGCAGTGCAGNAGGTGTTCCGGCTGGAGGAATACTGGTGCCAG	461
Qy	421	TGCGTGCATGAGTCTCTCGGGCACCAAGAGTCAAGAGTCAAGAGTCAATCCGCGATAGCC	480
Db	462	TGCGTGCATGAGTCTCTCGGGCACCAAGAGTCAAGAGTCAAGAGTCAATCCGCGATAGCC	521
Qy	481	AGATTGGCAAGAACTTCGAGCAGGAGCGCTGGCCAAAGAGTGTCCCTGGAGCAGGGC	540
Db	522	AGATTGGCAAGAACTTCGAGCAGGAGCGCTGGCCAAAGAGTGTCCCTGGAGCAGGGC	581
Qy	541	ATCGTGTGCCCTGCCGTGCACCGGAGGATCCCTCCAGCCGAGTGGAGTGCCTCCGG	600
Db	582	ATCGTGTGCCCTGCCGTGCACCGGAGGATCCCTCCAGCCGAGTGGAGTGCCTCCGG	641
Qy	601	AACGAGACCTGTGTGACCCGCTCCCTGGACCCCAATGTATACATCACGCGGGACACAGC	660
Db	642	AACGAGACCTGTGTGACCCGCTCCCTGGACCCCAATGTATACATCACGCGGGACACAGC	701
Qy	661	CTGTGTGTGACAGGCGCGCTGTGTGACACGCGCAATACATCACGCTGCGTGGCCAAAGAC	720
Db	702	CTGTGTGTGACAGGCGCGCTGTGTGACACGCGCAATACATCACGCTGCGTGGCCAAAGAC	761
Qy	721	ATCGTGCACGTGCCCGCAGCGCTCCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	780
Db	762	ATCGTGCACGTGCCCGCAGCGCTCCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	821
Qy	781	TCGACGTGGACCGAGTGGTCCGTCTGACGCGCCACAGTGTGGGCGCGCTGCGCAAAACGG	840
Db	822	TCGACGTGGACCGAGTGGTCCGTCTGACGCGCCACAGTGTGGGCGCGCTGCGCAAAACGG	881
Qy	841	AGCCGGAGCTGCACCAACCGGCGCTCTCAACGGGGCGCTTCTGTGTGAGGGGACAGAT	900
Db	882	AGCCGGAGCTGCACCAACCGGCGCTCTCAACGGGGCGCTTCTGTGTGAGGGGACAGAT	941
Qy	901	GTCCAGAA---AACAGCTGCGCCACCCCTGTGTGCCAGTAGACGGCAGCTGGAGCCCGTGG	957
Db	942	GTCCATGACCGCACCGTCTCTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1001
Qy	958	AGCAAGTGTGTGCGCTGTGGCTGGAATGACCAACCACTGGCGGAGCGGTGTGTGTGTGTGT	1017
Db	1002	AGCAAGTGTGTGCGCTGTGGCTGGAATGACCAACCACTGGCGGAGCGCGGTGTGTGTGTGT	1061
Qy	1018	CCAGACCCCGCACACGAGGGGAGGTGCGAGGGCACTGACCTGGACACCCCGCACTGT	1077
Db	1062	CCAGACCCCGCACACGAGGGGAGGTGCGAGGGCACTGACCTGGACACCCCGCACTGT	1121
Qy	1078	ACCAGTGACCTCTGTGTACAGTGTCTTGTGGCCCTGAGGACGTGGCCCTCTATGTGGGC	1137
Db	1122	ACCAGTGACCTCTGTGTACAGTGTCTTGTGGCCCTGAGGACGTGGCCCTCTATGTGGGC	1181
Qy	1138	CTCATCCGCTGGCCGTCTGCTGGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1197
Db	1182	CTCATCCGCTGGCCGTCTGCTGGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1241

Qy	1198	CGGAAGAAAGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTCACCCTCAGGGCTTC	1257
Db	1242	CGGAAGAAAGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTCACCCTCAGGGCTTC	1301
Qy	1258	CAGCCGCTCAGCATCAAGCCCAAGCAGACAAACCCCATCTGTCTCACCATTCCAGCCG	1317
Db	1302	CAGCCGCTCAGCATCAAGCCCAAGCAGACAAACCCCATCTGTCTCACCATTCCAGCCG	1361
Qy	1318	GACCTCAGCACCAACCAACCACTACCAAGGAGTCTCTGTCTCCCGGCAAGATGGGCC	1377
Db	1362	GACCTCAG---CACCACCAACCACTACCAAGGAGTCTCTGTCTCCCGGCAAGATGGGCC	1418
Qy	1378	AGCCCAAGTTTCAGCTCAGCTACCAATGGGACCTCTCTCAGCCCCCTGGTGGCGGCGCCAC	1437
Db	1419	AGCCCAAGTTTCAGCTCAGCTACCAATGGGACCTCTCTCAGCCCCCTGGTGGCGGCGCCAC	1478
Qy	1438	ACACTGCACACACAGTCTCCACCTCTGAGGCGGAGAGTTCGTCTCCCGCTCTCCACC	1497
Db	1479	ACACTGCACACACAGTCTCCACCTCTGAGGCGGAGAGTTCGTCTCCCGCTCTCTCCACC	1538
Qy	1498	CAGAACTACTTCCGCTCCCTGCCCCGAGGACACAGCAACATGACCTATGGGACCTTCAAC	1557
Db	1539	CAGAACTACTTCCGCTCCCTGCCCCGAGGACACAGCAACATGACCTATGGGACCTTCAAC	1598
Qy	1558	TTCTTCCGGGGCGGCTGATGCCCTAATACAGGTATCAGCCCTCCTCATCCCCCCAGAT	1617
Db	1599	TTCTTCCGGGGCGGCTGATGCCCTAATACAGGTATCAGCCCTCCTCATCCCCCCAGAT	1658
Qy	1618	GCCATACCCCGAGGGAAGATCTATGAGATCTACTCTCAGCTGCACAAGCCGGAAGAGCTG	1677
Db	1659	GCCATACCCCGAGGGAAGATCTATGAGATCTACTCTCAGCTGCACAAGCCGGAAGAGCTG	1718
Qy	1678	AGTTTCCCTTACTGCTGT	1737
Db	1719	AGTTTCCCTTACTGCTGT	1778
Qy	1738	GGGCTCTGCTTCAACCGGCGGCTGATCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1797
Db	1779	GGGCTCTGCTTCAACCGGCGGCTGATCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1838
Qy	1798	GACAGCTGGAGCTGCGCTTCAAAAAGCAGTCTGTGGGAGGCGAGCTGGG---AGGATGTG	1854
Db	1839	GACAGCTGGAGCTGCGCTTCAAAAAGCAGTCTGTGGGAGGCGAGCTGGGAGGAGATGTG	1898
Qy	1855	CTGCACTTGGGCGGAGGAGCGCTCCACCTCTCTACTCTGAGCTGGAGGCGAGTGC	1914
Db	1899	CTGCACTTGGGCGGAGGAGCGCTCCACCTCTCTACTCTGAGCTGGAGGCGAGTGC	1958
Qy	1915	TGCTTACTTCAACCGAGCAGTGGGCGCTTGTGGTGGGAGGAGGCGCTCAGCGTG	1974
Db	1959	TGCTTACTTCAACCGAGCAGTGGGCGCTTGTGGTGGGAGGAGGCGCTCAGCGTG	2018
Qy	1975	GCTTCCCGCCAAAGCGCTTCAAGCTGCTTGTGTGGCGCGGTGGCTGCACTCCCTCGAG	2034
Db	2019	GCTTCCCGCCAAAGCGCTTCAAGCTGCTTGTGTGGCGCGGTGGCTGCACTCCCTCGAG	2078
Qy	2035	TACAAATCCGGTCTTACTGCTGTGATGACCCCAAGTGTGCTTCAAGGAGTGGTGAG	2094
Db	2079	TACAAATCCGGTCTTACTGCTGTGATGACCCCAAGTGTGCTTCAAGGAGTGGTGAG	2138
Qy	2095	CTGGAGAGCAGCTGGGGGAGCAGCTGATCCAGGAGCAGGCTCTGTGCACTTCAAGGAC	2154
Db	2139	CTGGAGAGCAGCTGGGGGAGCAGCTGATCCAGGAGCAGGCTCTGTGCACTTCAAGGAC	2198
Qy	2155	AGTTACCAACCTTGGCGCTTATCCATCCAGATGTGCCAGCTCCCTGTGGAGAGTAAAG	2214
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Qy	2215	CTCTTGTGAGCTACAGGAGATCCCTTTTATCAGATCTGGAAATGGCAGCGGTAC	2274
Db	2259	CTCTTGTGAGCTACAGGAGATCCCTTTTATCAGATCTGGAAATGGCAGCGGTAC	2318
Qy	2275	TTGCACTGCACTTCACTCCCTGGAGCGTGTGAGCCCGCAGCACTAGTGACCTGGGCTGCAAG	2334

Db 2319 TTGCACTGCACCTTCAACCTGAGCGTGTGAGCCCGACCACTAGTGCCTGGCCCTGCAAG 2378
Qy 2335 CTGTGGGTGGCAGTGGAGGCGACGGGCGAGCTTTCAGCATCAACTTCAATCACC 2394
Db 2379 CTGTGGGTGGCAGTGGAGGCGACGGGCGAGCTTTCAGCATCAACTTCAATCACC 2438
Qy 2395 AAGGACACAAAGTTTGTCTGAGCTGTGCTCTGAGAGTGAAGCGGGGGTCCAGCCCTG 2454
Db 2439 AAGGACACAAAGTTTGTCTGAGCTGTGCTCTGAGAGTGAAGCGGGGGTCCAGCCCTG 2498
Qy 2455 GTGGCCCCAGTGCCTTCAAGATCCCTTCTCATTCGGCGAAGATTAATTTCCAGCCTG 2514
Db 2499 GTGGCCCCAGTGCCTTCAAGATCCCTTCTCATTCGGCGAAGATTAATTTCCAGCCTG 2558
Qy 2515 GACCCACCTGTAGCGGGGTGGCGACTGCGGGAATCTGGCCCGCAAACTCCACTGGAC 2574
Db 2559 GACCCACCTGTAGCGGGGTGGCGACTGCGGGAATCTGGCCCGCAAACTCCACTGGAC 2618
Qy 2575 AGCCATCTCAGCTTCTTTGCTTCAAGCCCGAGCCCGCAGCATGATCCTCAACTGTGG 2634
Db 2619 AGCCATCTCAGCTTCTTTGCTTCAAGCCCGAGCCCGCAGCATGATCCTCAACTGTGG 2678
Qy 2635 GAGCGCGGCACTTCCCGCAACGGCAACCTCAGCCAGCTGGCTGCAGCATGGCTGGACTG 2694
Db 2679 GAGCGCGGCACTTCCCGCAACGGCAACCTCAGCCAGCTGGCTGCAGCATGGCTGGACTG 2738
Qy 2695 GCGCAGCCAGACGCTGGCGCTTTCACAGTTCGGAGGCTGAGTCTGAGGCGCGGCCAG 2752
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RESULT 5
ADH71609
ID ADH71609 standard; DNA; 2881 BP.
XX AC ADH71609;
XX AC
XX AC
DT 25-MAR-2004 (first entry)
DE Human gene of the invention NOV21a SEQ ID NO:505.
XX ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
KW anorectic; antidiabetic; antimicrobial; antilipemic; gene therapy;
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW obesity; diabetes; infectious disease; metabolic syndrome X;
KW dyslipidaemia.
XX Homo sapiens.
XX OS
XX PN WO2003102155-A2.
XX PD 11-DEC-2003.
XX PF
XX PF 03-JUN-2003; 2003WO-US017430.
XX PF
XX PF 03-JUN-2002; 2002US-0385120P.
XX PF 04-JUN-2002; 2002US-0385784P.
XX PF 05-JUN-2002; 2002US-0386041P.
XX PF 05-JUN-2002; 2002US-0386047P.
XX PF 06-JUN-2002; 2002US-0386376P.
XX PF 06-JUN-2002; 2002US-0386453P.
XX PF 06-JUN-2002; 2002US-0386864P.
XX PF 06-JUN-2002; 2002US-0387016P.
XX PF 07-JUN-2002; 2002US-0386796P.
XX PF 07-JUN-2002; 2002US-0386816P.
XX PF 07-JUN-2002; 2002US-0386931P.
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XX PF 08-JUN-2002; 2002US-0296960P.
XX PF 10-JUN-2002; 2002US-0387400P.
XX PF 10-JUN-2002; 2002US-0387535P.

PR 11-JUN-2002; 2002US-0387610P.
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PR 12-JUN-2002; 2002US-0388022P.
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PR 13-JUN-2002; 2002US-0389123P.
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PR 14-JUN-2002; 2002US-0389120P.
PR 14-JUN-2002; 2002US-0389144P.
PR 14-JUN-2002; 2002US-0389146P.
PR 17-JUN-2002; 2002US-0389729P.
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PR 21-JUL-2002; 2002US-0396706P.
PR 06-AUG-2002; 2002US-0401628P.
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PR 12-AUG-2002; 2002US-0402786P.
PR 12-AUG-2002; 2002US-0402816P.
PR 12-AUG-2002; 2002US-0402821P.
PR 12-AUG-2002; 2002US-0402832P.
PR 13-AUG-2002; 2002US-0403448P.
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PR 13-AUG-2002; 2002US-0403631P.
PR 15-AUG-2002; 2002US-0403617P.
PR 26-AUG-2002; 2002US-0406182P.
PR 26-AUG-2002; 2002US-0406355P.
PR 27-AUG-2002; 2002US-0406240P.
PR 12-SEP-2002; 2002US-0410084P.
PR 20-SEP-2002; 2002US-0412528P.
PR 23-SEP-2002; 2002US-0412731P.
PR 30-SEP-2002; 2002US-0414801P.
PR 30-SEP-2002; 2002US-0414839P.
PR 30-SEP-2002; 2002US-0414840P.
PR 30-SEP-2002; 2002US-0414954P.
PR 09-OCT-2002; 2002US-0417186P.
PR 09-OCT-2002; 2002US-0417406P.
PR 23-OCT-2002; 2002US-0420639P.
PR 28-OCT-2002; 2002US-0421156P.
PR 31-OCT-2002; 2002US-0422690P.
PR 01-NOV-2002; 2002US-0423130P.
PR 05-NOV-2002; 2002US-00423798.
PR 05-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.
PA (CURA-) CURAGEN CORP.
XX PA
XX PA
XX PI Alsbrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ,
PI Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
PI Etenberg S, Gargoli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
PI Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
PI MacLachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS,
PI Padigaru M, Patturajan M, Pena CE, Peyman JA, Raha D, Rastelli L;
PI Rieger DX, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA;
PI Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
PI Zhong H;
XX WPI; 2004-081935/08.
DR

Qy 1738 GGCGTCTGCTCACCGGCCAGTGCATCTGCTGATGACCACTGTGGGGAGCCAGCCCT 1797
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Qy 1798 GACAGCTGGAGCCTGGCGCTCAAAAGCAGTCGTGGAGGCGACCTGGG---AGGATGTG 1854
Db 1839 GACAGCTGGAGCCTGGCGCTCAAAAGCAGTCGTGGAGGCGACCTGGGAGCAGGATGTG 1898
Qy 1855 CTGCACTCTGGCGGAGGAGGCGCCCTCCACCTCTACTACTGCGAGCTGGAGGCGCAGTGCC 1914
Db 1899 CTGCACTCTGGCGGAGGAGGCGCCCTCCACCTCTACTACTGCGAGCTGGAGGCGCAGTGCC 1958
Qy 1915 TGCTACGTCCTTACCGAGCAGCTGGCGCGCTTTGCCCTGTGGAGAGGCGCTCAGCGTG 1974
Db 1959 TGCTACGTCCTTACCGAGCAGCTGGCGCGCTTTGCCCTGTGGAGAGGCGCTCAGCGTG 2018
Qy 1975 GCTGCGCGCAAGCGCCTCAAGCTGCTTCTGTTTGGCGCGGTGGCTGCACCTCCCTCGAG 2034
Db 2019 GCTGCGCGCAAGCGCCTCAAGCTGCTTCTGTTTGGCGCGGTGGCTGCACCTCCCTCGAG 2078
Qy 2035 TACAACATCCGGGTCTACTGCTGCATGACACCCACGATGCACCTCAAGGAGGTGGTCAG 2094
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Db 2199 AGTTACCAACACCTGCGCCTATCCATCCAGATGTGCCAGCTCCCTGTGGAAGAGTAAG 2258
Qy 2215 CTCCTGTGACGTACACGAGGATCCCTTTTATCACAATCTGGAATGCGACGCGGTAC 2274
Db 2259 CTCCTGTGACGTACACGAGGATCCCTTTTATCACAATCTGGAATGCGACGCGGTAC 2318
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Db 2319 TTGCATCTGCACCTTCAACCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTGGCGCTGCAAG 2378
Qy 2335 CTGTGGGTGTGGCAGGTGGAGGGGAGCGGCGAGCTTCAGCATCAACTTCAACATCACC 2394
Db 2379 CTGTGGGTGTGGCAGGTGGAGGGGAGCGGCGAGCTTCAGCATCAACTTCAACATCACC 2438
Qy 2395 AAGGACACAAGTTTGTGTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGTCCAGGCCCTG 2454
Db 2439 AAGGACACAAGTTTGTGTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGTCCAGGCCCTG 2498
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Qy 2635 GAGCGCGGCACTTCCCAACGGCAACCTCAGCAGCTGTGTCAGCAGTGGCTGGACTG 2694
Db 2679 GAGCGCGGCACTTCCCAACGGCAACCTCAGCAGCTGTGTCAGCAGTGGCTGGACTG 2738
Qy 2695 GGCAGGCGAGCAGCTGGCCTTTCACAGTGTGGAGGCTGAGTGTGAGGCGGCGCAG 2752
Db 2739 GGCAGGCGAGCAGCTGGCCTTTCACAGTGTGGAGGCTGAGTGTGAGGCGGCGCAG 2796

RESULT 6

ADH71649

ID ADH71649 standard; DNA; 2881 BP.

XX

AC ADH71649;
XX DT 25-MAR-2004 (first entry)
XX DE Human gene of the invention NOV21u SEQ ID NO:545.
XX KW ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
KW anorectic; antidiabetic; antimicrobial; antilipaeamic; gene therapy;
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW obesity; diabetes; infectious disease; metabolic syndrome X;
KW dyslipidaemia.
XX OS Homo sapiens.
XX PN WO2003102155-A2.
XX PD 11-DEC-2003.
XX PP 03-JUN-2003; 2003WO-US017430.
XX PR 03-JUN-2002; 2002US-0385120P.
PR 04-JUN-2002; 2002US-0385784P.
PR 05-JUN-2002; 2002US-0386041P.
PR 05-JUN-2002; 2002US-0386047P.
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PR 07-JUN-2002; 2002US-0387262P.
PR 08-JUN-2002; 2002US-0296960P.
PR 10-JUN-2002; 2002US-0387400P.
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PR 11-JUN-2002; 2002US-0387625P.
PR 11-JUN-2002; 2002US-0387634P.
PR 11-JUN-2002; 2002US-0387668P.
PR 11-JUN-2002; 2002US-0387696P.
PR 11-JUN-2002; 2002US-0387702P.
PR 11-JUN-2002; 2002US-0387836P.
PR 11-JUN-2002; 2002US-0387859P.
PR 12-JUN-2002; 2002US-0387933P.
PR 12-JUN-2002; 2002US-0387934P.
PR 12-JUN-2002; 2002US-0387960P.
PR 12-JUN-2002; 2002US-0388022P.
PR 12-JUN-2002; 2002US-0388096P.
PR 13-JUN-2002; 2002US-0389123P.
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PR 17-JUL-2002; 2002US-0396706P.
PR 06-AUG-2002; 2002US-0401628P.
PR 09-AUG-2002; 2002US-0402156P.
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PR 09-AUG-2002; 2002US-0402389P.
PR 12-AUG-2002; 2002US-0402786P.
PR 12-AUG-2002; 2002US-0402816P.
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PR 12-AUG-2002; 2002US-0402832P.
PR 13-AUG-2002; 2002US-0403448P.
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QY 1855 CTGCACCTGGGAGGAGGCGCCCTCCCACTTACTACTGCGAGCTGGAGGCGAGTGGC 1914
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QY 2215 CTCCTTGTGACTACCAAGGAGATCCCTTTTATCAGATCTGGAATGGCAAGCAGCGGTAC 2274
Db 2259 CTCCTTGTGACTACCAAGGAGATCCCTTTTATCAGATCTGGAATGGCAAGCAGCGGTAC 2318

QY 2275 TTGCACTGCACCTTCAACCTGGAGCGTGTGAGCCCGAGCACTAGTGAACCTGGCCTGCAAG 2334
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QY 2335 CTGTGGGTGTGGCAGGTGGAGGGCGACGGGCGAGAGCTTTCAGCATCAACTTCAACATCACC 2394
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QY 2695 GGCAGCGCAGACGCTGCGCTTTCACAGTGTGAGAGCTGAGTGTGAGGCGCGGCCAG 2752
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RESULT 7
ADH71635
ID ADH71635 standard; DNA; 2881 BP.
XX
AC ADH71635;
XX
DT 25-MAR-2004 (first entry)
XX
Human gene of the invention NOV21n SEQ ID NO:531.
ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
anorectic; antidiabetic; antimicrobial; antilipase; gene therapy;
vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
obesity; diabetes; infectious disease; metabolic syndrome X;
dyslipidaemia.
XX
OS Homo sapiens.
XX
PN W02003102155-A2.
XX
PD 11-DEC-2003.
XX
PF 03-JUN-2003; 2003WO-US017430.
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PR 03-JUN-2002; 2002US-0385120P.
PR 04-JUN-2002; 2002US-0385784P.
PR 05-JUN-2002; 2002US-0386041P.
PR 05-JUN-2002; 2002US-0386047P.
PR 06-JUN-2002; 2002US-0386376P.
PR 06-JUN-2002; 2002US-0386453P.
PR 06-JUN-2002; 2002US-0386864P.
PR 06-JUN-2002; 2002US-0387016P.
PR 07-JUN-2002; 2002US-0386796P.
PR 07-JUN-2002; 2002US-0386816P.
PR 07-JUN-2002; 2002US-0386931P.
PR 07-JUN-2002; 2002US-0386942P.
PR 07-JUN-2002; 2002US-0386971P.
PR 07-JUN-2002; 2002US-0387262P.
PR 08-JUN-2002; 2002US-0296960P.
PR 10-JUN-2002; 2002US-0387400P.

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721 ATCTGGGCACTGGTGGCCGAGCGCTCCGCTGCTGTCTATCGTCTAAGTGAACGGTGGGTGG 780
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762 ATCTGGGCACTGGTGGCCGAGCGCTCCGCTGCTGTCTATCGTCTAAGTGAACGGTGGGTGG 821
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781 TCGAGCTGGACCGAGTGGTTCGGTCTGACAGCGCCAGCTGTGGCGCGGTGCGCAAGAACGG 840
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901 GTCCAGAA --- AACAGCTGCGCCACCTGTGTGCCAGTGAAGCGGAGCGCCGTGG 957
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942 GTCCATGACCGCACCGTCTCTCTCTGCTGTGTGAGCGGAGCTGGAGCGCCGTGG 1001
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958 AGCAAGTGGTGGCGCTGTGGCTGGACTGACACCACTGGCGGAGCGGTGAGTGTCTTGAC 1017
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1002 AGCAAGTGGTGGCGCTGTGGCTGGACTGACACCACTGGCGGAGCGGTGAGTGTCTTGAC 1061
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1062 CCAGCACCCCGCAACCGAGGGGAGAGTGGCAGGGGCACTGACCTGGAGCACCCGCAACTGT 1121
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1078 ACCAGTGACCTCTGTGTACACAGTGTCTTGGCCCTGAGAGAGTGGCCCTCTATGTGGGC 1137
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1558 TTCTCGGGGCGCGCTGATGATCCCTAATACAGTATCAGCTTCCTCATCCCCCAGAT 1617
Db
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1618 GCCATACCCCGAGGGAAGATCTATGAGATCTATGAGTCTACCTCAGCTGCAAGCCCGGAAAGAGCTG 1677
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1678 AGGTGCCCCCTAGCTGGCTGTGACACCCCTGTGAGTCCCATCTGTTAGCTGGACCCCT 1737
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RESULT 8
ADH71637
ID ADH71637 standard; DNA; 2881 BP.

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1855 CTGCACTTGGGCGAGGAGGCGCCCTCCCACTCTACTACTGCGCAGCTGGAGGCGCAGTGCC 1914
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1899 CTGCACTTGGGCGAGGAGGCGCCCTCCCACTCTACTACTGCGCAGCTGGAGGCGCAGTGCC 1958
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1959 TGCTTACATCTTCCAGCAGCAGCTGGCGCTTTGCCCTGTGGTGGAGAGGCGCTCAGCGTG 2018
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1975 GCTGCCGCCAAGCGCTCAAGCTGCTTCTGTTTGGCGCGGTGGCTGCGACTCTCCCTCGAG 2034
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2095 CTGGAGAGCAGCTGGGGGACAGCTGATCCAGGAGCAGCGGTCTCTGCACTTCAAGGAC 2154
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2275 TTGCACTGCACTTCAACCTTGGAGCGTGTGAGCGCCAGCACTAGTGAACCTGGCTGCAAG 2334
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2335 CTGTGGTGTGGCAGTGGAGGCGAGCGGCGAGCTTCAAGCATCAACTTCAACATCAC 2394
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Db 102 GGCCTGTGGCCAGCGCTCTCGGCATAGTCTCGCGCTTGCTCCGCGCTCGGCTGCC 161
Qy 121 CAGCAGAGTGCCACCGTGGCCAAACCCAGTGCCTGGTGCACACCGGACCTGCTTCCGCAC 180
Db 162 CAGCAGAGTGCCACCGTGGCCAAACCCAGTGCCTGGTGCACACCGGACCTGCTTCCGCAC 221
Qy 181 TTCCTGGTGGAGCCCGAGAGTGTGTACATCGTCAAGAACAGCCAGTGCCTGTGTGTGC 240
Db 222 TTCCTGGTGGAGCCCGAGAGTGTGTACATCGTCAAGAACAGCCAGTGCCTGTGTGTGC 281
Qy 241 AAGCCCGTGGCCGCCACGACATCTTCTTAAGTGCACACCGGGAGTGGTGCGCCAGGTG 300
Db 282 AAGCCCGTGGCCGCCACGACATCTTCTTAAGTGCACACCGGGAGTGGTGCGCCAGGTG 341
Qy 301 GACCACGTGTCGAGCGGACGACAGCGGAGCAGTGGCTGCCACCATGGAGGTCCGC 360
Db 342 GACCACGTGTCGAGCGGACGACAGCGGAGCAGTGGTGGAGCGACCATGGAGGTCCGC 401
Qy 361 ATTAATGTCTCAAGGACAGCGTGCAGAAAGGTGTTCCGGCTGGAGGAATACGTGTGCCAG 420
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Qy 1378 AGCCCAAGTTCAGCTCACAATGGGCACTGTGCTAGCCCCCTGGGTGGGGCGCGCCAC 1437
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Qy 1855 CTGCACTGGGCGAGAGGCGCCCTCCACCTCTACTACTGTGCCAGCTGGAGGCGCAGTGCC 1914
Db 1899 CTGCACTGGGCGAGAGGCGCCCTCCACCTCTACTACTGTGCCAGCTGGAGGCGCAGTGCC 1958
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Qy 1975 GCTGCGCCCAAGCGCTCAAGCTGCTTCTGTTTGGCGCGGTGGCTGCACCTCCCTCCAG 2034
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Qy 2035 TACAACATCCGGTCTACTGCTTGCATGACACCCACGATGCACTCAAGAGGAGTGGTGAG 2094
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Qy 2335 CTGTGGGTGTGGCAGTGTGGAGGGGAGCGGCGAGAGCTTTCAGCATCAACTTCAACATCAC 2394
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Db 2559 GACCCACCTGTAGCGGGGTGCCGACTGTGGCGACTCTGGCCAGAACTCCACCTGGAC 2618
Qy 2575 AGCCATCTCAGCTTCTTTTGCTTCAAGCCAGCCGAGCCCAAGCCATGATCTCAACCTGTGG 2634
Db 2619 AGCCATCTCAGCTTCTTTTGCTTCAAGCCAGCCGAGCCCAAGCCATGATCTCAACCTGTGG 2678
Qy 2635 GAGCGCGGCACTTCCCAACGGCAACTCAGCCAGCTGGCTGAGAGTGGCTGGA 2694
Db 2679 GAGCGCGGCACTTCCCAACGGCAACTCAGCCAGCTGGCTGAGAGTGGCTGGA 2738
Qy 2695 GGCAGCGCAGAGCTGGCTTTCACAGTGTGGAGGCTGAGTGTGAGCGCGCCAG 2752
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RESULT 9
ADH71641
ID ADH71641 standard; DNA; 2881 BP.
AC ADH71641;
XX
XX 25-MAR-2004 (first entry)
XX Human gene of the invention NOV21q SEQ ID NO:537.
XX
XX ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
XX anorectic; antidiabetic; antimicrobial; antiipaeamic; gene therapy;
XX vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
XX obesity; diabetes; infectious disease; metabolic syndrome X;
XX dyalipdaemia.
XX Homo sapiens.
XX
XX WO2003102155-A2.
XX
XX 11-DEC-2003.
XX
XX 03-JUN-2003; 2003WO-US017430.
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XX 03-JUN-2002; 2002US-0385120P.
XX 04-JUN-2002; 2002US-0385784P.
XX 05-JUN-2002; 2002US-0386041P.
XX 05-JUN-2002; 2002US-0386047P.
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PR 10-JUN-2002; 2002US-0387400P.
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PR 11-JUN-2002; 2002US-0387634P.
PR 11-JUN-2002; 2002US-0387668P.
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PR 12-JUN-2002; 2002US-0388096P.
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PR 17-JUL-2002; 2002US-0396706P.
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PR 28-OCT-2002; 2002US-0421156P.
PR 31-OCT-2002; 2002US-0422690P.
PR 01-NOV-2002; 2002US-0423130P.
PR 05-NOV-2002; 2002US-00423798.
PR 05-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
XX Carterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
XX Btenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
XX Gusev VV, Hermann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
XX MacLachlan T, Malyankar UM, Mezick AU, Millet I, Mishra VS;
XX Padigaru M, Patturajan M, Pena CEA, Peyman JA, Raha D, Rastelli L;
XX Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shinkets RA;
XX Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
XX Zhong H;

Db 1719 AGTTGCCCCCTAGCTGGCTGTCTCAGACCCCTGCTGAGTCCCATCGTTAGCTGTGGACCCCT 1778
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Db 1779 GGGGTCTGTCTACCCGGCCAGTCACTCTGGCTATGACCACTGTGGGGAGCCCGCCCT 1838
Qy 1798 GACAGCTGGAGCCTGGCGCTCAAAAGCAGTCTGCGAGGGCAGCTGGG---AGGATGTG 1854
Db 1839 GACAGCTGGAGCCTGGCGCTCAAAAGCAGTCTGCGAGGGCAGCTGGGGAGGATGTG 1898
Qy 1855 CTGACCTGGCGGAGGAGGGCCCTCCACCTCTACTACTGCAAGCTGGAGGGCAGGTC 1914
Db 1899 CTGACCTGGCGGAGGAGGGCCCTCCACCTCTACTACTGCAAGCTGGAGGGCAGGTC 1958
Qy 1915 TGCTACTCTTCAACCGAGCAGCTGGCGCTTTGCTGTTGGGAGAGGCCCTCAAGCGTG 1974
Db 1959 TGCTACTCTTCAACCGAGCAGCTGGCGCTTTGCTGTTGGGAGAGGCCCTCAGCGTG 2018
Qy 1975 GCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTGGCGGGTGGCTGCACTCCCTCGAG 2034
Db 2019 GCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTGGCGGGTGGCTGCACTCCCTCGAG 2078
Qy 2035 TACAACATCCGGGTCTACTGCTCATGACACCCACGATGCATCAAGGAGGTGGTGCAG 2094
Db 2079 TACAACATCCGGGTCTACTGCTCATGACACCCACGATGCATCAAGGAGGTGGTGCAG 2138
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Qy 2635 GAGCGGGGCACTTCCCAACGGGAACCTGACGAGCTGGCTGAGCAGTGGCTGGACTG 2694
Db 2679 GAGCGGGGCACTTCCCAACGGGAACCTGAGCAGCTGGCTGAGCAGTGGCTGGACTG 2738
Qy 2695 GGGCAGCAGACGCTGCGCTCTTCAAGAGTGTGGAGGCTGAGTGTGAGGCGCGGCCAG 2752
Db 2739 GGGCAGCAGACGCTGCGCTCTTCAAGAGTGTGGAGGCTGAGTGTGAGGCGCGGCCAG 2796

ADH71629 standard; DNA; 2881 BP.
ADH71629;
25-MAR-2004 (first entry)
Human gene of the invention NOV21k SEQ ID NO:525.
db; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
anorectic; antidiabetic; antimicrobial; antiipaeamic; gene therapy;
vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
obesity; diabetes; infectious disease; metabolic syndrome X;
dyslipidaemia.
Homo sapiens.
WO2003102155-A2.
11-DEC-2003.
03-JUN-2003; 2003WO-US017430.
03-JUN-2002; 2002US-0385120P.
04-JUN-2002; 2002US-0385784P.
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06-JUN-2002; 2002US-0387016P.
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13-AUG-2002; 2002US-0403448P.

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102 GGCCTGTGGCAGCGCTCTCTGGGCATAGTCTCTCCCGCTTGGCTCCCGGCTCGGGTGCC 161
Qy |||||
Db 121 CAGCAGAGTGCACCGCTGGCCNACCCAGTGCCTGGTGCACCCGGACCTGCTTCCCCAC 180
162 CAGCAGAGTGCACCGCTGGCCNACCCAGTGCCTGGTGCACCCGGACCTGCTTCCCCAC 221
Qy |||||
Db 181 TTCTGTGTGGAGCCCGGAGGATGTGTACATCGTCAAGAAACAAGCCAGTGCCTGTGTGTGC 240
222 TTCTGTGTGGAGCCCGGAGGATGTGTACATCGTCAAGAAACAAGCCAGTGCCTGTGTGTGC 281
Qy |||||
Db 241 AAGCCGTGTCGCCCAACGACATCTTCTCAAGTGCACCGGGAGTGGGTGCGCCAGGTG 300
282 AAGCCGTGTCGCCCAACGACATCTTCTCAAGTGCACCGGGAGTGGGTGCGCCAGGTG 341
Qy |||||
Db 301 GACCACGTGATCGAGCCGACAGACGAGCGGAGCAGTGGGCTGCCACCATGGAGTCCGC 360
342 GACCACGTGATCGAGCCGACAGACGAGCGGAGCAGTGGTGAAGCCGACATGGAGTCCGC 401
Qy |||||
Db 361 ATTAATGTCTCAAGCAGCAGGTTCGAGAGGTGTTCCGGCTGGAGGAATACTGTGTGCCAG 420
402 ATTAATGTCTCAAGCAGCAGGTTCGAGAGGTGTTCCGGCTGGAGGAATACTGTGTGCCAG 461
Qy |||||
Db 421 TGCCTGGATGGAGCTCTCTGGGCACCAACAAGTGCAGAAAGCCTACATCCGCGATAGCC 480
462 TGCCTGGATGGAGCTCTCTGGGCACCAACAAGTGCAGAAAGCCTACATCCGCGATAGCC 521
Qy |||||
Db 481 AGATTGGCGAGAACTTCGAGCAGGAGCCGCTGCCCAAGAGGTGCTCCCTGGAGCAGGC 540
522 AGATTGGCGAGAACTTCGAGCAGGAGCCGCTGCCCAAGAGGTGCTCCCTGGAGCAGGC 581
Qy |||||
Db 541 ATCGTGTGCTCCCTGCGCTCAACCGGAGGATCCCTCCAGCCGAGGTGGAGTGGCTCCGG 600
582 ATCGTGTGCTCCCTGCGCTCAACCGGAGGATCCCTCCAGCCGAGGTGGAGTGGCTCCGG 641
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Db 601 AACGAGACCTGTGTGGACCGCTCTCCAGACCCCAATGTATACATCAACCGGAGCAGC 660
642 AACGAGACCTGTGTGGACCGCTCTCCAGACCCCAATGTATACATCAACCGGAGCAGC 701
Qy |||||
Db 661 CTGTGTGTGACAGGCGCCGCTTGTGACACGCGCAACTACACCTCGCTGGCCCAAGAAC 720
702 CTGTGTGTGACAGGCGCCGCTTGTGACACGCGCAACTACACCTCGCTGGCCCAAGAAC 761
Qy |||||
Db 721 ATCGTGTGACGTCCCGCAGCGCTCCGCTGCTCATCGTCTACGTGAAACGCTGGGTGG 780
762 ATCGTGTGACGTCCCGCAGCGCTCCGCTGCTCATCGTCTACGTGAAACGCTGGGTGG 821
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822 TCGACGTGGACCGAGTGGTCCGTCTGACGCGCCAGCTGTGGGCGCGCTGGCAGAAACGG 881
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1062 CCAGACCCCGCAACGAGGGGAGGTGCGCAGGGCACTGACCTGGACACCCCGCAACTGT 1121
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Qy 1138 CTCAATCGCCGTGGCGCTGTGCCTGTGCTCTGCTGTGCTTGTCTCTCATCTCTGTTTATTGC 1197
Db |||||
1182 CTCAATCGCCGTGGCCGCTGTGCCTGTGCTCTGCTGTGCTTGTCTCTCATCTCTGTTTATTGC 1241
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1362 GACTCTAG---CACCCACCACTTACAGGGGAGTCTCTGTCCCCTGGGAGGATGGGCC 1418
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1959 TGCTAGCTCTTCAACCGAGCAGCTGGGCGCTTTGGCTGTGGGAGAGGCGCTCAGCGTG 2018
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Db 2035 TACAACATCCGGGTCTACTGCTTCATGACACCCAGCATGCACTCAAGGAGGTGGTGCAG 2094
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Qy |||||
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Qy |||||
Db 2155 AGTTACCAACCTCGGCTTATCCATCCAGATGTGCCAGCTCCCTGTGTGAGAGTAAG 2214
2199 AGTTACCAACCTCGGCTTATCCATCCAGATGTGCCAGCTCCCTGTGTGAGAGTAAG 2258
Qy |||||
Db 2215 CTCTTGTGAGCTACCGAGGAGATCCCTTTTATACATCTGGAATGGCAGCGAGGTAC 2274

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Db 2319 TTGCAACCGACCTTCACCTGTGAGAGGTGTGAGCCCGACACTAGTGCCTGGCTGGCAAG 2378
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Db 2679 GAGCGCGGCACTTCCCAAGCGCAACTCAGCCAGCTGGCTGAGCAGTGGCTGGACTG 2738
Qy 2695 GCGCAGCCAGAGCTGGCTCTTTCACAGTGTGAGAGTGTGAGGCGGCGCCAG 2752
Db 2739 GCGCAGCCAGAGCTGGCTCTTTCACAGTGTGAGAGTGTGAGGCGGCGCCAG 2796

RESULT 13

ID ADH71627 standard; DNA; 2881 BP.
XX AC ADH71627;
XX DT 25-MAR-2004 (first entry)
XX DE Human gene of the invention NOV21j SEQ ID NO:523.
XX ds; gene; human; cytosolic; immunomodulator; neuroprotective; nootropic;
XX anorectic; antidiabetic; antimicrobial; antileptemic; gene therapy;
XX vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
XX obesity; diabetes; infectious disease; metabolic syndrome X;
XX dyslipidaemia.
XX Homo sapiens.
XX WO2003102155-A2.
XX 11-DEC-2003.
XX 03-JUN-2003; 2003WO-US017430.
XX 03-JUN-2002; 2002US-0385120P.
XX 04-JUN-2002; 2002US-0385784P.
XX 05-JUN-2002; 2002US-0386041P.
XX 05-JUN-2002; 2002US-0386047P.
XX 06-JUN-2002; 2002US-0386376P.
XX 06-JUN-2002; 2002US-0386453P.
XX 06-JUN-2002; 2002US-0386864P.
XX 07-JUN-2002; 2002US-0387016P.
XX 07-JUN-2002; 2002US-0386796P.
XX 07-JUN-2002; 2002US-0386816P.
XX 07-JUN-2002; 2002US-0386931P.
XX 07-JUN-2002; 2002US-0386942P.
XX 07-JUN-2002; 2002US-0386971P.

PR 07-JUN-2002; 2002US-0387262P.
PR 08-JUN-2002; 2002US-0296960P.
PR 10-JUN-2002; 2002US-0387400P.
PR 10-JUN-2002; 2002US-0387535P.
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PR 12-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.

(CURA-) CURAGEN CORP.

PI Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
PI Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
PI Eitenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
PI Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
PI MacIachlan T, Malyankar UM, Mezick AU, Millet I, Mishra VS;
PI Padigaru M, Patturajan M, Pena CEA, Peyman JA, Raha D, Rastelli L;
PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA;

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XX
DT 25-MAR-2004 (first entry)
XX
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anorectic; antidiabetic; antimicrobial; antilipemic; gene therapy;
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW obesity; diabetes; infectious disease; metabolic syndrome X;
KW dyslipidaemia.

XX Homo sapiens.

OS Homo sapiens.

XX WO2003102155-A2.

XX 11-DEC-2003.

XX 03-JUN-2003; 2003WO-US017430.

XX 03-JUN-2002; 2002US-0385120P.

PR 04-JUN-2002; 2002US-0385784P.

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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5	841.4	30.6	2831	2	US-08-808-982-3
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7	833.6	30.3	3008	4	US-09-949-016-4794
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ALIGNMENTS

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; Patent No. 5939271
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; APPLICANT: Leonardo, E. David
; APPLICANT: Hink, Lindsay
; APPLICANT: Masu, Masayuki
; APPLICANT: Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/808,982
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UC96-217
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3014 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-808-982-1

Query Match 82.1%; Score 2259; DB 2; Length 3014;
Best Local Similarity 89.7%; Pred. No. 0;
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Qy 886 TGTGAGGGGCGAATGTCCAGAAACAGCTGCGCCACCTGTGCCAGTACAGCGAGC 945
Db 841 TGTGAGGGGCGAATGTCCAGAAACAGCTTGGCCCACTCTGTGCCCAGTGGATGGAGC 900
Qy 946 TGGAGCCCGTGGACAAAGTGTGGCCGTGGGCTGGACTGTGACCCCACTGGCGGAGCGCT 1005
Db 901 TGGAGTTCGTGGAGTAAGTGTGAGCTGTGGGCTTGACTGTGCCCACTGGCGGAGCGCG 960
Qy 1006 GAGTGTCTGACCCAGCACCCCGCAACGAGAGGAGAGTGGCAAGGGCACTGACCTGGAC 1065
Db 961 GAGTGTCTGACCCAGCACCCCGCAATGGAGGTGAGAGTGTGGGGTGTGACCTGGAC 1020
Qy 1066 ACCGCAACTGTACCAAGTACCTGTGTGACAGTGTCTGCGCCCTGAGAGCGTGGCC 1125
Db 1021 ACCGCAACTGTACCAAGTACCTGTGTGACAGTGTCTGCGCCCTGAGAGCGTGGCT 1080
Qy 1126 CTCTATGTGGGCGCTCATCGCGGTGGCGGTCTGCGCTGGTGTGCTGTGCTGTCTCATC 1185
Db 1081 CTCTATACATCGGCCCTGTGCTGTGGCTGTGCGCTCTTCTGTGCTGTGGCCCTTGA 1140

Qy 1186 CTGCTTTATTGCGGGAAGAGGGGCTGAGCTCAGATGTGGCTGACTCGTCCATTCTC 1245
Db 1141 CTCAATTTACTGTGCAAGAAAGAGGGTGAATCCGATGTGGCGGACTCGTCCATCCTC 1200
Qy 1246 ACCTCAGGCTTTCAGGCCGTGAGCTCAAGCCAGCAAGCAACACCCCATCTGCTC 1305
Db 1201 ACCTCGGGCTTTCAGGCCGTGTGAGCTCAAGCCAGCAAGCAACACCCCATCTGCTC 1260
Qy 1306 ACCATCCAGCGGACCTCAGCACACACCAACCACTTACCAGGGCAGTCTCTGTCCCGG 1365
Db 1261 ACCATCCAGCGGACCTCAGCACACCACTTACCAGGGCAGTCTATGTTGAGG 1320
Qy 1366 CAGGATGGGCCCCAGGCCCAAGTTTCCAGCTCAACAAATGAGGCACTGTCTAGCCCCCTGGGT 1425
Db 1321 CAGGATGGACCCAGGCCCAAGTTTCCAGCTCTCTAATGGTCACTGTCTAGCCCCACCTGGG 1380
Qy 1426 GGCGGCGGCACACACTGACACAGCTCTCCACCTCTGAGGCGGAGGATTCGTCTCC 1485
Db 1381 AGTGGCGGCATACGTTGCAACCACTCACCACCTCTGAGGCTGAGGATTCGTCTCC 1440
Qy 1486 CGCTCTCTCACCCAGAACTACTTCCGCTCCCTGCCCCGAGGCAACCAAGCAATGACCTAT 1545
Db 1441 CGCTCTCTCACCCAAACTACTTTCGTTCCCTGCCCCGCGCACCAAGCAATGGCTAC 1500
Qy 1546 GGACCTTCAACTTCTCGGGGCGCGCTGATGATCCCTAATAACAGGTATCAGCTCTC 1605
Db 1501 GGGACCTTCAACTTCTCGGGGCGCGCTGATGATCCCTAATAACAGGGATCAGCTCTC 1560
Qy 1606 ATCCGCCAGATGCCATACCCGAGGAGATCTATGAGATCTACCTCAGCTGCACAAG 1665
Db 1561 ATACCCCGGATGCCATCCCGAGGAAAGATCTACGAGATCTACCTCAGCTGCACAAG 1620
Qy 1666 CCGGAAGAAGTGAAGTTGCCCCCTAGCTGGTGTGAGACCTCTGAGTCCCATCTGTTAGC 1725
Db 1621 CCAGAGAAGTGAAGTTGCCCCCTAGCTGGTGTGAGACCTCTGAGTCCAGTCTGAGC 1680
Qy 1726 TGTGAGCCCGCTGGCTCTGTGCTCAACCGGCGAGTCACTCTGAGTATGAGCACTGTGGG 1785
Db 1681 TGTGGGCCCCAGAGTCTCTGTCTACCGGCGAGTCACTCTGCAATGGAACCACTGTGGA 1740
Qy 1786 GAGCCAGCCCTCAGAGCTGGAGCTCGGCTCAAAAAGCAGTCTGCGAGGCGAGCTGG 1845
Db 1741 GAGCCAGCCCTCAGAGCTGGAGTGTGCGCTCAAAAAGCAGTCTGCGAGGCGAGTGG 1800
Qy 1846 GAGGATGTGTGACCTTGGGCGAGGAGCGCCCTCCACCTCTACTACTCTCCAGCTGGAG 1905
Db 1801 GAGGATGTGTGACCTTGGTGAAGGAGTCACTTCCACCTCTACTTCCAGCTGGAG 1860
Qy 1906 GCAGTGGCTGTGCTAGTCTTCCAGGAGCTGGGCGGCTTTCGCTGTGGGAGAGGCC 1965
Db 1861 GCGGGGCGCTGTCTATGCTTTCAGGAGCAGTGGGCGGCTTTCGCTGTGGGAGAGGCC 1920
Qy 1966 CTGAGGTGGCTGCGCGCAAGCGCTCAAGCTCTTCTGTTTTCGCGCGGTGGCTGCACC 2025
Db 1921 CTGAGGTGGCTGCGCAAGCGCTCTCAGGCTCTTCTGTTTGTCCGCTGGCTGTAGC 1980
Qy 2026 TCCCTCGAGTACAACTCCGGGTCTACTGCTCGATGACACCCCAAGTGCATCAAGGAG 2085
Db 1981 TCCCTTGAAGTACAACTCCGGGTCTACTGCTTACAGACACCCCAAGCTCTCAAGGAG 2040
Qy 2086 GTGCTGAGCTGAGAGAGCTGGGGGAGCAGTATCCAGGAGCCACGGGTCTCTGCAC 2145
Db 2041 GTGCTGAGCTGAGAGAGCTAGGTGGAGCAGTATCCAGGAGCCTCGCGTCTCTGCAC 2100
Qy 2146 TTCAAGGAGAGTTTACCAACACTGCGCTTATCCATCCAGCATGTGCCAGTCCCTGTGG 2205
Db 2101 TTCAAGGAGAGTTTACCAACACTTACGCTCTCCATCCAGCAGTGGCCAGCTCCCTGTGG 2160
Qy 2206 AAGAGTAAGTCTCTGTGAGTACAGGAGATCCCTTTTATCAGATCTCGAATGGCAGC 2265
Db 2161 AAGAGCAAGCTACTTGTGAGTACAGGAGATCCCTTTTATCAGATCTCGAATGGCAGC 2220

Qy	946	TGGAGCCCGTGGAGCAAGTGTGTGGCGCTGTGGGTGTGACTGCACCCACTGTGGCGAGCCGT	1005
Db	901	TGGAGTTTCGTGGAGTAAGTGTGTGAGCTGTGGGCTTGACTGCACCCACTGGCGGAGCCGC	960
Qy	1006	GAGTGTCTGTGACCCAGCAGCACCCGCAACGGAGGGGAGGAGTGCACAGGSCACTGACCTGGAC	1065
Db	961	GAGTGTCTGTACCCAGCAGCACCCGCAATGGAGGTGAGGAGTGTGGGTGTGACCTTGGAC	1020
Qy	1066	ACCCGCAACTGTATACAGTGAACCTCTGTGTATACACAGTGTCTTGGGCCCTCGAGGACGTGGCC	1125
Db	1021	ACCCGCAACTGTATACAGTGAACCTCTGCTGTGACACCGCTTCTTGCCCCGAGAGACGTGGCT	1080
Qy	1126	CTCTATGTGGGCTCATGCGCGTGGCCGTCTGCTGTGCTGTGCTGTGCTGTGCTCTCATC	1185
Db	1081	CTCTACATCGGCCCTGTGCTGTGGCTGTGTGCCTCTCTTGTGCTTGTGCTGGCCCTTGGGA	1140
Qy	1186	CTCGTTTATTCGCGGAAGAGGAGGGGCTGGACTCAGATGTGTGGCTGACTGTGTCAATTCTC	1245
Db	1141	CTCATTTACCTGTCCGAAGAAGAAAGGCTGTGACTTCOGATGTGGCGCGACTGTGTCCATCCTC	1200
Qy	1246	ACCTCAGGCTTCCAGCCGCTCAGCATCAAGCCAGCAAGCAAGACAGACAAACCCCATCTGCTC	1305
Db	1201	ACCTCGGGCTTCCAGCCTGTGAGCATCAAGCCAGCAAGCAGACAAACCCCACTGCTC	1260
Qy	1306	ACCATCCAGCCGAGCTCAGCACCAACCAACCACTACCAAGGSCAGTCTCTGTCCCGG	1365
Db	1261	ACCATCCAGCCAGACCTCAGCACCAACCACTACCACTACCAAGGSCAGTCTATGTTGAGG	1320
Qy	1366	CAGATGGGCTCAGCGCCCAAGTTCAGCTCACAAATGGGCACTGTGTACGCCCTCTGGGT	1425
Db	1321	CAGATGGACCCAGCCCAAGTTTCAGCTCTCTAATGGTCACTGTCTCAGCCCACTGGG	1380
Qy	1426	GGCGGCGGCCACACACTGTCACCAAGCTCTCCCACTCTGAGGCGCAGGAGTTCGTCTCC	1485
Db	1381	AGTGGCGGCCATAGTTTGACCAAGCTCACCACTCTGAGGCTGAGGACTTCGTCTCC	1440
Qy	1486	CGCCTCTCCACCCAGAACTACTTCCGCTCCCTGCGCGAGGCAACGACAACTAGACCTAT	1545
Db	1441	CGCCTCTCCACCCAAACTACTTTCGTTCCCTGCGCCCGGCAACACATGGCCTAC	1500
Qy	1546	GGGACCTTCAACTTCTCTGGGGGCGGCTGATGATTCCTTAATCAGATATCAGCTTCCTC	1605
Db	1501	GGGACCTTCAACTTCTCTGGGGGCGGCTGATGATTCCTTAATCAGGGGATCAGCTCCTC	1560
Qy	1606	ATCCCCCAGATGCATACCCGAGGGAAGATCTATGAGATCTACCTCAGCTGCACAAG	1665
Db	1561	ATACCCCGGATGCCATCCCCCGAGGAAGATCTACGAGATCTACCTCACTGCAACAAG	1620
Qy	1666	CCGGAAGACGTGAGGTTGCCCTAGCTGGGTGTGAGACCTGTGAGTCCCATCGTTAGC	1725
Db	1621	CCAGAAGCGTGAAGTTGCCCTAGCTGGCTGTGTCAGACCTGTGTAGTCCAGTCTGTAGC	1680
Qy	1726	TGTGGACCCCTGGCGTCTGTCAACCCGGCCAGTCAATCTTGGCTATGGAACCACTGTGG	1785
Db	1681	TGTGGGCCCCAGGAGTCTGTCAACCCGGCCAGTCAATCTTGGCAATGGACCACTGTGGA	1740
Qy	1786	GAGCCGAGCCTTGACAGCTGGAGCTGGGCTCAAAAAGCAGTCTGTGCGAGGGCAGCTGG	1845
Db	1741	GAGCCGAGCCTTGACAGCTGGAGTCTGCGCTCAAAAAGCAGTCTGTGCGAGGGCAGTGG	1800
Qy	1846	GAGGATGTGCTGACCTCTGGGCGAGGCGGCCCTCCCACTCTACTACTGCCAGCTGGAG	1905
Db	1801	GAGGATGTGCTGACCTTGTGTGAGGATCACTTCCCACTCTACTACTGCCAGCTGGAG	1860
Qy	1906	GCCAGTGCCTGACTAGCTTTCAACCGAGCAGTGGGCGGCTTTGCCCTGTGGGAGAGGCC	1965
Db	1861	GCCGGGGCTGTATGTCTTCAACCGAGCAGCTGGGCGGCTTTGCCCTGTGTAGGAGGCC	1920
Qy	1966	CTCAGCTGGCTGGCCGCAAGCGCCTCAAGCTGTCTCTGTGCTGGCGGCTGGGCTGCACC	2025
Db	1921	CTCAGCTGGCTGGCCCAAGAGCGCTCAGGCTCCTCTGTGTTGCTCCCGTGGGCTGTAGC	1980
Qy	2026	TCCCTCGAGTACAACATCCGGGCTACTGTGCTGATGACACCAACGATGACACTCAAGGAG	2085

[illegible]

```

RESULT 3
US-08-808-982-2
; Sequence 2, Application US/0808982
; Patent No. 5939271
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; APPLICANT: Leonardo, E. David
; APPLICANT: Hink, Lindsay
; APPLICANT: Masu, Masayuki
; APPLICANT: Kazuo, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSER: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

```

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/808,982

FILING DATE:

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: OSMAN, RICHARD A

REGISTRATION NUMBER: 36,627

REFERENCE/DOCKET NUMBER: UC96-217

TELEPHONE: (415) 343-4341

TELEFAX: (415) 343-4342

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 1787 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

US-08-808-982-2

Query Match 56.8%; Score 1562.4; DB 2; Length 1787;

Best Local Similarity 98.5%; Pred. No. 0;

Matches 1661; Conservative 0; Mismatches 16; Indels 9; Gaps 8;

QY	1070	GCAACTGTACAGTACCTCTGTGTACACAGTCTCTGGCCCTGAGACGTGGCCCTCT	1129
DB	1	GCAACTGTACAGTACCTCTGTGTACACAGTCTCTGGCCCTGAGACGTGGCCCTCT	59
QY	1130	ATGTGGGCTCATCGCCGTGGCGCTGTGTACAGTCTCTGGCTGTCTGTCTCTATCTCG	1189
DB	60	ATGTGGGCTCATCGCCGTGGCGCTGTGTACAGTCTCTGGCTGTCTGTCTCTATCTCG	119
QY	1190	TTTATTGCGGAAGAGAGGGGTGGAGTCAAGTGTGGTGTGATCTGTCTCTATCTCACT	1249
DB	120	TTTATTGCGGAAGAGAGGGGTGGAGTCAAGTGTGGTGTGATCTGTCTCTATCTCACT	179
QY	1250	CAGGCTTCCAGCCGTGAGATC-AAGCCAGCAAGAGAGAGAGAGAGAGAGAGAGAG	1308
DB	180	CAGGCTTCCAGCCGTGAGATC-AAGCCAGCAAGAGAGAGAGAGAGAGAGAGAGAG	239
QY	1309	ATCCAGCGGACCTCAGACACCAACACCACTACAGGCGAGTCTGTCTCTCTCTCACC	1368
DB	240	ATCCAGCGGACCTCAGACACCAACACCACTACAGGCGAGTCTGTCTCTCTCACC	299
QY	1369	GATGGGCCAGCCCAAGTTCCAGTCAACCAATGGGCACTGTCTCAGCCCTCTGGTGGC	1428
DB	300	GATGGGCCAGCCCAAGTTCCAGTCAACCAATGGGCACTGTCTCAGCCCTCTGGTGGC	359
QY	1429	GGCCGCCACACATGCAACAGTCTCTCCACCTCTGAGGCGAGGAGTTCCTCTCCGC	1488
DB	360	GGCCGCCACACATGCAACAGTCTCTCCACCTCTGAGGCGAGGAGTTCCTCTCCGC	419
QY	1489	CTCTCCACCAAGAACTACTTCCGCTCTCCGCTCCGCGAGGACCAACATGACCTATGGG	1548
DB	420	CTCTCCACCAAGAACTACTTCCGCTCTCCGCTCTCCGCGAGGACCAACATGACCTATGGG	479
QY	1549	ACCTTCAACTTCTCGGGGGCGGCTGATGATATCCCTAATACAGTATCAGCTCTCTATC	1608
DB	480	ACCTTCAACTTCTCGGGGGCGGCTGATGATATCCCTAATACAGTATCAGCTCTCTATC	539
QY	1609	CCCCCAGATGCATACCCCGAGGAGAGATCTATGATCTACCTCAGCTGCACAGCCG	1668
DB	540	CCCCCAGATGCATACCCCGAGGAGAGATCTATGATCTACCTCAGCTGCACAGCCG	599
QY	1669	GAAAGCTGAGGTTGCCCTGAGCTGTGTGAGACCTCTGAGTCTCCATCGTTAGCTGT	1728
DB	600	GAAAGCTGAGGTTGCCCTGAGCTGTGTGAGACCTCTGAGTCTCCATCGTTAGCTGT	659
QY	1729	GGACCCCTGCGCTCTCTCACCCTGAGTCACTCTGCTGTGCTATGAGCACTGTGGGAG	1788

RESULT 4

US-09-306-902A-2

QY 1304 T-----CACCATCCAGCGGACCTCAGCACCACCAACCACTTACCAGGCGAGTCTCT 1357
Db 1304 TGCACCCATCCGCCCTCCGAGCCTAACCGCCAGTGTGCGCATCTACCGCGGACCTGTGT 1363
QY 1358 GTCCCGGCGAGGA-----TG 1372
Db 1364 ATGCCCTTGCAGGACTTGGCCGACAGAGATCCCTATGACTAATTAACCCCTTCTGTGATCCCT 1423
QY 1373 GGCCAGCCCCAAGTTCCAGTCCACCAATGGGACCTGTCTCAGCCC-----CCTGG 1423
Db 1424 TGCCAGCCTCAAGATCAAGGTCTATGACTCCAGCACCATCGGCTCTGGGCGCTGGCCTGG 1483
QY 1424 GTGGCGCGCCACACACTGCACACAGCTCTCCACCTCTGAGGCCGAGAGTTGCTCT 1483
Db 1484 CTGATGAGCGGACCTCTGGGTGTCTTACACCCGGTATATACCCAGGCGATTTCTCCC 1543
QY 1484 CCGCCTCTCACCCGAAC-----TACTTCGCTCCC 1516
Db 1544 GGGACACCACTTCTGCACTGTGGCAGCGCCAGCCTTGGTCCAGCACTCTCTGGGCC 1603
QY 1517 TGCCCGAGGACACAGCAACATGACCTATGGGACCTTCAACTTCTCGGGGCGCGGTGA 1576
Db 1604 TCCCTCGAGACCCCGAGCAGAGTGTCAGTGGCACCTTTGGTTGCTGGGTGGGAGGCTGA 1663
QY 1577 TGATCCCTAATACAGGTATCAGCTCTCATCCCCCAGATGCCATACCCCGGAGGAG 1636
Db 1664 CCAFTCCCGGCACAGGGGTGAGCCTGTGTGTACCAATGAGGCAATTCCTCCAGGGCAAGT 1723
QY 1637 TCTATGAGATCTACTCAGCTGACCAAGCGGAGACGTGAGGTTCGCCCTTACTGTGCT 1696
Db 1724 TCTATGACTTGTATCTAGTATCAACAAGACTGAAAGCACCTCCCACTTTCCGAAAGTT 1783
QY 1697 GTGAGACCTGTGAGTCCCATGTTAGCTGTGAGACCCCTGGCGTCTGTCTCACCCGGC 1756
Db 1784 CCCAGACAGTATTGAGCCCTCGGTGACCTCGGGCCCAAGGGCTCTCTCTGTGCCGCC 1843
QY 1757 CAGTCATCCTGGCTATGAGCACCTGTGGGAGCCAGCCCTGACAGCTGGAGCTGGGCC 1816
Db 1844 CTGTGTCTCTACTGTGCCCACTGTCTGAAGTCAATTGGCGGAGACTGTATCTTCAGC 1903
QY 1817 TCAAAAAGCAJTCGTGGCGAGGCGAGCTGGGAGGATGTCTGACCTGGGCGAGGAGCGC 1876
Db 1904 TCAAGACCCAGGCCCATCAGGCCACTGGGAGGAGTGTGACTTTGATGAGGAGACTC 1963
QY 1877 CTTCCCACTTACTACTCAGCTGAGGCGAGTGTCTGTAGTCTTCAAGGAGCAGC 1936
Db 1964 TGAACACCCCTGTACTGCCAGCTAGAGGCTAAATCTGCCACATCTCTGTGGACAGC 2023
QY 1937 TGGCCGCTTTGGCCGTGGGAGAGCCCTCAGCGTGGCTGCCGCAAGCGCTCAAGC 1996
Db 2024 TGGTACTACTGTTCAGGGCGAGTCTTACTCCCGCTCGCAGTCAAGCGGCTCAGC 2083
QY 1997 TGCTTCTGTTTGGCCCGGTGGCCTGCACTCCCTCGAGTACAAATCCGGGTCTACTGCC 2056
Db 2084 TAGCCATCTTGCGCCCAAGCCCTCTGCACCTCCCTGGAGTATAGTCTCAGGGTCTACTGTC 2143
QY 2057 TGCATGACACCCAGATGCACTAAGAGAGTGTGACAGCTGGAGAACAGCTGGGGGAG 2116
Db 2144 TGGAGGACACTCTCTGCAGCACTGAAGGAGGTCTTAGAGCTGGAGAGGACTCTGGGTGGCT 2203
QY 2117 AGCTGATCCAGGAGCCAGGCTCTGCACTTCAAGGACAGTTACCAACCTCGCCCTAT 2176
Db 2204 ACTTGGTGGAGGAGCCCAAGACTTGTCTTTAAGGACAGTTACCAACCTAGC-CTCT 2262
QY 2177 CCATCCACGATGTGCCAGCTCCCTGTGGAAGAGTAAGCTCCTTGTGAGCTACAGGAGA 2236
Db 2263 CCTCCATGACATCCCCCACTGCCACTGGAGGACAAACTACTGGCCAACTACAGGAGA 2322
QY 2237 TCCCTTTTATACATCTGGAATGGCAGCAGCGGTACTTGCATGCACTTCACTCTG 2296
Db 2323 TTCCCTTTCTACATGTGTGGAACGCGCAGCAAGCCCTGCACTGCACTTCACTCTG 2382
QY 2297 AGCGTGTGAGCCCGCAGCACTAGTCACTGGCGCTGCAAGCTGTGGGTGTGGCAGTGGAGG 2356

Db 2383 AGAGACATAGCCTAGCCTCCACTGAGTTCACTGAGTCTCGTGGCGAGGTAGAAG 2442
QY 2357 GCACCGGCGAGAGCTTTCAGCATCAACTTCAATATCAC---CAAAGGACACAAGGTTTGTCTG 2413
Db 2443 GGGAGGCCAGATTTTCCAGCTGCACACACGCTGGCTGAGAGCGCTGCTGCCCTGG 2502
QY 2414 AGCTGTGGCTCTGGAGAGTGAAGCGGGGTCCAGCCTGTGGGCCCCAGTGCCTTCA 2473
Db 2503 ATGCACTCTGCTCTGCCCCCTGGCAATGCTGCCACCAACACAGCTGGGACCCCTATGCTTCA 2562
QY 2474 AGATCCCTCTCCCTCATTCGGCAGAAGATAATTTCCAGCCTGGACCCACCCCTGTAGCGGG 2533
Db 2563 AGATACCACTGTCTCCCGCCAGAAGATCTGCAACAGCCTGGACGCCCCCACTCAGCGG 2622
QY 2534 GTGCCAGCTGGCGGACTCTTGGCCCCAGAAACTCCACCTGGACAGCCATCTCAGCTTCTTTG 2593
Db 2623 GCAATGACTGGCGGCTTGGCACAGAGCTCTCCATGGACCGGTACTGAACTACTTCG 2682
QY 2594 CTTCGAAGCCAGCCCCACAGCCATGATCTCAACTGTGGGAGGCGCGGCACTTCCCCA 2653
Db 2683 CCACCAAGCTAGTCCCAAGGCGTGTCTTAGACCTCTGGGAAGCTCGGCAGCAGATG 2742
QY 2654 ACCGCAACCTCAGCCAGCTGGCTGCAGCAGTGTGCTGAGCTGGGCCAGCCAGCGCTGGCC 2713
Db 2743 ATGGGACCTCAACAGCCTGGCCAGTGTCTTGGAGGAGATGGGCAAGAGTGAGATGCTGG 2802
QY 2714 TCTTCAGTGTCTGGAGGCTGAGTGTGA 2742
Db 2803 TAGCCATGACCACTGATGGCGATTGCTGA 2831

RESULT 6

US-09-306-902A-3
; Sequence 3, Application US/09306902A
; Patent No. 6277585
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; Leonardo, E. David
; Hink, Lindsay
; Masu, Masayuki
; Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/306,902A
; FILING DATE: 07-May-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2831 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear

QY 1103 CTTCTGGCC-----CTGAGACGTGGCCCTCT 1129

1064	AGGAACTCTAAACGACCTTAAAGCGCGCCCTGGAGCGCTCGGAGAGCGTGGCGGTGT	1123
Qy	ATGTGGGCGCTC--ATCGCGGTGGCGGTCTGCTGTGCTGTGCTGTGCTGTGCTCATCC	1186
Db	ATCGGGGCTCTGTGGTGGCGGTCTTTGTGTGTTCTGGCAGTTCTCATGGCTGTAGGAGTGA	1183
Qy	TCGTTTATTCGCGAAGAAGAGGGGTGGACTCAGATGTGGCTGACTCGTCAATT--C	1243
Db	TCGTGTACGGAGAAATCGCGGACTTCGACACGGACATCACTGACTCTCTGCTGCGCC	1243
Qy	TCACCTCAGGCTTCCAGCGCGTTCAGCATCAGGCCAGCAAGAGACAACCCCATCTGC	1303
Db	TCACGTGTGTTTCCACCCCGTCAACTTCAGACTTCGAAGGCCAGCAACCCACAGCTCC	1303
Qy	T-----CACCATTCAGCGGACCTCAGCACCAACCACCACTACCAAGGGCAGTCTCT	1357
Db	TGCACCATCGCGCTTCGACCTTAACGGCAGTCTGGCATCTACCGCGACCTGTGT	1363
Qy	GTCCCCGGCAGGA-----TG	1372
Db	ATGCCCTGCAGGACTCTGCGACAAGATCCCTATGACTAATTCACCCCTTCTGGATCCCT	1423
Qy	GGCCAGCCCAAGTTCAGCTCACAATGGGCACCTGTCTCAGCCC-----CTGG	1423
Db	TGCCACGCTTCAAGATCAAGGTCTATGACTTCCAGCACCATCGGCTCTGGGGCTGGCGCTGG	1483
Qy	GTGGCGCGCCACACACTGCAACACAGCTCTCCACCTCTGAGGGCGAGGAGTTCGTCT	1483
Db	CTGATGAGCGGACCTGTCTGGGTCTTACCAACCGGTACATACCAGCGGATTTCTCCC	1543
Qy	CCGGCTCTCCACCCAGAAC-----TACTTCCGCTCCC	1516
Db	GGGACACCACTTCCTGCACCTGCGCAGCGCAGCCTTGGTTCCCAGCACTCTCTGGGCC	1603
Qy	TGCCCGGAGGCAACAGACAATGACTATGGAGCTTCAACTTCTCTGGGGGCGGCTGA	1576
Db	TCGCTCGAGACCCAGCAGCAGTGTCAGTGGCACCTTTGTGTGCTGTGGGTGGGAGCTGA	1663
Qy	TGATCCTTAATCAGGTATCAGCTCTCATCCCCCAGATGCCATACCCCGAGGGAAGA	1636
Db	CCATTCGCGCAAGGGGTGAGCTTGGTACCAATGGAGGCCATTCGCCAGGGCAAGT	1723
Qy	TCTATGAGATCTACCTCACGCTGCACAAGCGGAGACGTGAGGTTGCCCTAGCTGGCT	1696
Db	TCTATGACTTGTATCTACGTATCAACAAGACTGAAAGCACCTCCCACCTTCGGAAGTT	1783
Qy	GTCAAGACCTGTGTAGTCCCATGTGTAGCTGTGGACCCCTGTGGGTCTGTCTCACCGGC	1756
Db	CCCAGACAGTATTGAGCCCTCGGTGACCTTGCGGGCCACGGGCTCTCTCTGTGCGGC	1843
Qy	CAGTCATCTTGGCTATGAGCACTGTGGGAGCCAGCCCTGCACGCTGCAGGCTTCGCGC	1816
Db	CTGTGTCTTCACTGTGCCCCACTGTGTGAAGTCAATGCCGAGACTGGATCTTCCAGC	1903
Qy	TCAAAGACAGTCTGTGCGAGGGCAGCTGGGAGGATGTGTGCACCTTGGCGAGGAGCGCG	1876
Db	TCAAGACCCAGGCCCATAGGGCCACTGGGAGGAGTGTGTGACTTTGGATGAGGAGCTC	1963
Qy	CTTCCACCTCTACTACTGCACTGGAGCCAGTGCCTGTCTAGCGTTCACCGAGCAGC	1936
Db	TGAACACCCCTGTCTACTGCACTAGAGGCTAAATCTCTGCCACATCTCTTGTGGACAGC	2023
Qy	TGGGCGCTTTCCTGTGTGGGAGGGCCCTCAGGTGGCTGCCCGCAAGCGCTCAAGC	1996
Db	TGGGTACCTACGTGTTCAGGGGAGTCTTACTTCCCGCTCCGAGGTCAAGCGGCTCCAGC	2083
Qy	TGCTTCTGTGTGGCGGTGGCTGTCACTCTCCCTCGAGTACAACATCCGGGTCTACTGCC	2056
Db	TAGCCATCTTGCGCCAGCCCTCTGCACCTCCCTGGAGTATAGTCTCAGGGTCTACTGTC	2143
Qy	TGCATGACACCCACGATGCATCAAGAGGTGGTGCAGCTGGAGAGCAGCTGGGGGAC	2116


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Db 2144 TGGAGGACACTCCTCGACGACCTGAAGGAGGTCTCTAGAGCTGGAGAGACTCTGGGTGGCT 2203
Qy 2117 AGCTGATCCAGGAGCCACGGGTCTCTGCACTTTCAAGACAGTTTACCACAACTCGGCTAT 2176
Db 2204 ACTTGGTGGAGGAGCCCAAGACTTTTGTCTTTAAGGACAGTTTACCACAACTACG-CTCT 2262
Qy 2177 CCATCCAGGATGTGCCAGCTCCTCTGGAGAGTAGTCTTGTGAGTACCGAGGA 2236
Db 2263 CCCTCCATGACATCCCCCATGCCCCACTGGAGGAGCAAACTACTGGCCAAAGTACCGAGA 2322
Qy 2237 TCCCTTTTATCATCATCTGGAATGGCACGCGAGGGTACTTTGCACTGCACTTCACTCCCTGG 2296
Db 2323 TTCCCTTCTACCATGTGTGNA CGCAGCCAGAAAGCCCTGCACTGCACTTTCACTCTGG 2382
Qy 2297 AGCGTGTACGCCAGACACTAGTAGACCTGCGCTGCAAGCTGTGGGTGTGCGAGGTGAGG 2356
Db 2383 AGAGACATAGCCTAGCCTCCACTGAGTTCACTGTAGGTCTGCGTGGCGAGGTAGAAG 2442
Qy 2357 GCGAGGGGCGAGCTTCAGCATCAACTTCAACATCAC- --CAAGGACACAAGGTTTGCTG 2413
Db 2443 GGGAGGCCAGATTTTCCAGCTGCACACACAGCTGGCTGAGACGCTGTGGCTCCCTGG 2502
Qy 2414 AGCTGTGGCTCTGGAGAGTGAAGCGGGGTCCAGAGCCCTGTGGGGCCCCAGTGCCTTCA 2473
Db 2503 ATGCACTCTGCTGTGCCCTGGCAATGCTGCCACACACAGCTGGGACCCCTATGCTTCA 2562
Qy 2474 AGATCCCTTCTCATTTTCGGAGAGATAATTTCCAGCTGGAGCCCAACCTGTAGCGGG 2533
Db 2563 AGATACCACCTGTCCATCCGCGAGAAGATCTGCAACAGCTGGAGCGCCCCAACTCAGCGG 2622
Qy 2534 GTGCCAGCTGCGGACTCTGGCCAGAAATCCACCTGGACAGCCATCTCAGTCTCTTTG 2593
Db 2623 GCATGACTGCGGCTTTGGACAGAAAGTCTCCATGGACCGGTACTCTGAATCTACTTGG 2682
Qy 2594 CCTTCAAGCCAGCCCCACAGCCATGATCTCAACCTGTGGGAGCGCGGCACTTCCCCA 2653
Db 2683 CCACCAAGCTAGTCCACAGGGGTGATCTTAGACCTCTGGGAGCTCGGCAGCAGATG 2742
Qy 2654 ACGCAACCTCAGGCAGCTGCTGACAGCTGCTGAGCTGGGCGAGCCAGCAGCTGGCC 2713
Db 2743 ATGGGGACCTCAACAGCTGGCCAGTGCCTTGGAGGAGATGGGCAAGAGTGAGATGCTGG 2802
Qy 2714 TCTTCAAGTGTGGAGGCTGAGTGCTGA 2742
Db 2803 TAGCCATGACCATGATGGCGATGCTGA 2831
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RESULT 7

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US-09-949-016-4794
; Sequence 4794, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4794
; LENGTH: 3008
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-4794
Query Match 30.3%; Score 833.6; DB 4; Length 3008;
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Best Local Similarity 62.1%; Pred. No. 7.4e-177;
Matches 1435; Conservative 0; Mismatches 814; Indels 63; Gaps 5;
Qy 485 TGGCAGAAGACTTTGAGCAGGAGCCGCTGGCCAAAGAGGTGTCCCTGGAGCAGGAGCATCG 544
Db 10 TACGGAAGACATTTGAGCAGGAGAACCCCTAGGAAGGAGTGTCTTTGGAACAGGAAGTCT 69
Qy 545 TGTGCGCTGCGCTCCACCGGAGGGGCAATCCCTCCAGCCGAGGTGGAGTGGCTCCGGAAACG 604
Db 70 TACTCAGGTGTGACCAACCTGAAAGGATCCCACTGGCTGAGGTGGAATGGTTGAAAAATG 129
Qy 605 AGGACCTGTGTGGACCCGTCCTCGGACCCCAATGTATACATCACGCGGAGCAGACCTGG 664
Db 130 AAGACATAATTTGATCCCGTTGAAGATCGGAATTTTATATTATTTGATTCACAACCTCA 189
Qy 665 TGTGCGGACAGGCCCGCTTTGCTGACACGCGCAACTACACCTCGCTGGGCCAAGAACTCG 724
Db 190 TCATAAAGCAGGCCCGACTCTCTGATACATGCAAAATTTACACCTGTGTGCCAAAACATTG 249
Qy 725 TGGCAGTGTGCGCGCAGCGCTCCGCTGTGTGTCTATGCTGTACGTGAACGCTGGGTGCTGCA 784
Db 250 TTGCCAAGAGGAAAAAGTACAACTGCCACTGTCTATGTCTATGTCAACGGTGGCTGGTCCA 309
Qy 785 CGTGGACCGAGTGTGCTCGCTGCGAGCGCAGCTGTGGCGCGCTGGCAGAAAACGAGCC 844
Db 310 CTTGGAGCGGAGTGTGTGTGTAA CAGCGCTGTGGAAGGGGTATCAGAAACGTACAA 369
Qy 845 GAGACTGCAACCAACCGCGCGCTCTCAACGGGGCGCTTTCTGTGAGGGGAGAGATGTCC 904
Db 370 GGACTTGTACCAACCCCGCACCACTCAATGGGGGTGCTTCTGTGAAGGGCAGAGTGTGC 429
Qy 905 AGAAAACAGCTGTGCGCACCTGTGCGCAGTAGACGCGAGCTGGAGCCGTGGAGCAAGT 964
Db 430 AGAAAATAGCTGTACTGTATGCGCAGTGGATGGCAGGTGGAGCGCCATCGACATG 489
Qy 965 GGTGCGCTGTGTGGCTGGACTGCACCCACTGGCGGAGCGTGTGAGTGTCTGTACCCAGCAC 1024
Db 490 GGTCTACTTGTGGAACATGAGTGACCACTGGCGCAGGAGGAGTGCACGCGCCAGCCCC 549
Qy 1025 CCGCAACCGAGGGGAGGAGTGCCAGGGCACTGACCTGGACACCCGCAACTGTACCAAGTG 1084
Db 550 CCAAGAAATGGAGGCAAGGACTGCGACGGCTCTGCTTGTGCAATCCAAGAACTGCACATG 609
Qy 1085 ACCTCTGTGTACAGTGTCTTGGCGCTGTGAGACGCTGGCCCTCTATGTGG- --CCTCA 1141
Db 610 GGCTTTGCAATGACAGCTGCTCTGATTCAGATGATGTGCTCTCTATGTGGGATGTGA 669
Qy 1142 TCGCCGTGGCGTCTGCTGCTGCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1201
Db 670 TAGCAGTGTATGTTTGGCTGGCGATCTCTGTAGTGTGTGGCTTGTGTGTATCGGAGA 729
Qy 1202 AGAAGAGGGGCTGGACTCAGATGTGGCTGACTCTGTCCTCAATTTCTCACTCAGGTTCCAGC 1261
Db 730 ATCATCGTGACTTTGAGTCAGATATTTAGTCTCTTGGCACTCAATGGGGGCTTTTTCAGC 789
Qy 1262 CCGTACAGATCAAGCCCGCAAGCAGACACCCCATCTGTCTCACTCAGCATCCAGCCGAGCC 1321
Db 790 CTGTGAACATCAAG- --GCAGCAAGACAAAGATCTGTGGCTGTATCCCCCGAGCC 840
Qy 1322 TCAGCACCAACCAACCACTACAGGCGAGTCTCTGTCCCCCGCAGGATG- --GGCC 1376
Db 841 TCAGGTGAGTGTGAGCAGCAGTGTATGAGGAGCTGTCTATGCGCTGCACTGAGCTCTCAGACA 900
Qy 1377 CAGCCCCAAGTTCAGACTCACCAAT- --GGGCACTGTCTCAGCCCGCTGGGTGGCGGCC 1432
Db 901 AATCCCAATGACCAACTCTCCAATTTCTGGATCCACTGGCCCAACCTGAAAATCAAAGTGT 960
Qy 1433 GCCACACTGACACAGCTCTCCCACTCTGAGGCGGAGGATTCGTTCTCCCGCTCT 1492
Db 961 ACAACACCTCAGGTGTGTACCCCCCAAGATGACCTCTCTGAGTTTACGTTCAAGCTGT 1020
Qy 1493 CCACCCAGAACTACTTTCCGCTCCCTCCCGCAGGACCAACAGACATGA- -- 1540
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Db 1021 CCCCTCAGATGACCCAGTGGTGTGAGAAATGAAGCCCTCAGCCTCGAAGAACAGAGTC 1080
Qy 1541 -----CCTATGGAGCTTCAACTTCCTCGGGGCC 1570
Db 1081 TAGCAGGCAGACTGATCCATCTCTGACCGCAATTTGGAGCTTCAACTTCGCTGGAGGTC 1140
Qy 1571 GGCTGATGATCCCTAATAAGATATCAGCTCTCTCATCCCCCAGATGCCATACCCGAG 1630
Db 1141 ACCTTATTTGCCAAATTCAGAGTTCAGTGTCTGATTTCCGCTGGGGCCATTTCCCAAG 1200
Qy 1631 GGAAGATCTATGAGATCTACCTCAGCTGACAGCGGAGAGAGTGAAGTTGGCCCTAG 1690
Db 1201 GGAGAGTCTACGAAATGTATGTGATCTGTACACAGAAAGAACTATGAGGCCACCCATGG 1260
Qy 1691 CTGCTGTGCAGACCTCTGCTAGTCCCATCTGTAGCTGTGAGACCCCTCGGCTCCTGTCA 1750
Db 1261 ATGACTCTCAGACACTTTTGACCCCTGTGTGAGCTGTGGGCCCCAGAGACTCTGTCTCA 1320
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Qy 1811 TGGCCCTCAAAAAGCAGTGTGCGAGGCAGCTGGAGGATGTCTGACCTGGGCGAGG 1870
Db 1381 TACTGCTCAAGAACCCAGCAGCAGAGGACAGTGGAGGATGTGTGTGGTGGGAGG 1440
Qy 1871 AGGCGCCTCCCACTCTACTACTGCCAGCTGGAGGCCAGTGCCTGTACTCTTCAACG 1930
Db 1441 AAAACTTACACACCCCTGTCTACATTCAGCTGTGATGAGAGGCTGCCATCTCAAG 1500
Qy 1931 AGCAGCTGGGCGCTTTGCCCTGTGGAGAGGCCCTCAGCGTGGCTGCGGCCAAGGCC 1990
Db 1501 AGAACCTCAGCACCTACGCCCTGTGTAGGACATTCACCAACCAAGCGCTGGAGCGCC 1560
Qy 1991 TCAAGCTGCTTCTGTGTGGCGCGTGGCTGCACTCTCTCGAGTACAACATCCGGTCT 2050
Db 1561 TCAAGCTGGCCATCTTTGGGCCCTGTGCTCTCTCGCTGGAGTACAGCATCCGAGTCT 1620
Qy 2051 ACTGCCCTGATGACACCCAGCATCAAGGAGTGTGTCAGCTGAGAGGAGCAGCTGG 2110
Db 1621 ACTGTGTGATGACACCCAGATGCCCTGAAAGAAATTTTACATCTTGAGAGACAGATG 1680
Qy 2111 GGGACAGCTGATCCAGGAGCACGGGTCTGTGCACTTCAAGGACAGTTACCAACCTGC 2170
Db 1681 GAGGACAGCTCTTAGAAGAACCTTAAGCTCTTCAATTTAAAGGACAGCACCAACCTGC 1740
Qy 2171 GCCTATCCATCCAGATGTGCCAGCTCCCTGTGGAGAGATGAAGCTCCTTGTAGCTACC 2230
Db 1741 GCCTGTCAATTCAGATATCGCCCATTCCTCTGGAAGAGCAAAATTCGTGGCTAAATATC 1800
Qy 2231 AGGAGATCCCTTTTATACATCTGGAATGCGACGAGCGGTACTTGCACCTGCACCTTCA 2290
Db 1801 AGGAAATTCATTTTACATGTTTGGAGTGGATCTCAAGAAACCTGCATGCACTTCA 1860
Qy 2291 CCCTGGAGCTGTGAGCCCCAGCAGTGTAGTACCTGGCTTGAAGCTGTGGGTGTGGCAGG 2350
Db 1861 CTCTGGAAAGATTTAGCCTGGAACACAGTGGAGCTGTTTGAACACTCTGTGTGGCGAGG 1920
Qy 2351 TGGAGGGCGAGCGGCGAGCTTACAGCATCAACTTTCAACATCAACAGGACACAGGTTTG 2410
Db 1921 TGGAGGAGAGGGGAGATCTTCCAGCTCAACTGCACCTGTGAGAGGAACTTACTGGCA 1980
Qy 2411 CTGAGCTGTGGCTCTGAGAGTGAAGCGGGGTCCAGGCCCTGTGGTGGGCCCGAGTGCCT 2470
Db 1981 TCGATTTGCGCTGCTGATCTCTCGGAACCATCAACAGGTCACGGGGCCAGTGCCTT 2040
Qy 2471 TCAAGATCCCTCTCTTATTTGGCAGAGATAATTTCCAGCTGGACCCACCTCTGTAGGC 2530
Db 2041 TCAGCATCCCTCTCTCTATCCGGCAGAGCTCTGTAGCAGCTGTGATGCCCCCGACAGA 2100
Qy 2531 GGGGTGCGGACTGGCGGACTCTGCCCCAGAAAATCTCACTGGAGCAGCATCTCAGCTTCT 2590
Db 2101 GAGGCCATGACTGGAGGATGTGCCCCATAAGCTGAACCTTGAACAGGTACTTGAATTAAT 2160
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Qy 2591 TTGCTTCAAGCCAGCCCCACAGCCATGATCTCTCAACCTGTGTGGAGCGCGGCACTTCC 2650
Db 2161 TTGCCACAAATCAGGCCCACTGGCGTATATCTTGGATCTTTTGGGAAGCAGAACTTCC 2220
Qy 2651 CCAACGGCAACCTCAGCCAGCTGCTGACAGCAGTGGCTGGACTGGGCCAGCAGACGCTG 2710
Db 2221 CAGATGGAACCTTGAGCATCTGCGACGTGTCTTGGAGAATAATGGGAAGACATGAACGG 2280
Qy 2711 GCCTTTCACAGTGTGCGAGGCTGAGTGCTGA 2742
Db 2281 TGGTGTCTTTCAGCAGCAAGAGGCGCAGTATTAA 2312
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RESULT 8

US-09-969-532-9

; Sequence 9, Application US/09969532

; Patent No. 6777232

; GENERAL INFORMATION:

; APPLICANT: walke, D. Wade

; APPLICANT: Scoville, John

; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides Encodin

; FILE REFERENCE: LEX-0244-USA

; CURRENT APPLICATION NUMBER: US/09/969,532

; CURRENT FILING DATE: 2001-10-02

; PRIOR APPLICATION NUMBER: US 60/237,280

; PRIOR FILING DATE: 2000-10-02

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 9

; LENGTH: 2736

; TYPE: DNA

; ORGANISM: homo sapiens

US-09-969-532-9

Query Match 17.7%; Score 487; DB 4; Length 2736;

Best Local Similarity 50.9%; Pred. No. 2.7e-99;

Matches 1305; Conservative 0; Mismatches 1230; Indels 30; Gaps 5;

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Qy 172 CTTCCCCACTTCTGTGTGGAGCCCGAGGATGTGTACATCTCAAGAACAGCCAGTCTGT 231
Db 157 CTGCCTCATTTTCATAGAGGAGCCAGATGCTATATTATCAAGAGCAACCCCTATTGCA 216
Qy 232 CTTGTGTGAAGCCGCTGCGCCGCCACGACATCTTCTTCAAGTGAACGGAGTGGGTG 291
Db 217 CTGAGGTGCAAGCGAGCCAGCCATGCAATATTTCTTCAATGCAACGGAGTGGGTG 276
Qy 292 CGCCAGGTGGAACCACTGTATCGAGCCGACAGCAGCGGAGCAGTGGGCTGCCACCATG 351
Db 277 CATCAGAACGAGCACGCTCTCTGAAGAGACTCTGAGAGAGCTCAGGTTTGAAGGTCGC 336
Qy 352 GAGGTCCGCAATTAATGTCTCAAGGCGAGCGTCTGAGAGGTGTTCGGGCTGGAGGAATAC 411
Db 337 GAAGTGTTCATCAATGTACTTAGGCCAACAGGTGGAGACTTTCATGGGCCCGAGGACTAT 396
Qy 412 TGTGTCAGTGTGGCATGAGCTCTCTCGGGCACCAACAGAGTCAAGAGGCTACATC 471
Db 397 TGTGCCAGTGTGGGTGGAGCCACCTGGGTACCTTCCAAAGCAGCAAGGCTCTGTG 456
Qy 472 CGCATAGCCAGATTGCGCAAGAACTTTGAACAAGACCCCAAGAGGAGGTGTCCCTG 531
Db 457 CGCATAGCCTATTTCAGGAAAACTTTGAACAAGACCCCAAGAGGAGGAAAGTTCCCAT 516
Qy 532 GAGCAGGCACTGTGTCTGCCCTCCGCTCCACCGGAGGCACTCCTCCAGCCGAGGTGAG 591
Db 517 GAAGGCAATGATTGTACTGCACTGCCGCCACCCAGGAGGAGTCTCTGCTGCCAGGTGAA 576
Qy 592 TGGCTCCGGAACGAGGACCTGTGTGGACCCGCTCCCTGACCCCAATGTATACATCACCGG 651
Db 577 TGGCTGAAAAATGAAAGGCCATTTGACTGTGAACAAGACGAGAACATTTGACACAGGGCT 636
Qy 652 GAGCAGACCTGTGTGTGGACAGGCGCCGCTTGTGCTGACACGCCCAACTACCTCGGTG 711
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Db 637 GACCATAACTGATCATCAGGAGGACGGCTCTCGAGCTACAGGAATTAACACTGCGATG 696
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712 GCCAAGAACATCGTGGCACTGCGCCGAGCGCCTCGCTCTGTCATCGTCTACGTGAAC 771
Db
697 GCAGCCAACTCGTGGCTAAGAGGAGAAGCTGTGCGCCACTGTGTGGTCTACGTGGAT 756
Qy
772 GGTGGGTGGTGCAGCTGGACCGAGTGTCTGCTGACGCCAGCTGTGTGGCGCGGTGG 831
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757 GGGAGCTGGGAAGTGTGGAGCGAATGGTCTGTCAGATCCAGAGTGTGA-----A 807
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832 CAGAAACCGAGCGAGCTGCACCAACCGCGCTCTCAACGGGGCGCTTTCTGTGAG 891
Db
808 CATTTGGGATCCGGAGTGCACGACACACCCCGGAGAAATGGGGCAAAATTCGTGAA 867
Qy
892 GGGCAGAAATTCACAGAAAAAGCGCTGCGCCACCGCTGTGCCAGTAGACGCGAGCTGAGC 951
Db
868 GGTCTAAGCCAGGAATCTGAANAACCTGCACAGATGGTCTTTGGCATCTCTAGATAAAAACCT 927
Qy
952 CCGTGGAGCAAGTGGTGGCGCTGTGGCTGGACTGACACCCACTGGCGGAGCGGTGATGC 1011
Db
928 CTTTCATGAAATAAAACCCCAAGCATTTGAGAAATGCCAGCGACATTTGCTTTACTCGGGC 987
Qy
1012 TCTGACCCAGCACCCCGCAACGGAGGGAGAGTGCAGGGCACTGACCTGGGACACCCGC 1071
Db
988 TTGGGTCTGCGCTGCTGGCGGTGCACTCTGTCATTTGGTGTCACTTACAGACGG 1047
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1072 AACTGTACCAAGTACCTCTGTGTACACAGTGTCTTGGCCCTTGAGGAGCTGGCCCTCTAT 1131
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1048 AGCCAGAGTGACTATGTCGTGGAGCTCATTTGACTCTTCTGCAATGACAGGTGGCTTCCA- 1106
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1132 GTGGGCTCATCGCGTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1191
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1107 --GACCTTTCACTTTAAAAAGTCCCGTCAAGCAAGAAATATCATGGAATTAATGATACAA 1164
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1192 TATTGCCGGAAGAGGAGGGCTGGACTCAGATGTGGCTGACTCGTCCATTTCTCACCTCA 1251
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1165 GAAAAATCCTTTGGTAATCCTCTGCTCTGAAATCTGCAATGTCGATGAGCCAGATCTGACNGT 1224
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1252 GGCTTCCAGCCCGTACAGATCAAGCCGAGCAAGAGCAGAACCCCGCTCTGTCACCATC 1311
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1372 GGGCCCAAGCTTCCAGCTCACCAATGGGCACCTGCTCAGCCCGCTGGGTGGCGGC 1431
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1432 CGGCACACTGACACAGCTCTCCACCTCTGAGGCCGAGAGTTCGTCTCCCGCTC 1491
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1405 CCCCATGGAACCAACCAAGCTTTAGTACAAATGCAATGCAATCCAGAAATAAAATGCGCTACATC 1464
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1492 TCACCCAGAACTACTTTCGCTCCCTCCCGGAGGACCAAGCAACATGACCTATGGGACC 1551
Db
1465 CAATACTGTG-----ATCACTCCCAAGGACAACTGAGGACAACTGAGTGTG 1515
Qy
1552 TTCAACTTCTCGGGGCGCGCTGATGATCCCTAATAAGTATCAGCTTACGCTCTCATCCCC 1611
Db
1516 TTTGGCCATTTAGGGGGCGCTTAGTAATGCCAAATACAGGGGTGAGCTTACTCATACCA 1575
Qy
1612 CCAGATGCCATACCCGAGGGAAGTCTATGAGATCTACCTCAGCTGCAAGCCGGAA 1671
Db
1576 CACGGTGGCCATCCAGAGGAGAAATTTCTGGGAGATTTATATGTCCAT---CAACCAAGGT 1632
Qy
1672 GACGTGAGGTGTGCCCTAGCTGGCTGCAGACCTGCTGAGTCCCATCGTTAGCTGTGA 1731
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1633 GAACCCAGCTCCAGTCAGATGGCTCTGAGGTGCTCTGAGTCTCTGAGTCACTGTGCTG 1692
Qy
1732 CCCCTGGCTCTGCTCACCCGCGCAGTCACTCTGCTATGGACCACTGTGGGAGGCC 1791
Db
1693 CTTCCAGACATGATCGTCACTCTCCCTTTGTCATTTGACCATCCGCACTGTGCAGATGTC 1752

Qy 1792 AGCCCTGACAGCTGGAGCCCTGCGCCTCAAAAAGAGAGTGTGTGAGGGCAGCTGGAGGAT 1851
Db
1753 AGTTCTGAGCATTTGGAATATCCATTTAAAGAGAGGACACAGCAGGGCAAAATGGAGGAA 1812
Qy
1852 GTGCTGCACTGGCGGAGGCGCCTCCACCTCTACTACTGCGAGCTGGAGGCCAGT 1911
Db
1813 GTGATGTCAAGTGAAGATGAATCTACATC-----CTGTACTGCTTTTGGACCCCTTT 1866
Qy
1912 GCCTGTACTGCTTTCAACCGAGAGCTGGGCGCTTTTGCCTGTGGAGGAGGCGCTCAGC 1971
Db
1867 GCGTGTACTGTCTCTGAGACAGCTTTGGACCTATGCGCTCACTGGAGAGCCAAATCACA 1926
Qy
1972 GTGGCTGCGCCCAAGCGCTCAAGCTGTCTTGTGTGGCCGGTGGCTGCACTCCCTC 2031
Db
1927 GACTGTGCGCTGAAGCAACTGAAGTGGGGTGTGTGGCTGCACTGCTGTAATCTCCCTG 1986
Qy
2032 GACTACAACTCCGGGTACTGCTGCTGATGACACCCAGATGCACTCAAGGAGGTGGT 2091
Db
1987 GATTCAACTTTGAGAGTTTACTGTGTGGAATATACCCCTTTGTGCAATTCAGGAGGTGTT 2046
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2092 CAGCTGGAAGAGCAGCTGGGGGACAGCTGATCCAGGAGCCACGGGTCTCTGCACTTCAAG 2151
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2047 TCAGATGAAGGCAATCAAGGTGACAGCTCTTGAAGAACCAAAATGCTGCAATTTCAA 2106
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2152 GACAGTTACCAACCTGCGCTTATCATTCACAGATGTGCCAGCTCCCTGTGGAAGT 2211
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2107 GGGAAATACCTTTAGTCTTCAAGATTTCTGCTTTGATATTTCCCTTTCCTCTGAGAAAT 2166
Qy
2212 AGCTCCTTGTGAGCTTACAGGAGATCCCTTTTATCACTCTGGAATGCAACGACGCG 2271
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2167 AAACCAATTCATGCTGCTGCAAGAGTCCCGTTCTCCGCGTGTGTGTCAGTAAACCGCAG 2226
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2272 TACTTGCACTGCACTTCACTTCCCTGGAGCGTGTGAGCCCGCAGCACTAGTGAACCTGGCTGC 2331
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2227 CCCTGCACTGTGCTTCTCCCTGGAGCGTTATACGCCCACTACCAACCGCTGTCTGC 2286
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2332 AGCTGTGGTGTGGAGGTGGAGGGGAGCGGCGAGAGTTCAGCATCAACTTCAACATC 2391
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2287 AAAATCTGATTCGGAGCTCAAGGCCATGAACAGATCCTCCAAGTGCAGACATCAATC 2346
Qy
2392 ACCAAGACACAAAGTTTGTGAGCTGTGGCTCTGAGAGTGAAGCGGGTCCCAAGCC 2451
Db
2347 CTAGAGAGTGAACGAGAAACCATCACTTTCTCGCAAGAGAGACAGCACTTTCCCTGCA 2406
Qy
2452 CTGGTGGGCCCGAGTCCCTTCAAGATCCCTTCCCTCATTTGGCAGAGATAAATTTCCAGC 2511
Db
2407 CAGACTGGGCCCAAGCCCTTCAAAATTCCTACTCTCCATCAGACAGCGGATTTGTGCTACA 2466
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2512 CTGGACCCACCTGTAGGGGGTGGGAGTGGGAGTCTGGCCCGAGAACTCCACCTG 2571
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2467 TTTGATACCCCAATGCCAAGGAGCTGGCAGATGTTAGCAGAGAAAAACAGCATC 2526
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2572 GACAGCATCTCAGCTTCTTTGCTCCAAAGCCCGCCAGCCCAAGCCATGATCTCAACCTG 2631
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2527 AACAGAAATTTATCTTATTTGCTACAAAGTAGCCCATCTGCTCATTTTGAACCTG 2586
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2632 TGGAGGCGCGCACTTCCCAAGCGCAACTCAGCGAGCTGGCTGAGCAGTGGCTGGA 2691
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2587 TGGGAAGCTGTCATCAGCATGATGTGATCTTGACTCCCTGCGCTGTGCGCTTGAAGAG 2646
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2692 CTGGGCCAGCAGACGCTGCGCTCTTCAAGTGTGGGAGCTGAG 2736
Db
2647 ATTGGGAGGACACACAGAACTCTCAACATTTCAAGATCCCGAG 2691

RESULT 9

US-09-969-532-33
; Sequence 33, Application US/09969532
; Patent No. 6777232
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John

; TITLE OF INVENTION: No. 677723261 Human Membrane Proteins and Polynucleotides Encodinf

; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969,532
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 3411
; TYPE: DNA
; ORGANISM: homo sapiens
; US-09-969-532-33

Query Match 17.7%; Score 487; DB 4; Length 3411;
Best Local Similarity 50.9%; Pred. No. 2.9e-99;
Matches 1305; Conservative 0; Mismatches 1230; Indels 30; Gaps 5;

Qy	172	CTTCCCACTTCCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGAACAGCCAGTGTCTG	231
Db	271	CTGCCTCATTTTCAATAGAGGAGCCAGATGATGCTTATATATCAAGAGCAACCTTATTGCA	330
Qy	232	CTTGTGTGCAAGCCGTGCGCCACGAGATCTTCTTCAAGTCAAGGGGAGTGGGTG	291
Db	331	CTCAGGTGCAAGCGAGCCGACGATGAGATATTTCTTCAATGCAACGGCGAGTGGGTC	390
Qy	292	CGCCAGGTGGACACAGCTGATCGAGCGGACGACACAGCGGAGCAGTGGCTGCCACCATG	351
Db	391	CATCAGAACGACGACGCTCTGAAGAGACTCTGACGAGAGCTCAGGTTTGAAGGTCCGC	450
Qy	352	GAGTCCGCAATTAATGTCTCAAGGACGACGAGTGTGAGGAGGTTCGGGGCTGGAGGAATAC	411
Db	451	GAAGTGTTCATCAATGTTACTAGGCAACAGGTGAGGACTTCCATGGCGCCGAGGACTAT	510
Qy	412	TGTTGCCAGTCCGTGGGATGAGTCTCTCGGGACACCAAGAGTCAAGAGGCTTACATC	471
Db	511	TGGTCCAGTGTGTGGGTGGAGCCACTGGGTACCTTCCAGAGCAGGAGGCTCTGTG	570
Qy	472	CGCATGCCAGATTTGCCCAAGAACTTCAGCAGGAGCGCTGGCCCAAGGAGGTGTCCTG	531
Db	571	CGCATGCCATTTTACGGAAAACTTTTGAACAGACCACCAAGGAGGAGGTTCCTCAT	630
Qy	532	GAGCAGGCGATCTGTGCTGCCCTGCGCTCCACCGAGGCGCATCCCTCCAGCGCGAGGTGGAG	591
Db	631	GAAGGCATGATTTGACTGCACTGCGGCCACCGAGGAGTCCCTGTGTCGAGGTGGAA	690
Qy	592	TGGCTCGGAAACGAGGACCTGTGGACCGCTGCTCGAACCCCAATGTATACATCAGCGGG	651
Db	691	TGGCTGAAAAATGAAGAGCCCATTTGACTCTGAAACAGACGAGAACTTTGACACCGAGGCT	750
Qy	652	GAGCAGAGCTGTGTGGTGGACAGGCGCGCTTGTGACACGCGCAACTACACTGCTG	711
Db	751	GACCATTAACCTGATCATCAGGAGGACGCGCTCTGGAGCTCAGGAAATACCTGCA	810
Qy	712	GCCAAGAACATCTGTGGCAGCTGCGCGCAGCGCCTCCGCTGTGTATCTGCTACGTGAAC	771
Db	811	GCAGCCAACTCTGTGCTAAGAGGAGAACTGTGCGCACTGTGTGTGTCTACGTGGAT	870
Qy	772	GGTGGTGTGTGAGTGGACCGAGTGTGCTGTGACGCGCCAGCTGTGTGGCGCGGTG	831
Db	871	GGGAGCTGGGAAGTGTGGAGCGAATGTGCTGCTGTGCACTGAGTGTGCACTGCTG	921
Qy	832	CAGAAACGAGCGGAGCTGCACCAACCGCGCGCTCTCAACGGGGCGCTTCTGTGAG	891
Db	922	CATTGGCGATTCGGGAGTGCAGACCAACCCCGAGAAATGGGGGCAAAATTCGTGAA	981
Qy	892	GGGAGAAATTCAGAAAAACAGCTGTGCGCCACCTGTGCGCCAGTAGACGCGCAGCTGGAGC	951
Db	982	GGTCTAAGCCAGGAATCTGAAACTGCAAGATGGTCTTTGCACTCTTAGATAAAAACCT	1041
Qy	952	CCGTGGAGCAAGTGTGGCGCTGTGGCTGGATGACCACTGCGGAGCGGAGCGGTGATGC	1011
Db	1042	CTTCATGAAATAAAACCCCAAGCATTTGAGAAATGCCAGCGACATTTGCTTGTACTCGGGC	1101

Qy	1012	TCTGACCCAGACCCCGCAACGAGGGAGGAGTGCAGGGCACTGACCTGGACACCCGC	1071
Db	1102	TTGGGTGCTGCGCGTGTGGCGTTTGCAGTCTCTGTGTCAATGGTGTACACCTTTACAGCGG	1161
Qy	1072	AACGTGTACCACTGACCTCTGTGTACACAGTGTCTTCTGGCCCTGAGGAGCTGGCCCTCTAT	1131
Db	1162	AGCCAGAGTGAATATGCGGTGGAGCTCATTTGACTCTTCTGCAATTGACAGGTGGCTTCCA-	1220
Qy	1132	GTGGGCTCATCGCGGTGGCGGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG	1191
Db	1221	--GACCTTTCAACTTCAAAACAGTCCGTCAAGCCCAAGAAATATCATGGAACCAATGATACAA	1278
Qy	1192	TATTGCCGGAAGAGGAGGCGCTGGACTCAGATGTGGCTGACTCGTCTCATTTCTCACCTCA	1251
Db	1279	GAAAAATCTTTGTTAACTCTCCCTGTCTCTGAAATTTCTGCCATGACGACAGATCTGACAGTG	1338
Qy	1252	GGCTTCCAGCCCGTGTAGCATCAAGCCCGCAGCAAGACAGACCAACCCCATCTGCTCACCATC	1311
Db	1339	AGCGGACATACAGCGGACCCATCTGTCTGAGGACCTCTGGACAGGAGCTCATGACA	1398
Qy	1312	CAGCGGACCTCAGCACCAACCAACCACTTACAGGGGAGTCTCTGTCTCCCGGAGGAT	1371
Db	1399	GAGTCTCTCACTCTTTAACTCTTTCGAGCATCAAAAGTGAAGTCCAGAGCTCTGTTATG	1458
Qy	1372	GGGCCAGCCCAAGTTTCCAGCTCACCATGGGCACTGTCTCAGCCCTGGGTGGCGGC	1431
Db	1459	GTTTTCTTGGAGTGTCTGAGAGAGTGAATACACGCGCAAGAAATCAATTCAGGACTTTT	1518
Qy	1432	CGCCACACACTGCACACACAGCTCTCCACCTCTGAGGCGCAGGAGTTCGTCTCCCGCTC	1491
Db	1519	CCCATGGAACCAACACAGCTTTTAGTACAATGCAATCCAGAAATAAATGCTTACATC	1578
Qy	1492	TCCACCCAGAACTACTTTCCCTCTCTGCGCCCGAGGACACAGCAACATGACTATGGGACC	1551
Db	1579	CAAAATCTGTCT-----ATCACTCCCAACAGGACAGAACTGAGGACAACTGTGTGTC	1629
Qy	1552	TTCAACTTCTCGGGGCGCGCTGATGATCCCTTAATACAGGTATCAGCTTCTCATCCCC	1611
Db	1630	TTTGGCCATTTAGGGGCGCGCTTAGTAATGCCAAATACAGGGGTGAGCTTACTCATACCA	1689
Qy	1612	CCAGATGCCATATACCCGAGGGAAGATCTATGAGATCTACCTCAGCTGCAACAGCCCGAA	1671
Db	1690	CACGGTGCATCCAGAGGAGAAATCTTGGAGATTTATATGTTCAT--CAACCAAGGT	1746
Qy	1672	GAGTGAAGTGTGCGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG	1731
Db	1747	GAACCCAGCTCCAGTCAAGTGTGCTGTGAGTGTCTCTGAGTCTCTGAAAGTCACTGTGTG	1806
Qy	1732	CCCCCTGGGTCTGTCTCAGCCGCGCAGTCACTCTGCTATGACCACTCTGCGGAGCC	1791
Db	1807	CTTCCAGACATGATCGTCACT	1866
Qy	1792	AGCCTTGACAGCTGTGAGCTTCCCTCAAAAGACAGTCTGTGCGAGGAGCTGTGGAGGAT	1851
Db	1867	AGTTCTGAGCATTTGGAATATCCATTAAAGAGAGGACACAGCAGGCGCAATTTGGAGGAA	1926
Qy	1852	GTGCTGCACTGTGGCGAGGAGCGCCCTTCCCACTCTATCTGCTGCTGCTGCTGCTGCTG	1911
Db	1927	GTGATGTGATGGAAGATGAATCTATCATC-----CTGTTACTGCTCTTTTGGACCCCTTT	1980
Qy	1912	GCCTGTGCTGTCTTCAACGAGCAGTGGGCGCTTTTGGCTGTGGAGAGGCGCTCTGAGC	1971
Db	1981	GCCTGTGCTGTCTTCTGACAGCTTTTGGAGCTTATGCGCTCACTGTGAGGCAATACCA	2040
Qy	1972	GTGGCTGCGCCCAAGCGCTCAAGCTGTCTTCTGTTTGGCGCGGTGCTGCTGCTGCTGCTG	2031
Db	2041	GACTGTGCGGTGAGCACTGAGGTGGCGGTTTTGGGTGCTGCTGCTGCTGCTGCTGCTG	2100
Qy	2032	GAGTCAACATCCGGGTCTACTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTG	2091
Db	2101	GATTACAACTGAGAGTTTACTGTGTGGACAAATACCCCTTGTGCTTGTGCTTGTGCTTGTG	2160

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QY 2092 CAGCTGGAGAACGAGCTGGGGGACAGCTGATCCAGAGAGCCACGGGTCTCGACTTCAAG 2151
Db 2161 TCAGATGAAGAGGATCAAGGTGACAGCTCTCTGGAAGAACCAAAATTGCTGCAATTTCAA 2220
QY 2152 GACAGTTTACCACAACTCGCCCTATCCATCCAGATGTGCCAGCTCCCTGTGGAGAGT 2211
Db 2221 GGGNATACCTTTAGTCTTCAGATTTCTGTCTTGATATTCCTCCCATTCCTCTGAGNAT 2280
QY 2212 AAGCTCCTTGTACAGTACCAAGAGATCCCTTTTATACATCTGGAATGGACGCGCGG 2271
Db 2281 AAACCAATTCAGCTGCTGCCAGGAAGTCCCGTTCTCCCGCGTGTGGTGCAATAACCGGCG 2340
QY 2272 TACTTGACATGCACCTTCAGCTGGAGCGTGTAGCCCCAGCACTAGTGACCTGGCTGTC 2331
Db 2341 CCCTTGACATGTGCTTCTCCCTGGAGCGTTATACGCCCACTACCAACCCAGCTGTCTGTC 2400
QY 2332 AAGCTGTGGCTGTGGCAGGTGGAGGCGACGGGACAGAGCTTCAGCAATCAACTTCAACATC 2391
Db 2401 AAAATCTGCATTCGGCAGCTCAAGGCCATGAACAGATCTCCNAGTGCAAGATCAATC 2460
QY 2392 ACCAAGGACACAAGGTTTGTGAGTGTCTGGCTCTGGAGAGTGAAGCGGGTCCAGACC 2451
Db 2461 CTAGAGAGTCAAGAGAAAACATCACTTTCTTCGCAACAAGAGGACAGCACTTTCCCTGCA 2520
QY 2452 CTGGTGGCCCCAGTGCCTTCAGATCCCTTCTCATTCGGCAGAGATAAATTTCCAGC 2511
Db 2521 CAGACTGGCCCCAAGCCCTTCAAAATTCCTTCTCCATCAGACAGCGGATTTGTGTACA 2580
QY 2512 CTGGACCCACCTGTAGCGGGGTGCCGACTGGCGGACTCTGGCCAGAAAACCTCCACTG 2571
Db 2581 TTTGATACCCCAATGCCAAGGCAGGACTTGGCAGATGTAGCAGAAAACAGCATC 2640
QY 2572 GACAGCCATCTAGCTTTCTTGGCTTCCAAGCCAGCCCCACAGCATGATCTCTCAACCTG 2631
Db 2641 AACAGGAATTTATCTTATTTTCGTTACACAAAGTAGCCCATCTGTGTCAATTTTGAACCTG 2700
QY 2632 TGGGAGCGCGGACTTCCCAAGCAACCTCAGCAGCTGCTGCAGCAGTGCAGCTGGA 2691
Db 2701 TGGGAAGCTCGTATCAGCATGATGTGTGATCTTGACTTCCCTGGCTGTGCCCTTGAAGAG 2760
QY 2692 CTGGCCAGCAGACGCTGGCTCTTCCACAGTGTGGAGGCTGAG 2736
Db 2761 ATGGGAGGACACACAGAACTCTCAACATTTCAAGATCCCGAG 2805

RESULT 10
US-09-969-532-11
; Sequence 11, Application US/09969532
; Patent No. 6777232
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides Encodir
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969,532
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 2001-10-02
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 2703
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-969-532-11

Query Match 17.0%; Score 467; DB 4; Length 2703;
Best Local Similarity 51.0%; Pred. No. 8.1e-95;
Matches 1307; Conservative 0; Mismatches 1195; Indels 63; Gaps 6;

QY 172 CTTCCCCACTCTCTGGTGGAGCCGAGGATGTGTACATCGTCAAGAACAAAGCCAGTGTCTG 231
Db 157 CTGCTCATTTATAGAGGAGCCAGATGATGCTTATATTATCAAGAGCAACCCCTATTGCA 216
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QY 232 CTTGTGTGCAAGCCCGTGTGCCCGCCACGCAAGATCTTCTTCAAGTGCACCGGGAGTGGGTG 291
Db 217 CTGAGGTGCAAGCGAGGGCCAGCCATGACAGATATTTCTTCAATGCAACCGCGAGTGGGTG 276
QY 292 CGCAGGTGGACCACTGTATCGAGCGCAGACACAGCGGAGCAGTGGGCTGCCACCATG 351
Db 277 CATCAGAACGAGCAGCTCTCTGAAGAGACTCTCGACGAGAGCTCAGGTTTGAAGGTCCGC 336
QY 352 GAGGTCGCGATTAATGTCTCAAGGACAGAGGTTCAGAAAGGTGTTCGGGCTTGGAGGAATAC 411
Db 337 GAGTGTTCATCAATGTACTAGCAACAGGTGTGAGACTTCCATGGCCCCGAGGACTAT 396
QY 412 TGTGTGACAGTGTGTCATGAGTCTCTCGGGCACCACAGAGTCAAGAGGCTTATATC 471
Db 397 TGTGTGACAGTGTGTGGGTGGAGCCACTGGGTACCTTCCAAGAGCAGGAGGCTCTGTG 456
QY 472 CGCATAGCCAGATTTCGCAAGAACTTCGAGCAGAGCGCTGCCAGGAGGTGTCCCTG 531
Db 457 CGCATAGCCATTTTACGGAATACTTTTGAAACAAGACCCACAAGAAAGGAGGTTCCTCAT 516
QY 532 GAGCAGAGGATCTGTGTGCTTCCAGCCGAGGAGTCCCTCCAGCCGAGGTGGAG 591
Db 517 GAAGGATGATTTGCTGCACTGCGCCACACAGAGGAGTCTCTGCTGCCGAGGTGGAA 576
QY 592 TGGCTCCGGAAACGAGGACCTGTGTGACCCGCTCCCTGGAACCCCAATGTATATCAGCCGG 651
Db 577 TGGCTGAAATAATGAAGAGCCATTGACTCTGAAACAAGACGAGAACTTGAACACGAGGCT 636
QY 652 GAGCAGAGCTGTGTGGCAGAGGCGCTTGTGACACGCGCAACTACACTCGCTG 711
Db 637 GACATAACCTGATCATCAGGAGGACAGGCTCTCGGACTCAGGAAATTAACCTGATG 696
QY 712 GCCAAGAACATCTGTGACAGTGTGCGCAGCGCTCCGCTGCTGTCTATCTGCTACGTGAAC 771
Db 697 GCAGCCAAACATCTGTGCTAAGAGGAGAGCGCTGTGCGCCACTCTGTGTGGTCTACGTGAT 756
QY 772 GGTGGGTGTGAGTGTGACCGAGTGTGCTGTGACGCGCCAGCTGTGTGGGCGGGCTGG 831
Db 757 GGAGCTGGGAAGTGTGGAGCGAATGTGCTCGTCTGCAGTCCAGAGTGTG-----AA 807
QY 832 CAGAAACGGAGCGGAGCTGCACCAACCGGGCGCTCTCAACGGGGCGCTTTCTGTGAG 891
Db 808 CATTTGGGATCGGGAGTGCACAGCACACCCCGAGAAATGGGGGCAAAATTTCTGTGA 867
QY 892 GGGCAGAAATGCCAGAAAACAGCTTCGGCCACCTGTGTGCCATAGACGCGCAGCTGAGC 951
Db 868 GGTCTAAGCCAGGAATCTGAAAACTGCACAGATGTGCTTTTGCATCTCTAGGCAATTGAAAT 927
QY 952 CGGTGGAGCAAGTGTGTGGCTGTGGCTGTGACCTGCAACCCACTGGCGGAGCCGTGAGTGC 1011
Db 928 GCAGCGACATGCTTTGTACTCGGGCTTGG-----GTGC 962
QY 1012 TCTGACCCAGCACCCCGCAACGGAGGGAGGAGTGCAGGGCACTGACCTTGGACACCCGC 1071
Db 963 TGGGTGTGGCGCTTGTGAGTCTGTGCTCATTTGTGTGTCACTTACAGACGGA----- 1015
QY 1072 AACTGTACCAAGTACCTCTGTGTACAGTGTCTTGTGGCCCTGAGGAGCTGGGCCCTTAT 1131
Db 1016 ---GCCAGAGTGAATATGCGGTGAGCGTCAATGACTCTTCTGCAATTTGACAGGTGGCTTC 1071
QY 1132 GTGGGCTCATCGCGTGGCGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 1191
Db 1072 CAGACCTTCAACTTCAAAAACAGTCCCTCAAGCCAGAATAATCATGGAACCTAAATGATACAA 1131
QY 1192 TATTGCGGAAGAAAGGAGGGCTGGACTCAGATGTGGCTGACTGCTCCTCATTTCTCACCTCA 1251
Db 1132 GAAAAATCTTTTGGTAACCTTCTGCTCTCTGAAATCTTGCCATGCGAGCCAGATCTGACAGTG 1191
QY 1252 GGCTTCCAGCCCTGTAGACTCAAGCCCGAGCAAGCCCAATCTGCTTCAACCATC 1311
Db 1192 AGCCGGACATACAGCGGAGCCCATCTGTCTGAGGAGCCCTCTGAGCAAGGAGCTCATGACA 1251
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QY 1312 CAGCCGACCTCAGACCCACACACACCTACAGGGCAGTCTCTGTCCCGCCGAGGAT 1371
Db 1252 GAGTCTCTCACTTTTAACCTTTTTCGAGACATCAAGTGAAGTCCAGAGCTCGTTTCATG 1311
QY 1372 GGGCCAGCCCAAGTTCCAGCTCACMAATGGGCACCTGCTCAGCCCGCTGGTGGCGGC 1431
Db 1312 GTTTCCCTGGAGTGTCTGAGAGAGCTGAGTACACACGGCAAGATCATTCAGGACTTTT 1371
QY 1432 CGCCACACATGACACACAGCTCTCCACCTCTCAGAGCCGAGGAGTTCTGCTCCCGCTC 1491
Db 1372 CCCATGGAACAACACAGCTTTAGTACAATGATCCAGAAATAAATGCCCTATCATC 1431
QY 1492 TCCACCCAGAACTACTTCCGCTCCCTGCCCGAGGACACAGCAACATGACCTATGGACC 1551
Db 1432 CAAAATCTGTC-----ATCACTCCCAAGGACAGAACTGAGGACAACTGGTGTG 1482
QY 1552 TTCAACTCTCCGGGGCGGCTGATGATCCCTTAATACAGGTATCAGGCTCTCTCATCCC 1611
Db 1483 TTTGGCCATTTAGGGGGCGCTTAGTAAATGCCAAATACAGGGGTGAGCTTACTCATACCA 1542
QY 1612 CCAGATGCCATACCCCGAGGGAAGATCTATGAGATCTACCTCAGCTGCAACAGCCGAA 1671
Db 1543 CAGGTGCCATCCAGAGGAGATTTCTGGAGATTTATATGTCAT---CAACCAAGT 1599
QY 1672 GACGTGAGTTGCCCTAGCTGGCTGTGAGACCTGCTGATCCCATCGTTAGCTGTGA 1731
Db 1600 GAACCCAGCTCCAGTCAGATGGCTCTGAGGTGCTCTGAGTCTCTGAAGTCACCTGTGGT 1659
QY 1732 CCCCCTGGCTCTGCTCACCCGGCCAGTCACTCTGGCTATGACCACTGTGGGGAGCCC 1791
Db 1660 CTTCCAGACATGATCGTCAACCACTCCCTTTGCAATTGACCATCCGCACTGTGCAATGTC 1719
QY 1792 AGCCCTCAGAGCTGAGCTGCGCTCTCAAAAGCAGTCTGCGAGGCGAGCTGGAGGAT 1851
Db 1720 AGTTCTGAGCATTTGGAATATCCATTTAAGAAGAGGACACAGAGGGCAANTGGAGAA 1779
QY 1852 GTGCTGACCTGGCGAGGAGCGCCCTCCACCTCTACTACTGCCAGCTGGAGGCCAGT 1911
Db 1780 GTGATGTCAGTGAAGATGAATCTACATC-----CTGTTACTGCTTTTGGACCCCTTT 1833
QY 1912 GCCTGTACTGTTTACCGAGCAGCTGGCGCGCTTTGGCCCTGTGGAGAGGCCCTCAGC 1971
Db 1834 CGGTGTATGTCTCTGAGCAGCTTTGGGACCTATGCTCTCACTGGAGAGCCAAATCACA 1893
QY 1972 GTGCTCCGCGCAAGCGCTCAAGCTCTTCTGCTTTGCGCGGTGCTGCACCTCCCTC 2031
Db 1894 GACTGTCCGTGAAGCAACTGAAGTGGCGTTTTTGGCTGCACTGTCTGTAATCCCTG 1953
QY 2032 GAGTACAAACATCCGGGTCTACTGCTGCAATGACACCCACGATGCACTCAAGGAGGTGGT 2091
Db 1954 GATTACAACTTGAGAGTTTACTGTGTGCAATAATACCCCTTGTGCAATTCAGGAAGTGT 2013
QY 2092 CAGCTGAGAAGCAGCTGGGGGACAGCTGATCAGAGGACCAAGGCTCTGCACTTCAAG 2151
Db 2014 TCAGATGAAGAGGCATCAAGGTGGACAGCTCTCGTGAAGAACCAAAATTTGCTGCAATTC 2073
QY 2152 GACAGTTTACCACACCTCGCGCTATCCATCCAGCTGTGCCAGCTCCCTGTGGAAGT 2211
Db 2074 GGGATACCTTTAGCTTTTCAATTTCTGCTTGTATTTCCCAATTTCCCTGTGAGAT 2133
QY 2212 AAGCTCTTGTACGTACACAGGAGATCCCTTTTATCACATCTGGAATGGCACGCGG 2271
Db 2134 AAACCATTCAGCTGCCAGGAAGTCCCGTTCTCCCGCGTGTGTGTCAGTAAACGGCAG 2193
QY 2272 TACTTGACCTGCATCTTCACTGGAGGTGTAGCCCCAGCACTAGTGACCTGGCCCTGC 2331
Db 2194 CCCCCTGACCTGTGCTCTTCTCCCTGGAGGTTTATACGCCCACTACCAACCGAGCTGTCTGC 2253
QY 2332 AAGCTGTGGGTGTGCGAGGTGGGGCGAGGGCAGAGCTTTCAGCATCAACTTCAACATC 2391
Db 2254 AAAATCTGCATTCGGCAGCTCAAGGGCCATGAACAGATCTCTTCAAGTGCAGACATCAATC 2313
QY 2392 ACCAAGGACACAAGGTTTGTGAGCTGTGCTGTGAGAGTGAAGCGGGGTCCACGCC 2451
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Db 2314 CTAGAGAGTGAACGAGAAACCATCCTTTCTGCAACAAGAGGACAGACACTTTTCCCTGCA 2373
QY 2452 CTGGTGGGCCCGAGTGGCTTCAAGATCCCTTCTCTATTCGGCAGAAGATAAATTTCCAGC 2511
Db 2374 CAGACTGGCCCCCAAGCCTTTCAAAATTTCCCTACTCCATCAGACAGCGGATTTGTGCTACA 2433
QY 2512 CTGGACCCACCTGTAGCGGGGTGCGACTCTGGCGGACTCTGGCCAGAAACTCCACCTG 2571
Db 2434 TTTGATACCCCAATGCCAAAGGCAAGGACTGGCAGATGTTAGCACAGAAAAACAGATC 2493
QY 2572 GACAGCCATCTCAGCTTTTGTCTCAAGCCAGCCAGCCCAAGCATGATCTCTCAACTG 2631
Db 2494 AACAGGAATTTATCTTATTTATTCGCTACACAAAGTAGCCCATCTGCTGTCAATTTTGAACCTG 2553
QY 2632 TGGGAGCGGGCAGCTTCCCAACGCAACCTCAGCAGCTGGCTGACAGAGTGGCTTGA 2691
Db 2554 TGGGAAGCTCGTCAACAGCATGATGATCTTGAATCTCCCTGGCTGTGGCTTTGAAGAG 2613
QY 2692 CTGGGCCAGCAGACGCTGGCTCTTTCACAGTGTGGAGGCTGAG 2736
Db 2614 ATTGGGAGGACACACAGAACTCTCAAACTTTTCAGATCCCGAG 2658
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RESULT 11

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US-09-969-532-13
; Sequence 13, Application US/09969532
; Patent No. 677232
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; TITLE OF INVENTION: No. 677232el Human Membrane Proteins and Polynucleotides Encodin
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969,532
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-969-532-13
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Query Match 16.7%; Score 460.2; DB 4; Length 2694;
Best local Similarity 51.94; Pred. No. 2.7e-93;
Matches 1330; Conservative 0; Mismatches 1163; Indels 72; Gaps 10;
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QY 172 CTTCCCCACCTTCTGTTGGAGCCCGAGGATGTGTACATCGTCAAGAAACAAGCCAGTGTG 231
Db 157 CTGCTCATTTTCATAGAGGAGCCAGATGCTTATATTATCAAGAGCAACCTTATTGCA 216
QY 232 CTTGTGTGAAGCCGCTGCCCCGACGAGATCTTTCTCAAGTGCACCGGGAGTGGGTG 291
Db 217 CTCAGGTGCAAGCGAGGCCAGCCATGTCAGATATTTCTCAATGCAACCGCGAGTGGT 276
QY 292 CGCCAGGTGACCACTGATCTGAGCCGACGACAGCGGAGCAGTGGCTGCCACCCTG 351
Db 277 CATCAGAACGACGACGCTCTGGAAGAGACTCTGACGAGAGCTCAGGTTTGAAGTCCGC 336
QY 352 GAGTCTCGCATTAATGTCTCAAGCGAGCAGGTGCGAAGGTGTTTCGGCTGGAGGAATAC 411
Db 337 GAAGTGTTCATCAATGTTACTAGCAACAGTGGAGACTTCCATGGCCCCGAGGACTAT 396
QY 412 TGTGCCAGTGTGGCATGGAGCTCTCTCGGGCACCAACCAAGAGTCAAGAGGCTCATATC 471
Db 397 TGGTGCAGTGTGTGGCTGGAGCCACCTGGGTACCTTCCAAAGAGCAGGAAGGCTCTGTG 456
QY 472 CGCATAGCCAGATTTGCGCAAGAACTTCGAGCAGAGCCGCTGGCCAGAGGAGTGTCTCTG 531
Db 457 CGCATAGCTTATTTACGGAAAACTTTTGAACAAGACCCACAGAGGAGGAAGTTCCTCAT 516
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Db 2605 ATTGGAGGACACACGAAACTCTCAACATTTTCAGAAATCCAG 2649
RESULT 12
US-09-969-532-15
; Sequence 15, Application US/09969532
; Patent No. 6777232
; GENERAL INFORMATION:
; APPLICANT: Scoville, John
; APPLICANT: Walke, D. Wade
; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides Encodin
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969,532
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 2661
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-969-532-15
Query Match 16.0%; Score 439.8; DB 4; Length 2661;
Best Local Similarity 51.2%; Pred. No. 9.9e-89;
Matches 1313; Conservative 0; Mismatches 1147; Indels 105; Gaps 8;
Qy 172 CTTCCCCACTTCTGTTGGAGCCCGAGATGTGTACATCGTCAAGAACAGCCAGTCTG 231
Db 157 CTGCCTCATTTATAGAGGAGCCAGATGTGTATATATCAAGAGCAACCCCTATTGCA 216
Qy 232 CTTGTGTGCAAGGCGGTGCGCCGACGAGATCTTCTCAAGTGCACGCGGAGTGGTG 291
Db 217 CTAGGTGCAAGGAGCGCCAGCCGATGAGATATCTTCAATGCAACGCGAGTGGTC 276
Qy 292 CGCCAGGTGACACGCTGTATGAGCGGACGACAGACGAGGAGTGGGCTGCCACCATG 351
Db 277 CATCAGAACGAGCAGCTCTCTGAAGACTCTGACGAGAGCTCAGGTCTTGAAGTCCGC 336
Qy 352 GAGTCCGCATTATGTCTCAAGCAGCAGGTGAGAGGTGTCGGGCTGGAGGAATAC 411
Db 337 GAAGTGTTCATCATATGTTACTTAGGCAACAGGTGAGGACTTCCATGGGCGCCGAGGACTAT 396
Qy 412 TGGTCCAGTGTGCGGATGAGCTCTCGGGACACCAAGAGTCAAGAGGCTACATC 471
Db 397 TGGTCCAGTGTGCGGAGTGGAGCCACTGGTACCTCCAGAGCAGAGGCTCTGTG 456
Qy 472 CGCATAGCCAGATTGCGCAAGAACTTCAGCAGAGAGCGCTGGCCAGAGGAGTGTCCCTG 531
Db 457 CGCATAGCTATTATACGGNAAAACCTTTGAAACAGACCCCAAGGAGGAGTTCCTCAT 516
Qy 532 GAGCAGGACATCGTGTCCCTGCGCTCCAGCGGACCAAGAGGAGTTCCTCAGCGAGTGGAG 591
Db 517 GAAGGATGATGTTGACTGCTGCGCCCAAGAGGAGTTCCTGCTGCGGAGGTGGAA 576
Qy 592 TGGCTCCGGAACGAGGACCTGTGTGACCCGCTCGGACCCCAATGTATACATCAACCGG 651
Db 577 TGGCTGAAAATGAGAGCCATTGACTCTGAACAGACGAGAACTTGACACAGGGCT 636
Qy 652 GAGCAGCTGTGTGTCGACAGGCGCGCTTGTCTGACACGCGCAACTACACTGCGTG 711
Db 637 GACCATAACCTGATCATCAGGACGACGCTCTCGGACTCAGGAAATTAACCTGCATG 696
Qy 712 GCCAAGAACATCGTGGCAGCTGCGCGGAGCGCTCCGCTGTGTATCATCGTGTGAAC 771
Db 697 GCAGCCAACTCGTGGGTAAAGAGAGAGGCTGTGCGCCACTGTGTGGTCTACGTGGAT 756
Qy 772 GGTGGGTGTGACGTGGAACGAGTGTCTGCTGACAGCGCAGCTGTGGGCGGCTGG 831
Db 757 GGGAGCTGGGAGTGTGAGGAAATGTTCTGCTGTCAGTCCAGAGTGTG-----AA 807
Qy 832 CAGAAACGAGCGGAGCTGCACCAACCCGCGCTCTCTCAACGCGGCGCTTTCTGTGAG 891
Db 808 CATTTGCGGATCCGGAGTGCACAGCACCAACCCCGAGAAATGGGGGCAAAATCTCTGTGA 867
Qy 892 GGGCAGAAATGTCCAGAAAAACAGCTGCGCCACCCCTGTGCCAGTAGAGCGAGCTGGAGC 951
Db 868 GGTCTAAGCCAGGAAATCTGAAAACTGCACAGATGGTCTTTTGCATCTCTAGGCAATGAGA 927
Qy 952 CCGTGGAGCAAGTGTGCGGCTGTGGGCTGGAAGTGCACCCACCTGGCGGAGCCGTGAGTGC 1011
Db 928 GCCAGCGACATTGCTTTGTACTCGGCTTG----- 958
Qy 1012 TCTGACCCAGACACCCCGCAACGAGGAGGAGTGCAGGGGACATGACTGTGACACCGC 1071
Db 959 -----GTGCTGCGCTGCTGGCCGCTGAGTCTGAGTCAATTTGCTGCTCACTCTTTAACCCCTT 1002
Qy 1072 AACTGTACCATGACCTCTGTGTACACAGTCTTCTGGCCCTGAGGAGTGGCCCTCTAT 1131
Db 1003 CTTTACAGACGAGCCAGAGTACTATGGCGTGGACGTCAATGACTCTTCTGCAATGACA 1062
Qy 1132 GTGGGCTCATCGCGGTGGCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1191
Db 1063 GGTGGCTTCCAGACCTTCAACTTCAAAACAGTCCGTCAAGGTAACTCCCTGCTCTGAT 1122
Qy 1192 TATTGCCGGAAGAGGAGGCTGGACTCAGATGTGGTGTGACTGTGCTCAATTTCTCACCTCA 1251
Db 1123 TCTGCCATGCA-----GCCAGATCTGACAGTGGAGCGGACATACAGCGGACCCATCT 1174
Qy 1252 GGTTCAGGCGCTCAGCATCAAGCCCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1311
Db 1175 GTCTGAGGAGCCCTCTGGACAAGG---AGCTCATGACAGAGTCTCTCACTCTTTAACCCCTT 1231
Qy 1312 CAGCGGACCTCAGCAGCACCAACCACTACAGGGGAGTCTCTGCTGCCCGGACAGGAT 1371
Db 1232 TGTGGACATCAAGTGAAGTCCAGAGCTCGTTCATGGTTTCCCTGGGAGTGTCTGAGA 1291
Qy 1372 GGGCCAGACCCCAAGTTCAGCTCAACCAATGGGCACTGTGCTGAGCCCCCTGGGTGGCGGC 1431
Db 1292 GAGTGTAGTACCAGCGCAAGAAATCATTTCCAGGACTTTT----- 1329
Qy 1432 CGCCACACTGCGACACACAGCTCTCCACCTCTGAGGCGGAGGAGTTCGTCTCCCGCTC 1491
Db 1330 CCCATGGAACAAACACAGCTTTAGTACAATGATCCAGAAATAAAATAGCCCTATCATC 1389
Qy 1492 TCCACCCAGAACTACTTCCGCTCCCTGCGCCGAGGACACAGCAACATGACTATGGAGC 1551
Db 1390 CAAAATCTGT-----CATCACTCCCACAGGACAACTGAGGACAACTGGTGTG 1440
Qy 1552 TTCAACTTCTCGGGGCGCGCTGATGATCCCTTAATAACAGGTATCAGCTCTCTCATCCCC 1611
Db 1441 TTTGGCCATTTAGGGGGCGCTTAGTAAATGCCAAATACAGGGGTGAGCTTACTCATACCA 1500
Qy 1612 CCAGATGCCATACCCCGAGGAGATCTATGAGATCTACCTCAGCTCAGCTGCAACGCCGAA 1671
Db 1501 CACGGTGCCATCCAGAGGAGAAATCTTGGGAGATTTATATGTCAT---CAACCAAGGT 1557
Qy 1672 GAGTGTAGGTTGCGCTCTAGCTGTGACACCTGCTGAGTCCCATCTGTTAGTGTGGA 1731
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Db 1618 CTTCCAGACATGATCGTCAACCTCTTGTGATGAGTACCATCCGCACTGTGAGATGTC 1677
Qy 1792 AGCCCTGACAGCTGGAGCTCGGCTCAAAAGCAGTCTGTCGAGGAGGAGTGGAGGAT 1851
Db 1678 AGTTCTGAGCATTTGGAATATCCATTTAAAGAGAGGACACAGCAGGGGCAATGGAGGAA 1737
Qy 1852 GTCTGCACTGCGGAGGAGGCGCTCCACCTCTACTACTCTGAGCTGGAGGCGAGT 1911
Db 1738 GTGATGTGAGTGAAGATGATCTATCATC-----CTGTTACTGCTTTTGGACCCCTTT 1791
Qy 1912 GCCTGTGTCTTCTCCAGAGAGTGGGCGCTTTTGCCTGTGTGGAGAGGCGCTCAGC 1971
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Db 1792 GCGTGTCTATGCTCTCGGACAGCTTTGGGACCTATGCGCTCACTGGAGAGCCAAATCACA 1851
Qy 1792 GTGGCTGCGCCCAAGCGCCCTCAAGCTGCTTCTGTTTGGCGCGGTGGCTGCACCTCCCTC 2031
Db 1852 GACTGTGCGGTGAAGCAACTGAAGTGGCGGTTTGGCTGCTGCTCTTAACCTCCCTG 1911
Qy 2032 GAGTACAACTCCGGTCTACTGCTGCTGCTGATGACACCCACATGCACTCAAGGAGGTGGT 2091
Db 1912 GATTAACTTTGAGAGTTTACTGTGTGGACAAATACCCCTTGTGCATTTTCAGGAAGTGGT 1971
Qy 2092 CAGCTGAGAGACAGCTGGGGGACAGCTGATCAGGAGCACGGGTCTGCACTTCAAG 2151
Db 1972 TCAGATGAAGGCATCAAGTGGACAGCTCTGGAGAACAAATTTGCTGCAATTCAAA 2031
Qy 2152 GACAGTTTACCAACCTCGCCCTATCATCCAGATGTGCCAGCTCCCTGTGTGGAAGT 2211
Db 2032 GGGAAATACCTTTAGTCTTCAGATTTCTGTGCTTGTGATATCCCCATTCCTCTGGAAT 2091
Qy 2212 AAGCTCCTTGTACGCTACCAAGGATCCCTTTTATCAGATCTGGAATGGACGACGG 2271
Db 2092 AAACCATCTAGCTGCTGCCAGGAAGTCCCGTCTCCGCGTGTGGTGCAGTAACCGGAG 2151
Qy 2272 TACTTGCACTGCACCTTTCACCTCGGAGCGTGTGAGCCCGACAGCACTAGTACCTGGCTGC 2331
Db 2152 CCCTGCACTGCTTCTCCCTGGAGGTTATAGCCCACTACCAACCCAGCTGTCTGC 2211
Qy 2332 AAGCTGTGGGTGTGGCAGGTGGAGGGGACGGGAGAGCTTTCAGCATCAACTTCAACATC 2391
Db 2212 AAAATCTGCATTCGGCAGCTCAAAGGCGCATGAACAGATCTCCAAAGTGACAGATCAATC 2271
Qy 2392 ACCAAGGACACAGGTTTGTGAGCTGCTGGCTCTGGAGAGTGAAGGGGGTCCAGCC 2451
Db 2272 CTAGAGAGTGAACAGAAAACATCACTTTCTTGCGACAGAGCAGCACTTTCCTCGCA 2331
Qy 2452 CTGTGCGGCCCGAGTGCTTCAAGATCCCTTCTCATTCGGCAGAGATAATTTCCAGC 2511
Db 2332 CAGACTGCGCCCAAGGCTTCAAAATTCCTACTCCATCAGACAGCGGATTTGTGTACA 2391
Qy 2512 CTGACCCACCTGTAGCGGGGTGCGCACTGGGGAGCTTGGCCGAGAACTTCCAGCTG 2571
Db 2392 TTTGATACCCCAATGCAAGGCAAGCACTGGCAGATGTTAGCAGAAAAACAGCATC 2451
Qy 2572 GACAGCCATCTCAGCTTCTTGTGCTCCAGCCAGCCCGACAGCATGATCTCAACCTG 2631
Db 2452 AACAGGAATTTATCTTATTTGCTACACAAAGTAGCCCATCTGTGTCTTTTGAACCTG 2511
Qy 2632 TGGAGGCGGGCACTTCCCAAGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCTGGA 2691
Db 2512 TGGGAAGCTCGTCATCAGCATGATGGTGATCTTGACTCCCTGGCTGTGCCCTTGAAGAG 2571
Qy 2692 CTGGCCAGCCAGACGCTGGCTCTTTCACAGTGTGGAGGCTGAG 2736
Db 2572 ATTGGAGGACACACAGAAACTCTCAAACTTTCAGAAATCCCGAG 2616

RESULT 13
US-09-471-276-345
; Sequence 345, Application US/09471276
; Patent No. 6822072
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J. B.
; APPLICANT: Duclert A.
; APPLICANT: Giordano, J. Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: GENSET.025CP1
; CURRENT APPLICATION NUMBER: US/09/471.276
; CURRENT FILING DATE: 1999-12-21
; EARLIER APPLICATION NUMBER: 09/057, 719
; EARLIER FILING DATE: 1998-04-09
; EARLIER APPLICATION NUMBER: 09/069, 047
; EARLIER FILING DATE: 1998-04-28
; EARLIER APPLICATION NUMBER: PCT/IB99/00712

; EARLIER FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 1622
; SOFTWARE: Patent.pm
; SEQ ID NO 345
; LENGTH: 349
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 207..347
; NAME/KEY: sig peptide
; LOCATION: 207-278
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: score 5.40000009536743
; OTHER INFORMATION: seq SCCLSSSSSFIAG/RR
US-09-471-276-345

Query Match 11.7%; Score 323; DB 4; Length 349;
Best Local Similarity 98.8%; Pred.No.6.9e-63;
Matches 335; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

Qy 934 GTAGCGGAGCTGGAGCCCGTGGAGCAAGTGGTGGGCTGTGGGCTGGAGTGCACCCAC 993
Db 12 GTGAGCGGAGCTGGAGCCCGTGGAGCAAGTGGTGGGCTGTGGGCTGGAGTGCACCCAC 71
Qy 994 TGGCGAGCGGTGAGTGTCTGTACCCAGCACCCCGCAACGGAGGGAGGAGTCCAGGGC 1053
Db 72 TGGCGGA-CCGTGAGTGTCTGTACCCAGCACCCCGCAACGGAGGGAGGAGTCCAGGGC 130
Qy 1054 ACTGAGCTGGACACCCGCAACTGTACAGTAGCTCTGTGTACACAGTGTCTTGGGCCCT 1113
Db 131 ACTGAGCTGGACACCCGCAACTGTACAGTAGCTCTGTGTACACAGTGTCTTGGGCCCT 190
Qy 1114 GAGGAGCTGGGCCCTTATGTGGGCCCTCATCGCGTGGGCCCTTGTCTGTGCTGCTG 1173
Db 191 GAGGAGCTGGGCCCTTATGTGGGCCCTCATCGCGTGGGCCCTTGTCTGTGCTGCTG 250
Qy 1174 CTGTCTCTCATCTCTCTTTATTGCGGAGAGAGGAGGGCTGGAGTGCAGTGTGGCTGAC 1233
Db 251 CTGTCTCTCATCTCTCTTTATTGCGGAGAGAGGAGGGCTGGAGTGCAGTGTGGCTGAC 310
Qy 1234 TCGTCACTTCTCACTCAGCTTCCAGCCCGTCAGCATC 1272
Db 311 TCGTCACTTCTCACTCAGCTTCCAGCCCGTCAGCATC 349

RESULT 14
US-09-969-532-31
; Sequence 31, Application US/09969532
; Patent No. 677232
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides Encoding
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969,532
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-969-532-31

Query Match 10.7%; Score 293.2; DB 4; Length 1968;
Best Local Similarity 53.7%; Pred.No.5.8e-56;
Matches 657; Conservative 0; Mismatches 558; Indels 9; Gaps 2;

Qy 1513 TCCTGCCCCGAGGACCAACAGCAATGAGCTATGGACCTTCAACTTCTCGGGGCGCG 1572

Db 709 TCACTCCCCACAGGACAGAACTGAGGACAACTGGTGTCTTTGGCCATTTAGGGGGCGC 768
Qy 1573 CTGATGATCCCTTAATACAGGTATCAGCTCTCTATCCCGCCAGATGCCATACCCGAGGG 1632
Db 769 TTAGTAATGCACAAATACAGGGGTGAGCTTACTCATACACAGGTGCCATCCAGAGGAG 828
Qy 1633 AAGATCTATGAGATCTACCTCAGCTGCACAAAGCCGGAAGACGTGAGGTTGCCCTAGCT 1692
Db 829 AATTTCTTGGGAGATTTATATGTCTCATCAACAGGTGAACCC---AGCCTCCAGTCAGAT 885
Qy 1693 GGCTGTGAGACCCCTGCTGAGTCCATCTGTTAGCTGTGGACCCCTGCGCTCTGCTCAAC 1752
Db 886 GGCTGTGAGTGTCTCTGAGTCTGAACTGCTGAGTCACTGCTGCTCTCCAGACATGATGTCACC 945
Qy 1753 CGGCAGTCTCTGCTGATGACCACTGTGGGAGCCAGCCTGACAGCTGACAGCTGAGCCTG 1812
Db 946 ACTCCCTTTGCAATGACATCCCGCATGTGCAGATGTGATCTGAGCATTTGAAATATC 1005
Qy 1813 CGCTTCAAAAGCAGTCTGCGAGGCGAGCTGGGAGGATGTCTGCACTTGGCGGAGGAG 1872
Db 1006 CATTTAAAGAGGACACAGCAGGCGCAATGGGAGGATGTCTCAGTGGGAAGATGAA 1065
Qy 1873 GCGCCTCCACCTCTACTACTGCTGAGCTGAGGCGCAGTGTCTGCTACGCTTCCACCGAG 1932
Db 1066 TCTACATC-----CTGTACTGCTTTTGGACCCCTTTGCTGTCTCATGTCTCTGCTGAC 1119
Qy 1933 CAGCTGGCGCGCTTTGCTGCTGGGAGAGCCCTCAGCTGCTGCTGCGCCAGAGCGCTC 1992
Db 1120 AGCTTTGGGACCTATGCGCTCACTGGAGAGCCATCAACAGCTGTGCGCGTGAAGCAACTG 1179
Qy 1993 AAGCTGCTTCTGTTTGGCGCGGTGCTGCACTCTCCCTCGAGTACAACTCCGGGTCTAC 2052
Db 1180 AAGTGGCGGTTTGGCTGATGCTCTGTAACTCTCTGATTAACATTTGAGAGTTTAC 1239
Qy 2053 TGGCTGATGACACCCACGATGCACTCAAGAGGTGTGTGAGCTGTGAGAGAGCTGGGG 2112
Db 1240 TGTGTGACAAATACCCCTTGTGCAATTTTCAAGAGTGTGTTTTCAGATGAAGGCATCAAGGT 1299
Qy 2113 GGACAGCTGATCCAGGAGCAGCGGCTCTGCACTTCAAGGACAGTTTACCAACCTCGCG 2172
Db 1300 GGAAGCTCTGTGAAGAACAAATTTGCTGATTTCAAGGGATTAACCTTTAGTCTTTAG 1359
Qy 2173 CTATCCATCCAGATGTGCCAGCTCCCTGTGGAAGATGAAGCTCTTGTGAGTACCACTAC 2232
Db 1360 ATTTCTGTCTGTATATTCCTCCCACTCTCTGAGATTAACCACTTCACTGCTGCCAG 1419
Qy 2233 GAGATCCCTTTTATCACTCTGGAATGGCAGCGGCTACTTGTGCACTGCACTTCACTCACC 2292
Db 1420 GAAATCCCGTTCTCCCGCTGTGTGTCAGTAAACCGGCGAGCCCTGCACTGTGCTCTTCTCC 1479
Qy 2293 CTGGAGGCTGTGAGCCCGCAGCACTAGTGACCTGCGCTGCAAGCTGTGGGTGTGCGAGGTG 2352
Db 1480 CTGGAGGTTATAGCCCACTACCCAGCTGTCTGCAAAATCTGCAATTCGCGAGCTC 1539
Qy 2353 GAGGGCAGCGGAGAGCTTTCAGCATCAACTTCAACATCCAAAGGACACAAAGGTTTGCT 2412
Db 1540 AAGGCCATGAACAGATCTCTCAAGTCAGCATCAATCTAGAGAGTGAACGAGAAACC 1599
Qy 2413 GAGCTGTGCTGTGAGAGTGAAGCGGGGTCTCCAGCCCTGTGGGCCCCAGTGTGCTTC 2472
Db 1600 ATCACTTTCTTCGCAAGAGGACAGCACTTCCCTGCAAGAGTGTGCGCCCAAGGCTTC 1659
Qy 2473 AAGATCCCTCTCTCATTTCCGCGAGAGATATTTCCAGCTGAGCCACCCCTGTAGGCGG 2532
Db 1660 AAAATCCCTACTCATCAGACAGCGGATTTGTGCTACATTTGATATCCCCCAATGCGAAA 1719
Qy 2533 GGTGCCAGCTGGGGAATCTGGGCCAGAAACTCCACCTGGACAGCACTCTCAGCTTCTTT 2592
Db 1720 GGCAGAGACTGGCAGATGTTAGCACAGAAAACAGCATCAACAGGAATTTATCTTATTTTC 1779
Qy 2593 GCCTCAAGCCACGCCCAAGCCATGATCTCAACTGTGGAGGCGGCGCACTTCCCC 2652
Db 1780 GCTACAAAAGTAGCCCATCTGCTGTATTTTGAACCTGTGGGAGGCTGCTCATCAGCAT 1839

Qy 2653 AACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCTGGACTGGCCAGCCAGACGCTGGC 2712
Db 1840 GATGGTGAATCTTGAATCTCCCTGGCTGTGCCCTTTGAAGAGATTGGGAGGACACACAGAAA 1899
Qy 2713 CTCTTCCACAGTGTCCGAGGCTGAG 2736
Db 1900 CTCTCAACATTTTCAGAAATCCAG 1923

RESULT 15

US-09-969-532-29
; Sequence 29, Application US/09969532
; Patent No. 677232
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; TITLE OF INVENTION: No. 677232el Human Membrane Proteins and Polynucleotides Encodin
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969,532
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 2001
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-969-532-29

Query Match 10.7%; Score 293.2; DB 4; Length 2001;
Best Local Similarity 53.7%; Pred. No. 5.8e-56;
Matches 657; Conservative 0; Mismatches 558; Indels 9; Gaps 2;

Qy 1513 TCCTTCCCGGAGGACACCAACATGACCTATATGGACCTTCAACTTCTCGGGGGCGG 1572
Db 742 TCACTCCCGCACAGGACAGAACTGAGGACAACTGGTGTCTTTGGCCATTTAGGGGGCGC 801
Qy 1573 CTGATCATCCCTTAATACAGGTATCAGCTCTCTATCCCCCAGATGCCATACCCGAGGG 1632
Db 802 TTAGTAATGCCAAATACAGGGTGAAGCTTACTCATACACACAGGTGCCATCCAGAGAG 861
Qy 1633 AAGATCTATGAGATCTACCTCAGCTGCAAGCCGGAAGACGTGAGGTTGCCCTAGCT 1692
Db 862 AATCTTGGAGATTTATATGTCTCATCAACCAAGGTGAACCC---AGCCTCCAGTCAGAT 918
Qy 1693 GGCTGTGAGACCTCTGTGAGTCCCATCGTTAGTGTGGACCCCTTGGCTGCTGCTCAAC 1752
Db 919 GGCTGTGAGTGTCTCTGAGTCTGAAAGTCACTGTGGTCTCCAGACATGATCGTCAAC 978
Qy 1753 CGGCCAGTCACTCTGCTATGAGCACTGTGGGAGCCAGCCCTGACAGCTGGAGGCTG 1812
Db 979 ACTCCCTTTGCAATTTGACCATCCCGCACTGTGCAGATGTCTAGTCTTGAGCAATTTGAATATC 1038
Qy 1813 CGCCTCAAAAGCAGTCTGTCGAGGCGCAGCTGGGAGGATGTGTGCACCTTGGCGAGGAG 1872
Db 1039 CATTTAAGAGAGGACACAGCAGGCGCAATTTGGAGAGAGTGTGATGTCAGTGGAGATGAA 1098
Qy 1873 GCGCCCTCCCACTCTACTACTGCGAGCTGGAGCCAGTGTGCTGTACTACGCTTTCACCGAG 1932
Db 1099 TCTACATC-----CTGTTACTGCTTTTGGACCCCTTTTGGCTGTCTATGTCTCTGGAC 1152
Qy 1933 CAGCTGGCGCGCTTTTCCCTTGGTGGGAGAGGCCCTCAGCGTGGCTGCGCCAGACGCGCTC 1992
Db 1153 AGCTTTGGGACCTTATGCTCACTGGAGAGCCCAATCAAGACTGTGCGCGGAAAGCAACTG 1212
Qy 1993 AAGCTCTCTTGTGTTCCGCGGTGGCTGTCACTCTCGAGTACAACTCCGGGTCTAC 2052
Db 1213 AAGTGGCGGTTTGGTGCATGTCTGTAACTCTCTGATTTCAACTTTGAGAGTTTAC 1272
Qy 2053 TGCTTCATGACACCCCAAGCATGCACTCAAGGAGGTGTGAGCTGGAGAGAGCTGGGG 2112

Db 1273 TGTGTGACAAATACCCCTTGTGCATTTTCAGGAAGTGGTTTCAGATGAAGGCATCAAGGT 1332
Qy |||||
Db 2113 GGAAGTGTGATFCCAGGAGCAACGGGTCCTGCACCTTCAAGGACAGTTTACCACAAACCTGCGC 2172
Qy |||||
Db 1333 GGAAGTGTGATFCCAGGAGCAACGGGTCCTGCACCTTCAAGGAGTACCTTTAGTCTTCAG 1392
Qy |||||
Db 2173 CTATCCATCCACGATGCGCCAGCTCCCTGTGGAGAGTAAGCTCCTGTGTCAGTACCAG 2232
Qy |||||
Db 1393 ATTTCTGTCTTGATATTCGCCCATTCCTCTGGAGAAATTAACCAATTCACGTGCTGCCAG 1452
Qy |||||
Db 2233 GAGATCCCTTTTATACATCTGGAATGGCAGCGGTACTTGCACCTGCACCTTCACC 2292
Qy |||||
Db 1453 GAAGTCCCGTTCTCCCGGTTGGTGAGTAACCGGCGCCCTGCACCTGTGCTTCTCC 1512
Qy |||||
Db 2293 CTGAGGCTGTGAGCCCGCAGCACTAGTGAACCTGGCCCTGCAAGCTGTGGGTGTGGCAGGTG 2352
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Db 1513 CTGAGGCTGTATAGCGCCCACTACCCAGCTGTCTGCAAAATCTGCATTCGGCAGCTC 1572
Qy |||||
Db 2353 GAGGCGACGGCAGAGCTTCAGCATCAACTTCAACATCACCAGGACACAAGTTTGTCT 2412
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Db 1573 AAAGGCCATGAACAGATCTCCAAAGTGCAGACATCAATCTAGAGAGTGAACGAGAAACC 1632
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Db 2413 GAGCTGTGCTGTGGAGAGTGAAGCGGGGTCCAGCCCTGTGGGCCCGCAGTGCCTTC 2472
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Db 1633 ATCACTTTCTTCGCACAGAGGACAGCACTTCCCTGCACAGACTGGCCCCCAAGCCTTC 1692
Qy |||||
Db 2473 AAGATCCCTTCTCTCATTCGGCAGAGATTAATTTCCAGCCCTGGACCCACCTGTAGGCGG 2532
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Db 1693 AAAATTCCTTACTCCATCAGACAGCGGATTTGTGCTACATTTGATACCCCAATGCCAAA 1752
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Db 2533 GGTGCCGACTGGGGACTCTGGGCCAGAACTCCACCTGGGACAGCCATCTCAGCTTCTTT 2592
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Db 1753 GGCAGGACTGGGAGATGTTAGCACAGAAAACAGCATCAACAGGAATTTATCTTATTTT 1812
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Db 2593 GCCTCCAAGCCAGCCCCACAGCCATCATCTCAACCTGTGGAGCGCGGCACCTTCCCC 2652
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Db 1813 GCTACACAAAGTAGCCCATCTGCTGTCTATTTTGAACCTGTGGAGCTCGTCATCAGCAT 1872
Qy |||||
Db 2653 AAGGCAACCTCAGCCAGCTGGGTGACAGAGTGGCTGGAATGGGCCAGCCAGACGCTGGC 2712
Qy |||||
Db 1873 GATGGTGTCTTGACTCCCTGGCCTGTGCGCTTGAAGAGATTTGGGAGGACACACAGAAA 1932
Qy |||||
Db 2713 CTCTTACAGTGTGGAGGCTGAG 2736
Qy |||||
Db 1933 CTCTCAAAATTTCAAGATCCAG 1956

Search completed: August 7, 2005, 22:31:21
Job time : 647 secs

Result No.	Query			Description	
	Score	Match	Length	ID	
1	2752	100.0	2752	10	US-09-918-779-1
2	2752	100.0	2752	18	US-10-628-932-1
3	2676.4	97.3	2881	10	US-09-970-944-1
4	2356	85.6	3561	20	US-10-643-795A-77
5	2356	85.6	3561	21	US-10-948-518-77
6	2356	85.6	3580	17	US-10-311-623-13
7	2259	82.1	3014	10	US-09-933-261-1
					Sequence 1, Appl
					Sequence 1, Appl
					Sequence 1, Appl
					Sequence 77, App
					Sequence 77, App
					Sequence 13, App
					Sequence 1, Appl

RESULT 1
US-09-918-779-1
Sequence 1, Application US/09918779
Publication No. US20030064369A1
GENERAL INFORMATION:
APPLICANT: Taupier, Raymond
APPLICANT: Padigaru, Muralidhara
APPLICANT: Rastelli, Luca
APPLICANT: Padigara, Steven
APPLICANT: Shinkets, Richard
APPLICANT: Zerhusen, Bryan
APPLICANT: Spytek, Kimberly
APPLICANT: Shenoy, Suresh
APPLICANT: Li, Li
APPLICANT: Gusev, Vladimir
APPLICANT: Grosse, William
APPLICANT: Alsbrook, John
APPLICANT: Lepley, Denise
APPLICANT: Burgess, Catherine
APPLICANT: Gerlach, Valerie
APPLICANT: Ellerman, Karen
APPLICANT: MacDougall, John
APPLICANT: Stone, David
APPLICANT: Smithson, Glenda
TITLE OF INVENTION: Novel Proteins and Nucleic Acids
FILE REFERENCE: 21402-074 US
CURRENT APPLICATION NUMBER: US/09/918,779
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/221,409
PRIOR FILING DATE: 2000-07-28

QY 181 TTCTGTGTGAGCCGAGGATGTGTATCATCGTCAAGAAACAAGCCAGTGTCTGTGTGTC 240
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181 TTCTGTGTGAGCCGAGGATGTGTATCATCGTCAAGAAACAAGCCAGTGTCTGTGTGTC 240
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241 AAGCCGTGTCCGCGCACGACAGATCTTCTTCAAGTGCACACGGGAGTGGGTGCGCCAGGTG 300
Db |||||
241 AAGCCGTGTCCGCGCACGACAGATCTTCTTCAAGTGCACACGGGAGTGGGTGCGCCAGGTG 300
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301 GACCACTGTATCGAGCCGACACAGACGGAGCAGTGGGTGCCACCATCGAGGTCCGC 360
Db |||||
301 GACCACTGTATCGAGCCGACACAGACGGAGCAGTGGGTGCCACCATCGAGGTCCGC 360
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361 ATTAAATCTCTCAAGGACAGGTTCGAGAAAGTGTTCGGGCTGGAGGAATACTGGTGCAG 420
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361 ATTAAATCTCTCAAGGACAGGTTCGAGAAAGTGTTCGGGCTGGAGGAATACTGGTGCAG 420
QY |||||
421 TGCCTGTGCATGGAGTCTCTCGGGACCAACAAGAGTCAGAAAGGCTACATCCGCATAGCC 480
Db |||||
421 TGCCTGTGCATGGAGTCTCTCGGGACCAACAAGAGTCAGAAAGGCTACATCCGCATAGCC 480
QY |||||
481 AGATTGCGCAAGAACTTCGAGCAGAGCCGCTGCGCCAAAGAGGTGTCCCTGGAGCAGGC 540
Db |||||
481 AGATTGCGCAAGAACTTCGAGCAGAGCCGCTGCGCCAAAGAGGTGTCCCTGGAGCAGGC 540
QY |||||
541 ATCGTGTGCCCTCGCTCCACCGGAGGSCATCCCTCCAGCCGAGGTGGAGTGGCTCCGG 600
Db |||||
541 ATCGTGTGCCCTCGCTCCACCGGAGGSCATCCCTCCAGCCGAGGTGGAGTGGCTCCGG 600
QY |||||
601 AACGAGACCTGTGTGACCCGCTCCCTGGACCCCAATGTATATCATCACCGGGAGCAGC 660
Db |||||
601 AACGAGACCTGTGTGACCCGCTCCCTGGACCCCAATGTATATCATCACCGGGAGCAGC 660
QY |||||
661 CTGTGTGTGACAGGCCCGCTTGTGTGACACGGCCAACTACACCTCGTGGCCAAAGAAC 720
Db |||||
661 CTGTGTGTGACAGGCCCGCTTGTGTGACACGGCCAACTACACCTCGTGGCCAAAGAAC 720
QY |||||
721 ATCGTGTGACGTGCGCCGAGGCTCCGCTGTGTGTATCTGTGTGTGAAAGGTGGGTGG 780
Db |||||
721 ATCGTGTGACGTGCGCCGAGGCTCCGCTGTGTGTATCTGTGTGTGAAAGGTGGGTGG 780
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781 TCAGAGTGTGACAGGTGCTCGTCTGACAGGCCAGCTGTGGGCGCGCTGGCAGAAACGG 840
Db |||||
781 TCAGAGTGTGACAGGTGCTCGTCTGACAGGCCAGCTGTGGGCGCGCTGGCAGAAACGG 840
QY |||||
841 AGCCGAGTGTGACAAACCGCGCGCTCTCAAACGGGGCGCTTCTGTGAGGGGCAAGAT 900
Db |||||
841 AGCCGAGTGTGACAAACCGCGCGCTCTCAAACGGGGCGCTTCTGTGAGGGGCAAGAT 900
QY |||||
901 GTCCAGAAACAGCTTGGCCACCGCTGTGCGCCAGTACAGCGCAGCTGGAGCCCGTGGAGC 960
Db |||||
901 GTCCAGAAACAGCTTGGCCACCGCTGTGCGCCAGTACAGCGCAGCTGGAGCCCGTGGAGC 960
QY |||||
961 AAGTGTGTGAGTGTGGGCTGGACTGACCCACCTCTGGCGGAGCCGTGAGTGTCTGACCCCA 1020
Db |||||
961 AAGTGTGTGAGTGTGGGCTGGACTGACCCACCTCTGGCGGAGCCGTGAGTGTCTGACCCCA 1020
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1021 GCACCCCGCAACGGAGGGGAGGTGCGAGGCACTGACCTGGACACCCCGCAACTGTGACC 1080
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1021 GCACCCCGCAACGGAGGGGAGGTGCGAGGCACTGACCTGGACACCCCGCAACTGTGACC 1080
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1081 AGTGACCTCTGTGACACAGTGTTCGGCCCTGGAGCAGTGGCCCTCTATGTGGGCTC 1140
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1081 AGTGACCTCTGTGTGACACAGTGTTCGGCCCTGGAGCAGTGGCCCTCTATGTGGGCTC 1140
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1141 ATCGCCGTGGCCGTCTGCCTGGTCTGCTGTGTGTCTCATCTCTGTTTATTTGCGCG 1200
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1141 ATCGCCGTGGCCGTCTGCCTGGTCTGCTGTGTGTCTCATCTCTGTTTATTTGCGCG 1200
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1201 AAGAGAGGGGCTGGACTCAGATGTGGCTGACATCGTGTCCATTTCTCACTCAGGCTTCAG 1260
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1201 AAGAGAGGGGCTGGACTCAGATGTGGCTGACATCGTGTCCATTTCTCACTCAGGCTTCAG 1260
QY |||||
1261 CCGTGTGAGTCAAGCCCGACGAAAGCAGACAAACCCCATCTGTCTCACCATCCAGCCGAC 1320

Db |||||
1261 CCGTGTGAGTCAAGCCCGACGAAAGCAGACAAACCCCATCTGTCTCACCATCCAGCCGAC 1320
QY |||||
1321 CTGAGACCAACCAACCACTATCCAGGGCAGTCTCTGTCCCGGCGAGGATGGGCCCGAGC 1380
Db |||||
1321 CTGAGACCAACCAACCACTATCCAGGGCAGTCTCTGTCCCGGCGAGGATGGGCCCGAGC 1380
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1381 CCAGAGTTCAGTCTCAACCAATGGGCACCTGTCTCAGGCCCCCTGGGTGGCGGCGCCACACA 1440
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1381 CCAGAGTTCAGTCTCAACCAATGGGCACCTGTCTCAGGCCCCCTGGGTGGCGGCGCCACACA 1440
QY |||||
1441 CTGACCAACAGCTCTCCCACTCTGAGGCCGAGAGTTCGTCTCCCGCTCTCCACCCAG 1500
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1441 CTGACCAACAGCTCTCCCACTCTGAGGCCGAGAGTTCGTCTCCCGCTCTCCACCCAG 1500
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1501 AACTACTTTCGGCTCCCTGCGCCCGAGGCACACAGCAACATGACCTATATGGGAACTTTCAACTTC 1560
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1561 CTGCGGGGCGGCTGTATGATCCCTAATAAGGTATCAGCTCTCCTCATCCCCCAGATGCC 1620
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1621 ATACCCCGAGGGAAGATCTATGAGATCTACTCTCAGCTGCACAAAGCCGGAAGAGCTGAGG 1680
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1681 TTGCCCTTAGCTGGCTGTACAGACCCCTGCTGAGTCCCCTAGCTTGTGTGACCCCTGGC 1740
Db |||||
1681 TTGCCCTTAGCTGGCTGTACAGACCCCTGCTGAGTCCCCTAGCTTGTGTGACCCCTGGC 1740
QY |||||
1741 GTCTGTGTACCCGGCGAGTCATCTTGGCTATGTGAACATGTGTGGGAGGCCAGCCCTGAC 1800
Db |||||
1741 GTCTGTGTACCCGGCGAGTCATCTTGGCTATGTGAACATGTGTGGGAGGCCAGCCCTGAC 1800
QY |||||
1801 AGCTGTGAGCTGTGCTCTCAAAAGAGCAGTGTGTGAGGAGCTGTGGAGGATGTGTGAC 1860
Db |||||
1801 AGCTGTGAGCTGTGCTCTCAAAAGAGCAGTGTGTGAGGAGCTGTGGAGGATGTGTGAC 1860
QY |||||
1861 CTGGGAGGAGGCGCCCTCCCACTCTACTGTGCGAGCTGGAGGCGAGTGTGCTGTAC 1920
Db |||||
1861 CTGGGAGGAGGCGCCCTCCCACTCTACTGTGCGAGCTGGAGGCGAGTGTGCTGTAC 1920
QY |||||
1921 GTCTTACCGAGCAGCTGGGCCGCTTTCCTTGGTGGGAGAGGCCCTCAGCGTGGCTGCC 1980
Db |||||
1921 GTCTTACCGAGCAGCTGGGCCGCTTTCCTTGGTGGGAGAGGCCCTCAGCGTGGCTGCC 1980
QY |||||
1981 GCCAAGCGCTCAAGCTGTCTTCTGTTTGGCCCGGTGGCCCTGCACCTCCCTCGAGTACAAC 2040
Db |||||
1981 GCCAAGCGCTCAAGCTGTCTTCTGTTTGGCCCGGTGGCCCTGCACCTCCCTCGAGTACAAC 2040
QY |||||
2041 ATCCGGGTCTACTGCTGTGATGACCCACGATGCACCTCAAGGAGGTGTGCGAGCTGGAG 2100
Db |||||
2041 ATCCGGGTCTACTGCTGTGATGACCCACGATGCACCTCAAGGAGGTGTGCGAGCTGGAG 2100
QY |||||
2101 AAGCAGCTGGGGGGAAGCTGATCCAGGAGCAGGGTCTGCACTTCAGAGGACAGTTAC 2160
Db |||||
2101 AAGCAGCTGGGGGGAAGCTGATCCAGGAGCAGGGTCTGCACTTCAGAGGACAGTTAC 2160
QY |||||
2161 CACAACTGCGCCTATCTCCATCCAGATGTGCCACAGTCCCTGTGGAAAGAGTAAAGCTCCTT 2220
Db |||||
2161 CACAACTGCGCCTATCTCCATCCAGATGTGCCACAGTCCCTGTGGAAAGAGTAAAGCTCCTT 2220
QY |||||
2221 GTGAGCTTACAGAGATCCCTTTTATACATCTGGAATGGCAACGAGCGGTACTTGCAC 2280
Db |||||
2221 GTGAGCTTACAGAGATCCCTTTTATACATCTGGAATGGCAACGAGCGGTACTTGCAC 2280
QY |||||
2281 TGCACCTTACCTGGAGCGTGTACGCCCAGCACTAGTACCTGGCTGCGAGCTGTGG 2340
Db |||||
2281 TGCACCTTACCTGGAGCGTGTACGCCCAGCACTAGTACCTGGCTGCGAGCTGTGG 2340
QY |||||
2341 GTGTGGCAGGTGGAGGGCGACGGGCGAGAGTTCAGCATCAACTTCAACATCACCAAGGAC 2400

Db 2341 GTGTGGCAGTGGAGGGCGAGCGGCGAGAGCTTCAGCATCAACTTCAACATCACCAAGGAC 2400
Qy
2401 ACAAGGTTTGTGAGCTGCTGGCTCTGAGAGTGAAGCGGGGTCCAGCCCTGGTGGG 2460
Db
2401 ACAAGGTTTGTGAGCTGCTGGCTCTGAGAGTGAAGCGGGGTCCAGCCCTGGTGGG 2460
Qy
2461 CCCAGTGCCTTCAAGATCCCTTCTCTCATTCGGCAGAGATAAATTCAGCCTCGACCCA 2520
Db
2461 CCCAGTGCCTTCAAGATCCCTTCTCTCATTCGGCAGAGATAAATTCAGCCTCGACCCA 2520
Qy
2521 CCCTGTAGCGGGGTGGGACTGGGAGTCTGGCCAGCAAACTCCACTTGGACAGCAT 2580
Db
2521 CCCTGTAGCGGGGTGGGACTGGGAGTCTGGCCAGCAAACTCCACTTGGACAGCAT 2580
Qy
2581 CTGAGCTTCTTGGCTTCAAGCCAGCCAGCCAGCATGATCCCTCAACCTGTGGAGGCG 2640
Db
2581 CTGAGCTTCTTGGCTTCAAGCCAGCCAGCCAGCATGATCCCTCAACCTGTGGAGGCG 2640
Qy
2641 CGGCACCTTCCCAACGGCAACTCAGCCAGCTGGCTGCAGAGTGGCTGGACTGGCCAG 2700
Db
2641 CGGCACCTTCCCAACGGCAACTCAGCCAGCTGGCTGCAGAGTGGCTGGACTGGCCAG 2700
Qy
2701 CCAGACGCTGCCTTCTCAAGTGTGGAGGCTGAGTGTGAGCCGCGCCAG 2752
Db
2701 CCAGACGCTGCCTTCTCAAGTGTGGAGGCTGAGTGTGAGCCGCGCCAG 2752

RESULT 3
US-09-970-944-1
; Sequence 1, Application US/09970944
; Publication No. US20030204052A1
; GENERAL INFORMATION:
; APPLICANT: Heriman, John L
; APPLICANT: Restelli, Luca
; APPLICANT: Shimkets, Richard A
; TITLE OF INVENTION: No. US20030204052A1el Proteins and Nucleic Acids Encoding Same as
; TITLE OF INVENTION: Antibodies Directed Against these Proteins
; FILE REFERENCE: 21402-138
; CURRENT APPLICATION NUMBER: US/09/970,944
; CURRENT FILING DATE: 2002-05-02
; PRIOR FILING DATE: 2002-05-02
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2881
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-970-944-1

Query Match 97.3%; Score 2676.4; DB 10; Length 2881;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2728; Conservative 0; Mismatches 21; Indels 9; Gaps 3;
Qy 1 CCGGGGGCCCGCGCCCGCGCCCGCTGCGCCCGCGCGCCATGGCGCCCGCC 60
Db 42 CCGGGGGCCCGCGCCCGCGCCCGCTGCGCCCGCGCGCCATGGCGCCCGCC 101
Qy 61 GGCTGTGGCAGCGCTCTGGGAGTATGCTGCGCGCTGGCTGCGCGGCTGGGTC 120
Db 102 GGCTGTGGCAGCGCTCTGGGAGTATGCTGCGCGCTGGCTGCGCGGCTGGGTC 161
Qy 121 CAGCAGATGCCACCGTGGCCCAACCCAGTGCCTGGTGCACCCGAGCTGCTCCCCAC 180
Db 162 CAGCAGATGCCACCGTGGCCCAACCCAGTGCCTGGTGCACCCGAGCTGCTCCCCAC 221
Qy 181 TTCTGTGGAGCCCGAGGATGTATCATCGTCAAGAAACAGCAGTGTGCTTGTGTC 240
Db 222 TTCTGTGGAGCCCGAGGATGTATCATCGTCAAGAAACAGCAGTGTGCTTGTGTC 281
Qy 241 AAGCCGTGCGCCAGCAGATCTTCAAGTGAACCGGGAGTGGGTGCGCCAGGTG 300
Db 282 AAGCCGTGCGCCAGCAGATCTTCAAGTGAACCGGGAGTGGGTGCGCCAGGTG 341

Qy 301 GACACGCTGATCGAGCGCAGACAGACGGGAGAGTGGGCTGCCCAACATCGAGGTCGC 360
Db 342 GACACGCTGATCGAGCGCAGACAGACGGGAGAGTGGTGGAGCGACATCGAGGTCGC 401
Qy 361 ATTAATGTCTCAAGGCGACAGAGTTCGGAAGGTGTTCGGGCTGGAGGAATACTGTCGCAG 420
Db 402 ATTAATGTCTCAAGGCGACAGAGTTCGGAAGGTGTTCGGGCTGGAGGAATACTGTCGCAG 461
Qy 421 TGGTGTGCATGAGAGTCTCTCGGGCACCAAGAGTCAAGAGGCTTACATCCGATAGCC 480
Db 462 TGGTGTGCATGAGAGTCTCTCGGGCACCAAGAGTCAAGAGGCTTACATCCGATAGCC 521
Qy 481 AGATTGGCAAGAACTTCGAGCAGGAGCGCTGGCAAGGAGTGTCCCTGGACAGGCG 540
Db 522 AGATTGGCAAGAACTTCGAGCAGGAGCGCTGGCAAGGAGTGTCCCTGGACAGGCG 581
Qy 541 ATCGTGTGCTGCTGCCCTCCACCGGAGGCGATCCCTCCAGCCGAGGTGGAGTGGCTCCGG 600
Db 582 ATCGTGTGCTGCTGCCCTCCACCGGAGGCGATCCCTCCAGCCGAGGTGGAGTGGCTCCGG 641
Qy 601 AACGAGACCTGTGTGAGACCGCTCCCTGGACCCCAATGTATATACATCAGCGGGAGCAGC 660
Db 642 AACGAGACCTGTGTGAGACCGCTCCCTGGACCCCAATGTATATACATCAGCGGGAGCAGC 701
Qy 661 CTGTTGTGCGACAGGCGCGCTTGTGACACGCGCAACTACACCTGGTGGCCAAAGAC 720
Db 702 CTGTTGTGCGACAGGCGCGCTTGTGACACGCGCAACTACACCTGGTGGCCAAAGAC 761
Qy 721 ATCGTGTGACGCTGCGCGCAGCGCTCCGCTGTGTGTATCTGTACGTGAACCGTGGGTGG 780
Db 762 ATCGTGTGACGCTGCGCGCAGCGCTCCGCTGTGTGTATCTGTACGTGAACCGTGGGTGG 821
Qy 781 TCAGAGTGACCCAGTGTGCTGTGACGCGCAGCTGTGGCGCGCGCTGGCAGAAACCG 840
Db 822 TCAGAGTGACCCAGTGTGCTGTGACGCGCAGCTGTGGCGCGCGCTGGCAGAAACCG 881
Qy 841 AGCGGAGCTGACCAACCGCGCGCTTCAAGCGGGCGCTTCTGTGAGGGGCGAGAT 900
Db 882 AGCGGAGCTGACCAACCGCGCGCTTCAAGCGGGCGCTTCTGTGAGGGGCGAGAT 941
Qy 901 GTCCAGAA---AACAGCTGCGCCACCCCTGTGCGCCAGTAGACGCGAGCTGGAGCCGTTGG 957
Db 942 GTCCATGACCGCACCGCTCTCTCTGTGTTGTCTCTGTGAGCGGCGAGCTGGAGCCGTTGG 1001
Qy 958 AGCAAGTGTGCGCCTGTGGCTGTGAGCTGACCCCACTGGCGGAGCCGTGTGAGTGTCTGAC 1017
Db 1002 AGCAAGTGTGCGCCTGTGGCTGTGAGCTGACCCCACTGGCGGAGCCGTGTGAGTGTCTGAC 1061
Qy 1018 CCAGCACCCCGCAACCGAGGGAGGAGTGCACGGGCACTGACCTGGAGACCCCGCAACTGT 1077
Db 1062 CCAGCACCCCGCAACCGAGGGAGGAGTGCACGGGCACTGACCTGGAGACCCCGCAACTGT 1121
Qy 1078 ACCAGTGACCTGTGTGTACACAGTGTCTTGGCCCTGAGGACGTTGGCCCTCTATGTGGGC 1137
Db 1122 ACCAGTGACCTGTGTGTACACAGTGTCTTGGCCCTGAGGAGCTGGCCCTCTATGTGGGC 1181
Qy 1138 CTATGCGCGTGGCGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1197
Db 1182 CTATGCGCGTGGCGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1241
Qy 1198 CGGAAGAGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTCCTCAGGCTTC 1257
Db 1242 CGGAAGAGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTCCTCAGGCTTC 1301
Qy 1258 CAGCCGCTCAGCATCAAGCCCGCAGCAAGAGCAGACAGCCCATCTGTCTCAGCATCCAGCCG 1317
Db 1302 CAGCCGCTCAGCATCAAGCCCGCAGCAAGAGCAGACAGCCCATCTGTCTCAGCATCCAGCCG 1361
Qy 1318 GACCTCAGACACACACACACCTACAGGGGAGTGTCTGTCTCCCGGAGAGTGGGCC 1377
Db 1362 GACCTCAG---CACCAACCAACCTACAGGGGAGTGTCTGTCTCCCGGAGAGTGGGCC 1418

QY 1378 AGCCCCAAGTTCCAGCTCACCAATGGGCACTGCTCAGCCCCCTGGTGGGGCGGCCAC 1437
Db 1419 AGCCCCAAGTTCCAGCTCACCAATGGGCACTGCTCAGCCCCCTGGTGGGGCGGCCAC 1478
QY 1438 AACTGCACACAGCTCTCCACCTCTGAGGCCGAGAGTTGCTCCCGCCTCTCCACC 1497
Db 1479 AACTGCACACAGCTCTCCACCTCTGAGGCCGAGAGTTGCTCCCGCCTCTCCACC 1538
QY 1498 CAGAACTACTTCGGCTCCCTGCCCCGAGGACCAAGCAACATGACCTTATGGACCTTCAAC 1557
Db 1539 CAGAACTACTTCGGCTCCCTGCCCCGAGGACCAAGCAACATGACCTTATGGACCTTCAAC 1598
QY 1558 TTCTTCGGGGCGGCTGATGATCCCTAATACAGGTATCAGCTCTCCTCATCCCCCAGAT 1617
Db 1599 TTCTTCGGGGCGGCTGATGATCCCTAATACAGGTATCAGCTCTCCTCATCCCCCAGAT 1658
QY 1618 GCATATACCCGAGGGAAGATCTATGAGATCTACTCAGCTGCACAGCCGGAAGCGTG 1677
Db 1659 GCATATACCCGAGGGAAGATCTATGAGATCTACTCAGCTGCACAGCCGGAAGCGTG 1718
QY 1678 AGFTTGCCCTAGTGGCTGTACAGCCCTGCTGAGTCCCATCGTTAGTGTGACCCCT 1737
Db 1719 AGFTTGCCCTAGTGGCTGTACAGCCCTGCTGAGTCCCATCGTTAGTGTGACCCCT 1778
QY 1738 GGCGTCTGTCTACCCGGCCAGTCTCTGCTATGACCACTGTGGGGAGCCAGCCCT 1797
Db 1779 GGCGTCTGTCTACCCGGCCAGTCTCTGCTATGACCACTGTGGGGAGCCAGCCCT 1838
QY 1798 GACAGCTGAGAGCTGCGCCCTCAAAAGACGTCGTCGAGGCGAGCTGGG--AGGATGTG 1854
Db 1839 GACAGCTGAGAGCTGCGCCCTCAAAAGACGTCGTCGAGGCGAGCTGGGAGCAGATGTG 1898
QY 1855 CTGCACTCGGGCGAGGAGGCGCCCTCCCACTTACTTACTGTCAGCTGGAGGCGAGTGC 1914
Db 1899 CTGCACTCGGGCGAGGAGGCGCCCTCCCACTTACTTACTGTCAGCTGGAGGCGAGTGC 1958
QY 1915 TGCTACGTCTTACCGAGAGCTGGGCGCTTTGGCCCTGGTGGAGGCGCCCTCAGGCTG 1974
Db 1959 TGCTACGTCTTACCGAGAGCTGGGCGCTTTGGCCCTGGTGGAGGCGCCCTCAGGCTG 2018
QY 1975 GCTGCCGCCAAGGCGCTCAAGCTGCTTCTGTTGGCGCGGTGGCTGCACTCCCTCGAG 2034
Db 2019 GCTGCCGCCAAGGCGCTCAAGCTGCTTCTGTTGGCGCGGTGGCTGCACTCCCTCGAG 2078
QY 2035 TACAATCCGGGTCTACTGCTGCATGACCAACCATGATGCTCAAGAGGTTGGTGCAG 2094
Db 2079 TACAATCCGGGTCTACTGCTGCATGACCAACCATGATGCTCAAGAGGTTGGTGCAG 2138
QY 2095 CTGAGAGACAGCTGGGGGACAGCTGATCCAGAGCCACGGGTCTTGCATCTTCAAGGAC 2154
Db 2139 CTGAGAGACAGCTGGGGGACAGCTGATCCAGAGCCACGGGTCTTGCATCTTCAAGGAC 2198
QY 2155 AGTTACCAACCTTGCCTTATCCATCCAGATGTGCCAGCTCCCTGTGGAAGAGTAAG 2214
Db 2199 AGTTACCAACCTTGCCTTATCCATCCAGATGTGCCAGCTCCCTGTGGAAGAGTAAG 2258
QY 2215 CTCTTGTAGTACAGAGATCCCTTTTATCATACTGGAATGSCACGACGCGGTAC 2274
Db 2259 CTCTTGTAGTACAGAGATCCCTTTTATCATACTGGAATGSCACGACGCGGTAC 2318
QY 2275 TTGCATGCACTTACCCCTGGAGCGTGCAGCCCCAGCACTAGTGACCTGGCCTGCAAG 2334
Db 2319 TTGCATGCACTTACCCCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTGGCCTGCAAG 2378
QY 2335 CTGTGGGTGTGGAGGTGGAGGCGACGGGCGAGAGCTTACAGCATCACTTCAACATCACC 2394
Db 2379 CTGTGGGTGTGGAGGTGGAGGCGACGGGCGAGAGCTTACAGCATCACTTCAACATCACC 2438
QY 2395 AAGGACACAAGGTTTGTGATGCTGTGCTCTGAGAGTGAAGGGGGTCCAGCCCTG 2454
Db 2439 AAGGACACAAGGTTTGTGATGCTGTGCTCTGAGAGTGAAGGGGGTCCAGCCCTG 2498
QY 2455 GTGGGCCCCAGTGCCTTCAAGATCCCTTCTCATTCCGGCAGAAGATAATTTCCAGGCTG 2514

Db 2499 GTGGGGCCCCAGTGCCTTCAAGATCCCTTCTCATTCCGGCAGAAGATAATTTCCAGCTG 2558
QY 2515 GACCCACCTCTGATAGGGGGGTGCCGACTTGGCGGACTTGGCCCGAGAACTCCACCTGGAC 2574
Db 2559 GACCCACCTCTGATAGGGGGGTGCCGACTTGGCGGACTTGGCCCGAGAACTCCACCTGGAC 2618
QY 2575 AGCATCTCAGCTTCTTTGCTCCAAAGCCAGCCAGCCCAAGCCATGATCTCTCAACCTGTG 2634
Db 2619 AGCATCTCAGCTTCTTTGCTCCAAAGCCAGCCAGCCCAAGCCATGATCTCTCAACCTGTG 2678
QY 2635 GAGGCGGCGACTTCCCAACGGAACCTCAGCAGCTGGCTGCAGAGTGGCTGGACTG 2694
Db 2679 GAGGCGGCGACTTCCCAACGGAACCTCAGCAGCTGGCTGCAGAGTGGCTGGACTG 2738
QY 2695 GGCAGCAGACGCTGGCCTCTTTCACAGTGTCCGAGGCTGAGTGTGAGGCGGCCAC 2752
Db 2739 GGCAGCAGACGCTGGCCTCTTTCACAGTGTCCGAGGCTGAGTGTGAGGCGGCCAC 2796

RESULT 4
US-10-643-795A-77
; Sequence 77, Application US/10643795A
; Publication No. US20040241703A1
; GENERAL INFORMATION:
; APPLICANT: FREDERIC J. DESAUVAGE
; APPLICANT: KENNETH J. HILLAN
; APPLICANT: KENNETH J. HILLAN
; APPLICANT: PAUL POLAKIS
; APPLICANT: ANDREW POLSON
; APPLICANT: VICTORIA SMITH
; APPLICANT: SUSAN D. SPENCER
; APPLICANT: THOMAS D. WU
; APPLICANT: ZEMIN ZHANG
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; FILE OF INVENTION: TREATMENT OF TUMOR
; FILE REFERENCE: P5026R1-US
; CURRENT APPLICATION NUMBER: US/10/643, 795A
; CURRENT FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: US 60/404, 809
; PRIOR FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/405, 645
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/413, 192
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: US 60/419, 008
; PRIOR FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/426, 847
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/484, 959
; PRIOR FILING DATE: 2003-07-02
; NUMBER OF SEQ ID NOS: 158
; SEQ ID NO 77
; LENGTH: 3561
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-643-795A-77

Query Match 85.6%; Score 2356; DB 20; Length 3561;
Best Local Similarity 93.6%; Pred. No. 0;
Matches 2537; Conservative 0; Mismatches 5; Indels 168; Gaps 1;
QY 43 GCATGGCGCTCCGGCCCGGCTGTGGCAGCGCTCTCTGGGCATAGTCTCGCGCTTGG 102
Db 1 GCATGGCGCTCCGGCCCGGCTGTGGCAGCGCTCTCTGGGCATAGTCTCGCGCTTGG 60
QY 103 CTCGGCGGCTCGGGTCCCGAGAGTGCACCGTGCACCAACCCAGTGCCTGTGGTCCAAC 162
Db 61 CTCGGCGGCTCGGGTCCCGAGAGTGCACCGTGCACCAACCCAGTGCCTGTGGTCCAAC 120
QY 163 CCGGACCTGCTTCCCACTTCTTGGTGGAGCCCGGAGGATGTGTACATCGTCAAGAACAG 222
Db 121 CCGGACCTGCTTCCCACTTCTTGGTGGAGCCCGGAGGATGTGTACATCGTCAAGAACAG 180

Qy	223	CCAGTGTCTGTGTGCAAGGCGGTGCCCGCCAGCGAGATCTTCTTCAAGTGCACCGGG	282
Db	181	CCAGTGTCTGTGTGCAAGGCGGTGCCCGCCAGCGAGATCTTCTTCAAGTGCACCGGG	240
Qy	283	GAGTGGGTGCGCCAGGTGGGACCAAGTATGAGCGGACAGACAGCGGAGCAGTGGGCTG	342
Db	241	GAGTGGGTGCGCCAGGTGGGACCAAGTATGAGCGGACAGACAGCGGAGCAGTGGGCTG	300
Qy	343	CCACCATGGAGTCCCATTAATGTCTCAAGGCGAGCGTTCGAGAGGTGTTGGGCTG	402
Db	301	CCACCATGGAGTCCCATTAATGTCTCAAGGCGAGCGTTCGAGAGGTGTTGGGCTG	360
Qy	403	GAGGAATACTGGTCCAGTGGGCAATGGAGTCTCCGGGACACCAAGAGTCAAGAAG	462
Db	361	GAGGAATACTGGTCCAGTGGGCAATGGAGTCTCCGGGACACCAAGAGTCAAGAAG	420
Qy	463	GCCTACATCCGCATAGCCAGATTCGGCAAGAACTTCGAGCAGGAGCGCTGGCCAAAGAG	522
Db	421	GCCTACATCCGCATAGCCATTTTGGCAAGAACTTCGAGCAGGAGCGCTGGCCAAAGAG	480
Qy	523	GTGTCCCTGGAGCAGGCGCATCGTGTCCCTGCGGTCCACCGGAGGGCATCCCTCCAGCC	582
Db	481	GTGTCCCTGGAGCAGGCGCATCGTGTCCCTGCGGTCCACCGGAGGGCATCCCTCCAGCC	540
Qy	583	GAGGTGAGTGGCTCCGGAAACAGAGAACTGTGTGACCCGCTCCCTGGACCCCAATGTATAC	642
Db	541	GAGGTGAGTGGCTCCGGAAACAGAGAACTGTGTGACCCGCTCCCTGGACCCCAATGTATAC	600
Qy	643	ATCACGGGGAGCAGCTGTGTGGTGGCAGAGCGCCCGCTTGTGTGACAGCGGCAACTAC	702
Db	601	ATCACGGGGAGCAGCTGTGTGGTGGCAGAGCGCCCGCTTGTGTGACAGCGGCAACTAC	660
Qy	703	ACCTGCGTGGCCAGAACATCGTGGCAGCTGCGCGCAGCGCTCCGCTGTGTGTATCGTC	762
Db	661	ACCTGCGTGGCCAGAACATCGTGGCAGCTGCGCGCAGCGCTCCGCTGTGTGTATCGTC	720
Qy	763	TACGTGAACCGTGGTGGTTCGACGTGGAACGAGTGGTCCGCTCTGACGGCGCAGCTGTGGG	822
Db	721	TACGTG-----	726
Qy	823	CGCGGCTGGCAGAAACGGAGCGCGAGTGCACAAACCGCGGCGCTCTCAACGGGGCGCT	882
Db	727	-----	726
Qy	883	TTCTGTGAGGGGAGAAATGTCCAGAAACAGCCTGCGCCACCTGTGSCCCAGTAGACGGC	942
Db	727	-----GACGGC	732
Qy	943	AGCTGAGCCCGTGGAGCAAGTGGTCCGCTGTGGGCTGGACTGCACCCCACTGGCGGAGC	1002
Db	733	AGCTGAGCCCGTGGAGCAAGTGGTCCGCTGTGGGCTGGACTGCACCCCACTGGCGGAGC	792
Qy	1003	CGTGAAGTCTGTGACCCAGCAACCCGCAACGGAGGGAGGAGTGCAGGGGCACTGACCTG	1062
Db	793	CGTGAAGTCTGTGACCCAGCAACCCGCAACGGAGGGAGGAGTGCAGGGGCACTGACCTG	852
Qy	1063	GACACCCGCAACTGTACAGTGAACCTGTGTACACAGTGTCTTGGCCCTGAGGACGTG	1122
Db	853	GACACCCGCAACTGTACAGTGAACCTGTGTACACAGTGTCTTGGCCCTGAGGACGTG	912
Qy	1123	GCCCTCTATGTGGGCTCATCGCGCGTGGCGCTGTGCTGTGCTGTGCTGTGCTGCTC	1182
Db	913	GCCCTCTATGTGGGCTCATCGCGCGTGGCGCTGTGCTGTGCTGTGCTGTGCTGCTC	972
Qy	1183	ATCTCGTTTATTCGCGAAGAGGAGGGCTGGAATCAGATGTGGTGTGACTCGTCCATT	1242
Db	973	ATCTCGTTTATTCGCGAAGAGGAGGGCTGGAATCAGATGTGGTGTGACTCGTCCATT	1032
Qy	1243	CTCACCTCAGGCTTCCAGCCGCTCAGCATCAGCCGAGCAAGAGCAACCCCACTCTG	1302
Db	1033	CTCACCTCAGGCTTCCAGCCGCTCAGCATCAGCCGAGCAAGAGCAACCCCACTCTG	1092

Qy	1303	CTCACCTCAGCGCGACCTCAGCAACCAACCACTACACGAGGCGAGTCTCTGTCCC	1362
Db	1093	CTCACCTCAGCGCGACCTCAGCAACCAACCACTACACGAGGCGAGTCTCTGTCCC	1152
Qy	1363	CGGAGGATGGGCGCCAGCCCCAAAGTTCAGTCCAAATGGGACCTGTCTCAGCCCCCTG	1422
Db	1153	CGGAGGATGGGCGCCAGCCCCAAAGTTCAGTCCAAATGGGACCTGTCTCAGCCCCCTG	1212
Qy	1423	GGTGGGCGCGCCACACATCGACCAACAGCTCTCCCACTCTGAGGCGGAGGAGTTCGTC	1482
Db	1213	GGTGGGCGCGCCACACATCGACCAACAGCTCTCCCACTCTGAGGCGGAGGAGTTCGTC	1272
Qy	1483	TCGCGCTCTCCACCCAGAACTACTTCCGCTCCCTGCGCGGAGGACACAGCAATGACC	1542
Db	1273	TCGCGCTCTCCACCCAGAACTACTTCCGCTCCCTGCGCGGAGGACACAGCAATGACC	1332
Qy	1543	TATGGGACCTTCAACTTCTCGGGGCGCGTGTGATTCCTTAATAAGTATCAGGCTC	1602
Db	1333	TATGGGACCTTCAACTTCTCGGGGCGCGTGTGATTCCTTAATAAGGAAATCAGGCTC	1392
Qy	1603	CTCATCCCCCAGATGCCATACCCGAGGGAAGATCTATGAGATCTACCTCAGGCTGCAC	1662
Db	1393	CTCATCCCCCAGATGCCATACCCGAGGGAAGATCTATGAGATCTACCTCAGGCTGCAC	1452
Qy	1663	AAGCCGGAAGACGTGAGGTTGCCCCCTAGCTGGCTGTGAGACCCCTGTGAGTCCCATCGTT	1722
Db	1453	AAGCCGGAAGACGTGAGGTTGCCCCCTAGCTGGCTGTGAGACCCCTGTGAGTCCCATCGTT	1512
Qy	1723	AGCTGTGGAACCCCTGGCGTCTGTCAACCGGCGAGTCACTCTGGGCTATGGACACTGT	1782
Db	1513	AGCTGTGGAACCCCTGGCGTCTGTCAACCGGCGAGTCACTCTGGGCTATGGACACTGT	1572
Qy	1783	GGGAGCGCCAGCCCTGACAGCTGGAGCTCGGCTCAAAAGCAAGTGTGCGAGGGGAGC	1842
Db	1573	GGGAGCGCCAGCCCTGACAGCTGGAGCTCGGCTCAAAAGCAAGTGTGCGAGGGGAGC	1632
Qy	1843	TGGGAGGATGTGTGCACTCTGGGCGAGGAGCGCCCTCCACACCTCTACTACTGCGAGCTG	1902
Db	1633	TGGGAGGATGTGTGCACTCTGGGCGAGGAGCGCCCTCCACACCTCTACTACTGCGAGCTG	1692
Qy	1903	GAGGCGAGTGTGTCTGCTTCAACCGAGAGTGGGCGCGCTTGTGCGCTGTGGGAGAG	1962
Db	1693	GAGGCGAGTGTGTCTGCTTCAACCGAGAGTGGGCGCGCTTGTGCGCTGTGGGAGAG	1752
Qy	1963	GCCTCAGCGTGTGCGCCAGCGCTCAAGCTGCTTCTGTTGGCGCGTGGCCCTGC	2022
Db	1753	GCCTCAGCGTGTGCGCCAGCGCTCAAGCTGCTTCTGTTGGCGCGTGGCCCTGC	1812
Qy	2023	ACCTCCCTCGAGTACAACATCCGCGTCTACTGCTGCTGATGACACCCACGATGCACTCAAG	2082
Db	1813	ACCTCCCTCGAGTACAACATCCGCGTCTACTGCTGCTGATGACACCCACGATGCACTCAAG	1872
Qy	2083	GAGTGTGTGAGTGGAGAGAGTGTGGGGGAGCAGCTGATCCAGGAGCAGCGGCTCTG	2142
Db	1873	GAGTGTGTGAGTGGAGAGAGTGTGGGGGAGCAGCTGATCCAGGAGCAGCGGCTCTG	1932
Qy	2143	CACCTCAAGAGACATTTACCAACCTGCGCTTATCCATCCAGATGTGCCAGCTCCCTG	2202
Db	1933	CACCTCAAGAGACATTTACCAACCTGCGCTTATCCATCCAGATGTGCCAGCTCCCTG	1992
Qy	2203	TGGAAGAGTAAGTCTCTTGTGCTACACGAGATCCCTTTTATCACTCTGGAATGGC	2262
Db	1993	TGGAAGAGTAAGTCTCTTGTGCTACACGAGATCCCTTTTATCACTCTGGAATGGC	2052
Qy	2263	ACGAGGGGTACTTGCACTGTGCACTTCAACCTGGAGGCTGTGAGCCCGAGCTAGTGAC	2322
Db	2053	ACGAGGGGTACTTGCACTGTGCACTTCAACCTGGAGGCTGTGAGCCCGAGCTAGTGAC	2112
Qy	2323	CTGCGCTTGAAGCTGTGGGTGTGGAGGCGAGCGGCGAGAGCTTTCAGCATCAAC	2382
Db	2113	CTGCGCTTGAAGCTGTGGGTGTGGAGGCGAGCGGCGAGAGCTTTCAGCATCAAC	2172
Qy	2383	TTCAACATCAACCAAGGACACAAGGTTTGTGCTGTGCTCTGGAGAGTGAAGCGGGG	2442

Db 2173 TTCAACATACCAAGGACACAGGTTTGCTAGCTGTGGCTCTGGAGAGTGAAGCGGG 2232
Qy 2443 GTCCAGCCTGTGGGCCCCAGTGCCTTCAAGATCCCTTCTCATTTCCGCGAGAATATA 2502
Db 2233 GTCCAGCCTGTGTGGGCCCCAGTGCCTTCAAGATCCCTTCTCATTTCCGCGAGAGATA 2292
Qy 2503 ATTTCAGCCTGAGCCACACCTGTAGCGGGGTGCGAGCTGGCGGACTCTGGCCCGAGAA 2562
Db 2293 ATTTCAGCCTGAGCCACACCTGTAGCGGGGTGCGAGCTGGCGGACTCTGGCCCGAGAA 2352
Qy 2563 CTCACCTGTGACAGCAGCTCTAGCTTCTTTGCGCTTCCAAAGCCAGCCCCACAGCCATGATC 2622
Db 2353 CTCACCTGTGACAGCAGCTCTAGCTTCTTTGCGCTTCCAAAGCCAGCCCCACAGCCATGATC 2412
Qy 2623 CTCAACCTGTGGAGCGCGGCACTTCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCA 2682
Db 2413 CTCAACCTGTGGAGCGCGGCACTTCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCA 2472
Qy 2683 GTGGCTGGACTGGCCAGCAGAGCGCTGGCTCTTTCACAGTGTGCGAGGCTGAGTGCTGA 2742
Db 2473 GTGGCTGGACTGGCCAGCAGAGCGCTGGCTCTTTCACAGTGTGCGAGGCTGAGTGCTGA 2532
Qy 2743 GGCAGGCGAG 2752
Db 2533 GGCAGGCGAG 2542

RESULT 5

US-10-948-518-77
; Sequence 77, Application US/10948518
; Publication No. US20050064492A1
; GENERAL INFORMATION:
; APPLICANT: FREDERIC J. DESAUVAGE
; APPLICANT: GRETCHEN FRANTZ
; APPLICANT: KENNETH J. HILLAN
; APPLICANT: PAUL POLAKIS
; APPLICANT: ANDREW POLSON
; APPLICANT: VICTORIA SMITH
; APPLICANT: SUSAN D. SPENCER
; APPLICANT: THOMAS D. WU
; APPLICANT: ZEMIN ZHANG
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; FILE REFERENCE: P5028R1-US
; CURRENT APPLICATION NUMBER: US/10/948,518
; CURRENT FILING DATE: 2004-09-22
; PRIOR FILING DATE: US/10/643,795
; PRIOR FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: US 60/404,809
; PRIOR FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/405,645
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/413,192
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: US 60/419,008
; PRIOR FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/426,847
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/484,959
; PRIOR FILING DATE: 2003-07-02
; NUMBER OF SEQ ID NOS: 158
; SEQ ID NO 77
; LENGTH: 3561
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-948-518-77

Query Match 85.68; Score 2356; DB 21; Length 3561;
Best Local Similarity 93.68; Pred. No. 0;
Matches 2537; Conservative 0; Mismatches 5; Indels 168; Gaps 1;
Qy 43 GCCATGGCCGTCGGCGCCGCGCTGTGGCCAGCGCTCTCTGGGCATAGTCTCGCGGCTGG 102

Db 1 GCCATGGCCGTCGGCGCCGCGCTGTGGCCAGCGCTCTCTGGGCATAGTCTCTCGCGCTGG 60
Qy 103 CTCGGCGGCTCGGCTGCCAGCAGAGTGCCACCGTGGCCCAACCCAGTGCCTGTGTGCGCAAC 162
Db 61 CTCGGCGGCTCGGCTGCCAGCAGAGTGCCACCGTGGCCCAACCCAGTGCCTGTGTGCGCAAC 120
Qy 163 CCGGACCTGTCTCCCACTTCTCTGGTGGAGCCCGAGATGTGTACATCTGTCAAGAACAG 222
Db 121 CCGGACCTGTCTCCCACTTCTCTGGTGGAGCCCGAGATGTGTACATCTGTCAAGAACAG 180
Qy 223 CAGTGTCTGTCTGTGGAGGCGGTGCCGCCACCGAGATCTTCTCAAGTGCACCGGG 282
Db 181 CAGTGTCTGTCTGTGGAGGCGGTGCCGCCACCGAGATCTTCTCAAGTGCACCGGG 240
Qy 283 GAGTGGGTGGCGCAGGTGGACACGCTGATCGAGCGCAGCACACAGCGGAGCAGTGGGCTG 342
Db 241 GAGTGGGTGGCGCAGGTGGACACGCTGATCGAGCGCAGCACACAGCGGAGCAGTGGGCTG 300
Qy 343 CCACCATGAGAGTCCGCAATTAATGTCTAAGGCGAGAGTTCAGAGAGTGTTCGGGCTG 402
Db 301 CCACCATGAGAGTCCGCAATTAATGTCTAAGGCGAGAGTTCAGAGAGTGTTCGGGCTG 360
Qy 403 GAGGAATACTGTGGCCAGTCCGATGCGATGAGCTCTCGGGCACCCACCAAGAGTCAAGAG 462
Db 361 GAGGAATACTGTGGCCAGTCCGATGCGATGAGCTCTCGGGCACCCACCAAGAGTCAAGAG 420
Qy 463 GCCTACATCCGCATAGCCAGATTGCGCAAGAACTTCAGCAGGAGCGCTGGCCAAAGAG 522
Db 421 GCCTACATCCGCATAGCCATATTTGCGCAAGAACTTCAGCAGGAGCGCTGGCCAAAGAG 480
Qy 523 GTGTCCCTGGAGCAGGCGATCGTGTCTGCTGCTGCTGCCGTCCACCGAGGCGCATCCCTCCAGCC 582
Db 481 GTGTCCCTGGAGCAGGCGATCGTGTCTGCTGCTGCTGCCGTCCACCGAGGCGCATCCCTCCAGCC 540
Qy 583 GAGGTGGAGTGGTCTCCGGAACGAGGACCTGGTGGACCCGCTCCGAGCCCAATATGTATAC 642
Db 541 GAGGTGGAGTGGTCTCCGGAACGAGGACCTGGTGGACCCGCTCCGAGCCCAATATGTATAC 600
Qy 643 ATCACGGGAGCAGACGCTGTGGTGGCGACGCGCGCTTCTGTGACAGCGGCAACTAC 702
Db 601 ATCACGGGAGCAGACGCTGTGGTGGCGACGCGCGCTTCTGTGACAGCGGCAACTAC 660
Qy 703 ACCTGGTGGCCAAAGAACATCGTGGCAGCTGCGCGGAGGCGCTCCGCTGTGTCTCATCGTC 762
Db 661 ACCTGGTGGCCAAAGAACATCGTGGCAGCTGCGCGGAGGCGCTCCGCTGTGTCTCATCGTC 720
Qy 763 TACGTGAACCGTGGGTGGTGGACGCGAGTGGTCCGTCTGTGACGCGCAGCTGTGGG 822
Db 721 TACGTG----- 726
Qy 823 CGCGGCTGGCAGAAACGGAGCCGAGTGTGCA CCAACCCGCGCGCTCTTCAACGGGGGCGCT 882
Db 727 ----- 726
Qy 883 TTCTGTGAGGGGCGAGATGTCCAGAAAAACAGCCTGCGCCACCCTGTGTCCCGAGTAGACGC 942
Db 727 -----GACGGC 732
Qy 943 AGCTGGAGCCCGTGGAGCAAGTGGTGGCGCTGTGGGTGGAGCTGCA CCACTGCGCGGAGC 1002
Db 733 AGCTGGAGCCCGTGGAGCAAGTGGTGGCGCTGTGGGTGGAGCTGCA CCACTGCGCGGAGC 792
Qy 1003 CGTGAAGTGTCTGACCCAGCACCCCGCAACGGAGGGGAGAGTGCACAGGCGACTGACCTG 1062
Db 793 CGTGAAGTGTCTGACCCAGCACCCCGCAACGGAGGGGAGAGTGCACAGGCGACTGACCTG 852
Qy 1063 GACACCGGCAACTGTACCAAGTACCTGTGTGTACAGTCTTCTGSCCTGTGAGGAGCTG 1122
Db 853 GACACCGGCAACTGTACCAAGTACCTGTGTGTACACTCTTCTGTGCGCTGTGAGGAGCTG 912
Qy 1123 GCCTCTATGTGGGCTCTCATCGCGCGCTGTGGCGCTGTGCTGTGCTGTGCTGTGCTCTC 1182

; ORGANISM: Homo sapiens									
; FEATURE:									
; NAME/KEY: misc_feature									
; OTHER INFORMATION: Incyte ID No. US2004002344A1 6052371CB1									
US-10-311-623-13									
Query Match 85.6%; Score 2356; DB 17; Length 3580;									
Best Local Similarity 93.6%; Pred. No. 0;									
Matches 2537; Conservative 0; Mismatches 5; Indels 168; Gaps 1;									
Qy	43	GCCATGCGCTGCGGCGCGGCTGTGGCCAGCGCTCTGGGCATAGTCTCGCGCTGG	102						
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Qy	103	CTCGCGGCTGGGTGCCAGCAGAGTGCCACCGTGGCCAAACCAAGTCTGTGCAAC	162						
Db	61	CTCGCGGCTGGGTGCCAGCAGAGTGCCACCGTGGCCAAACCAAGTCTGTGCAAC	120						
Qy	163	CCGGACCTGCTCCCACTTCTTGGTGGAGCCGAGATGTACATCGTCAAGAACAG	222						
Db	121	CCGGACCTGCTCCCACTTCTTGGTGGAGCCGAGATGTACATCGTCAAGAACAG	180						
Qy	223	CCAGTGTCTGTGTGCAAGGCGTGCCTCCGCGCAGCAGATCTTCTCAAGTGCAACGG	282						
Db	181	CCAGTGTCTGTGTGCAAGGCGTGCCTCCGCGCAGCAGATCTTCTCAAGTGCAACGG	240						
Qy	283	GAGTGGTGGCCAGGTGGACCAAGTGATCGAGCGCAGCAGACGCGGAGCAGTGGGCTG	342						
Db	241	GAGTGGTGGCCAGGTGGACCAAGTGATCGAGCGCAGCAGACGCGGAGCAGTGGGCTG	300						
Qy	343	CCACCATGAGGTCCGCATTAATGTCTCAAGCAGAGGTGCGAGAGTTCGCGGCTG	402						
Db	301	CCACCATGAGGTCCGCATTAATGTCTCAAGCAGAGGTGCGAGAGTTCGCGGCTG	360						
Qy	403	GAGGAATCTGTGTGCCAGTGTGGCATGTGAGTCTCTCGGGCACCACCAAGAGTCAAGAG	462						
Db	361	GAGGAATCTGTGTGCCAGTGTGGCATGTGAGTCTCTCGGGCACCACCAAGAGTCAAGAG	420						
Qy	463	GCCTACATCCGCATPAGCCAGATTCGCAAGAACTTCGAGCAGAGCGCTGGCCAAAGAG	522						
Db	421	GCCTACATCCGCATPAGCCAGATTCGCAAGAACTTCGAGCAGAGCGCTGGCCAAAGAG	480						
Qy	523	GTGTCCCTGAGCAGGAGCATGTGCTGCTCCCTGCGCTCCACCGGAGGCGATCCCTCCAGCC	582						
Db	481	GTGTCCCTGAGCAGGAGCATGTGCTGCTCCCTGCGCTCCACCGGAGGCGATCCCTCCAGCC	540						
Qy	583	GAGTGGAGTGGTTCGCGAACGAGGACCTGGTGGACCCGCTCGGACCCCAATGTATAC	642						
Db	541	GAGTGGAGTGGTTCGCGAACGAGGACCTGGTGGACCCGCTCGGACCCCAATGTATAC	600						
Qy	643	ATCACGGGAGCAGACGCTGTGTGCGACAGGCCCGCTTGTGTGACACGGCCAACTAC	702						
Db	601	ATCACGGGAGCAGACGCTGTGTGCGACAGGCCCGCTTGTGTGACACGGCCAACTAC	660						
Qy	703	ACCTGCGTGGCCAGAACATCTGGGACGCTCGCGCAGCGCTCCGCTGTGTGATCGTC	762						
Db	661	ACCTGCGTGGCCAGAACATCTGGGACGCTCGCGCAGCGCTCCGCTGTGTGATCGTC	720						
Qy	763	TAGCTGAACCGGTGGTGGTGGACCGAGTGGTCCGCTCTGCGAGCGCAGCTGTGGG	822						
Db	721	TACGTG-----	726						
Qy	823	CGCGGTGGCAGAAACGGAGCCGAGGTGCACCAACCCGCGCGCTCTCAACCGGGGGCGCT	882						
Db	727	-----	726						
Qy	883	TTCTGTGAGGGCAGATGTCCAGAAACAGCCTGCGCCACCCTGTGCCCCAGTAGACGGC	942						
Db	727	-----GACGGC	732						
Qy	943	AGCTGGAGCCGTGGAGCAAGTGTGGGCTGTGGGCTGTGACCTGCACCCACTGCGGAGC	1002						
Db	733	AGCTGGAGCCGTGGAGCAAGTGTGGGCTGTGGGCTGTGACCTGCACCCACTGCGGAGC	792						

Qy	1003	CGTGAAGTCTCTGACCCAGCACCCCGCAACGAGGAGGAGGTGCCAGGCACTGACCTG	1062						
Db	793	CGTGAAGTCTCTGACCCAGCACCCCGCAACGAGGAGGAGGTGCCAGGCACTGACCTG	852						
Qy	1063	GACACCGGCAACTGTACCAAGTGTGTGTACACAGTGTCTTGGCCCTGAGGAGGTG	1122						
Db	853	GACACCGGCAACTGTACCAAGTGTGTGTACACAGTGTCTTGGCCCTGAGGAGGTG	912						
Qy	1123	GCCTCTATGTGGGCTCATCGCGGTGGCGCTGTGCTTGGTCTGTGCTGTGTGCTC	1182						
Db	913	GCCTCTATGTGGGCTCATCGCGGTGGCGCTGTGCTTGGTCTGTGCTGTGTGCTC	972						
Qy	1183	ATCCTCGTTTATGCGGAGAAAGAGGGGCTGGAATCAGATGTGGTGAATCGTCAATT	1242						
Db	973	ATCCTCGTTTATGCGGAGAAAGAGGGGCTGGAATCAGATGTGGTGAATCGTCAATT	1302						
Qy	1243	CTCACCTCAGGCTTCAGGCCGTCAGCATCAAGCCAGCAAAAGCAGACACCCCACTG	1302						
Db	1033	CTCACCTCAGGCTTCAGGCCGTCAGCATCAAGCCAGCAAAAGCAGACACCCCACTG	1092						
Qy	1303	CTCACCATCAGCGGACCTCAGCACCAACCAACCACTTACCAGGGCAGTCTCTGTCCC	1362						
Db	1093	CTCACCATCAGCGGACCTCAGCACCAACCAACCACTTACCAGGGCAGTCTCTGTCCC	1152						
Qy	1363	CGGCAAGATGGGCGCCAGGCCAAAGTTCAGCTCCAAATGGGCACTGTCTCAGCCCTG	1422						
Db	1153	CGGCAAGATGGGCGCCAGGCCAAAGTTCAGCTCCAAATGGGCACTGTCTCAGCCCTG	1212						
Qy	1423	GGTGGCGGCGCCACACATGTGACCAAGTCTCCACCTCTCAGGCCGAGGAGTTCGTC	1482						
Db	1213	GGTGGCGGCGCCACACATGTGACCAAGTCTCCACCTCTCAGGCCGAGGAGTTCGTC	1272						
Qy	1483	TCCCGCTCTTCCACCCAGAACTACTTCCGCTCCCTCCCGCGGACACCAAGCATGACC	1542						
Db	1273	TCCCGCTCTTCCACCCAGAACTACTTCCGCTCCCTCCCGCGGACACCAAGCATGACC	1332						
Qy	1543	TATGGAGACTTAACTCTTCCGGGCGCGCTGATATCCCTAATACAGGTATCAGGCTC	1602						
Db	1333	TATGGAGACTTAACTCTTCCGGGCGCGCTGATATCCCTAATACAGGAAATCAGGCTC	1392						
Qy	1603	CTCATCCCCCAGATGCCATACCCCGAGGGAAGATCTATGAGATCTACCTCAGCTGCAC	1662						
Db	1393	CTCATCCCCCAGATGCCATACCCCGAGGGAAGATCTATGAGATCTACCTCAGCTGCAC	1452						
Qy	1663	AAGCCGGAGACGTGAGGTTCGCCCTAGCTGGCTGTGAGACCTCTGAGTCCCATCGTT	1722						
Db	1453	AAGCCGGAGACGTGAGGTTCGCCCTAGCTGGCTGTGAGACCTCTGAGTCCCATCGTT	1512						
Qy	1723	AGCTGTGGACCCCTCGGCTCTGCTCAACCGGCGAGTCACTCTGGCTATGGACCACTGT	1782						
Db	1513	AGCTGTGGACCCCTCGGCTCTGCTCAACCGGCGAGTCACTCTGGCTATGGACCACTGT	1572						
Qy	1783	GGGAGCCAGCCCTGACAGCTGAGCCTGCGCTCAAAAAGCAGTCTGCCAGGGGAGC	1842						
Db	1573	GGGAGCCAGCCCTGACAGCTGAGCCTGCGCTCAAAAAGCAGTCTGCCAGGGGAGC	1632						
Qy	1843	TGGGAGGATGTGTGCACTTGGGCGAGGCGCCCTCCACCTCTACTCTGCTCCAGCTG	1902						
Db	1633	TGGGAGGATGTGTGCACTTGGGCGAGGCGCCCTCCACCTCTACTCTGCTCCAGCTG	1692						
Qy	1903	GAGCCAGTGTGCTGTGCTTTCAGGACAGCTGGGCGGCTTGGCTTGGTGGGAGAG	1962						
Db	1693	GAGCCAGTGTGCTGTGCTTTCAGGACAGCTGGGCGGCTTGGCTTGGTGGGAGAG	1752						
Qy	1963	GCCTCAGCGTGGCTCGCGCAAGCGCTCAAGCTGCTTCTGCTTGGCGCGGTGGCTGC	2022						
Db	1753	GCCTCAGCGTGGCTCGCGCAAGCGCTCAAGCTGCTTCTGCTTGGCGCGGTGGCTGC	1812						
Qy	2023	ACCTCCCTCGAGTAAACATCCGGGTCTACTGTCTGTGACACCAACCAAGTCACTCAAG	2082						
Db	1813	ACCTCCCTCGAGTAAACATCCGGGTCTACTGTCTGTGACACCAACCAAGTCACTCAAG	1872						

Leonardo, E. David
Hink, Lindsey
Masu, Masayuki
Kazuko, Keino-Masu
TITLE OF INVENTION: Netrin Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/256,702
FILING DATE: 27-Sep-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/933,261
FILING DATE: 20-Aug-2001
APPLICATION NUMBER: 08/808,982
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UC96-217
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3014 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-256-702-1
Query Match 82.1%; Score 2259; DB 14; Length 3014;
Best Local Similarity 89.7%; Pred. No. 0;
Matches 2427; Conservative 0; Mismatches 280; Indels 0; Gaps 0;
Qy 46 ATGGCCGTCCGGCCCGCCCTGTGCGCAGTGTCTCTGGGCATAGTCTCTCGCGCTGGCTT 60
Db 1 ATGGCCGTCCGGCCCGCCCTGTGCGCAGTGTCTCTGGGCATAGTCTCTCGCGCTGGCTT 60
Qy 106 CGGGCTCGGGTCCGACAGAGTGCACCGTGGCCAAACCGAGTGCCTGTGGCCAAACCG 165
Db 61 CGTGGTTCGGGTCCGACAGAGTGCACCGTGGCCAAACCGAGTGCCTGTGGCCAAACCG 120
Qy 166 GACCTGCTTCCCACTTCTGCTGAGCGCGGAGATGTACATGCTGCTGCTGCTGCTGCTGCT 225
Db 121 GACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
Qy 226 GTGTGCTGTGTGTCAGAGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 285
Db 181 GTGTGCTGTGTGTCAGAGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
Qy 286 TGGTGGCCAGGTGGACAGTGTATCGAGGCGAGCAGACGGGAGCAGTGGCTGCC 345
Db 241 TGGTTCGCGCAGGTTCGATCAGTAAATTGAACGACGACCCGACAGCAGCAGCGGATTGCCA 300
Qy 346 ACCATGAGGTCCGCAATTAATGCTCAAGGCGAGCGAGTGCAGAGGTTTCGGGCTGGAG 405
Db 301 ACCATGAGGTCCGCAATTAATGCTCAAGGCGAGCGAGTGCAGAGGTTTCGGGCTGGAG 360
Qy 406 GAATACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 465

361 GAATACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
Qy 466 TACATCCGATAGCAGCATTGGCCAGAAATTTGAGCAGGAGCGCTGGCCAAAGAGGTG 525
Db 421 TACATCCGATAGCAGCATTGGCCAGAAATTTGAGCAGGAGCGCTGGCCAAAGAGGTG 480
Qy 526 TCCCTGGAGCAGGAGCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 585
Db 481 TCACTGGAGCAGGAGCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
Qy 586 GTGAGTGGCTCCGGAACGAGGACCTGGTGGACCCGCTCCCTGGACCCCAATGTATATATC 645
Db 541 GTGAGTGGCTCCGGAATGAGGACCTGGTGGACCCGCTCCCTGGATCCCAATGTATATATC 600
Qy 646 ACGCGGAGCAGCAGCCTGGTGGCAGAGCGCGCTGCTGACAGCGCGCTGCTGACAGCGCGCTGCT 705
Db 601 ACGCGGAGCAGCAGCCTGGTGGCAGAGCGCGCTGCTGACAGCGCGCTGCTGACAGCGCGCTGCT 660
Qy 706 TGGCTGGCCAAAGAACATCGTGGCAGCAGTGGCGGAGCGCTCCGCTGCTGCTGCTGCTGCTGCT 765
Db 661 TGTGTGGCCAAAGAACATCGTGGCGGAGCGCTGCTGCGGAGCAGCTCTGACAGCGCTCATTTTAT 720
Qy 766 GTGAAACGGTGGTGGTGCAGCTGGACCCGAGTGTGCTGCTGACAGCGCAGCTGTGGGCGC 825
Db 721 GTGAAACGGTGGTGGTGCAGCTGGACCCGAGTGTGCTGCTGACAGCGCAGCTGTGGGCGC 780
Qy 826 GGCCTGGCAGAAACGGAGCGGAGTGCACCAACCGCGGCTCTCAACGGGGCGCTTTC 885
Db 781 GGCCTGGCAGAAACGGAGCGGAGTGCACCAACCGCGGCTCTCTCAACGGGGCGCTTTC 840
Qy 886 TGTGAGGGGCGAGAAATGTCAGAAAAACAGCTGGCGCCACCTGTGCGCCAGTAGACGGGAGC 945
Db 841 TGTGAGGGGCGAGAAATGTCAGAAAAACAGCTGGCGCCACCTGTGCGCCAGTAGAGTGGAGC 900
Qy 946 TGGAGCCCTGTGGAGCAAGTGGTGGGCTGTGGGCTGGAAGTGCACCCACTGCGCGAGCGCT 1005
Db 901 TGGAGTTCGTGGAGTAAAGTGGTGGGCTGTGGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
Qy 1006 GAGTGTCTGACCCAGCAGCCCGCAACGGAGGGGAGAGTGCAGGGGAGTGCAGGGGAGTGCAG 1065
Db 961 GAGTGTCTGACCCAGCAGCCCGCAACGGAGGGTGGAGTGTGCGGGTGTGCTGCTGCTGCTGCT 1020
Qy 1066 ACCCGCAACTGTACAGTACCTCTGTGTACACAGTGTCTGTGCGCTGTGCGCTGTGCGCTGTGCGC 1125
Db 1021 ACCCGCAACTGTACAGTACCTCTGTGTGCAACAGCTGTGCTGCGCCAGGAGCGTGGCT 1080
Qy 1126 CTCTATGTGGGCTCATGCGCGTGGGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1185
Db 1081 CTCTATGTGGGCTCATGCGCGTGGGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
Qy 1186 CTGTTTTATTGCGGAGAGAGGGGCTGGAAGTGCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1245
Db 1141 CTCAATTTACTGTGCGAAGAGAGGGCTGGAATCCGATGTGCGCGAGTGTGCTGCTGCTGCTGCT 1200
Qy 1246 ACCTCAGGCTTCCAGCCCGTGCAGCATCAAGCCAGCAAGAGAGAGAGAGAGAGAGAGAGAGAG 1305
Db 1201 ACCTCAGGCTTCCAGCCCGTGCAGCATCAAGCCAGCAAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
Qy 1306 ACCATCCAGCCGAGCTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1365
Db 1261 ACCATCCAGCCGAGCTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1320
Qy 1366 CAGATGGGCGCAGCCAGCTTCCAGCTACCAATGGGAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCT 1425
Db 1321 CAGATGGGCGCAGCCAGCTTCCAGCTACCAATGGGAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
Qy 1426 GGGGCGCGCAGCAGCTGACAGCAGCTCTCCAGCTCTGAGCGCGAGGAGTTCGCTCTCC 1485
Db 1381 AGTGGCGCGCATAGTTGACACAGCTTACCCAGCTCTGAGGCTGAGGAGTTCGCTCTCC 1440
Qy 1486 CGCTCTTCCACCCAGAACTACTTCCGCTCCCTCCCGGAGCCAGCAACATGACCTAT 1545

Db 1441 CGCTCTCCACCCAAACTACTTTGTTCCCTGCCCCCGCGCACCAACATGGCCCTAC 1500
Qy 1546 GGGACCTTCAACTTCCTCGGGGGCGGCTGATGATCCCTAATAACAGGTATCAGCCTCCTC 1605
Db 1501 GGGACCTTCAACTTCCTCGGGGGCGGCTGATGATCCCTAATAACGGGGATCAGCCTCCTC 1560
Qy 1606 ATCCCCCAGATGCCATACCCCGAGGGAAGATCTATGAGATCTACCTCAGCTGCACAAG 1665
Db 1561 ATACCCCGGATGCCATCCCGCGAGGAAGATCTACAGATCTACCTCACACTGCACAAG 1620
Qy 1666 CCGAAGACGTGAGGTTGCCCTAGCTGGCTGTGAGACCTGTGAGTCCCATCTGTTAGC 1725
Db 1621 CCAGAAAGCTGAGTTGCCCTAGCTGGCTGTGAGACCTGTGAGTCCCATCTGTTAGC 1680
Qy 1726 TGTGACCCCTGGCTGCTGCTCACCCGSCCAAGTCACTCTGGCTATGGAACCACTGTGGG 1785
Db 1681 TGTGGGCCCCAGAGTCTCTGCTCACCCGSCCAAGTCACTCTGGCTATGGAACCACTGTGGG 1740
Qy 1786 GAGCCACGCTGACAGCTGGAGCTGGGCTCAAAAAGCAGTCTGCGAGGGGAGCTGG 1845
Db 1741 GAGCCACGCTGACAGCTGGAGTCTGGGCTCAAAAAGCAGTCTGCGAGGGGAGCTGG 1800
Qy 1846 GAGGATGTGCTGACCTGGGCGAGGAGCGCCCTCCCACTCTACTACTGCCAGCTGGAG 1905
Db 1801 GAGGATGTGCTGACCTGGTGGAGAGTCACTTCCCACTCTACTACTGCCAGCTGGAG 1860
Qy 1906 GCCAGTGCCTGCTACGTCTTCAACGAGCAGCTGGGCGGCTTTGCTGCTGGTGGAGAGGCC 1965
Db 1861 GCCGGGCGCTGCTATGCTTTCACGAGCAGCTGGGCGGCTTTGCTGCTGGTGGAGAGGCC 1920
Qy 1966 CTCAGCTGCTGCTGCGCCAGCGGCTCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2025
Db 1921 CTCAGCTGCTGCTGCGCCAGCGGCTCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1980
Qy 2026 TCCCTCGAGTACAACATCCCGGCTTACTGCTGCTGATGACACCAACGATGCACTCAAGGAG 2085
Db 1981 TCCCTCGAGTACAACATCCCGGCTTACTGCTGCTGATGACACCAACGATGCTCAAGGAG 2040
Qy 2086 GTGCTGAGCTGGAGAGCAGCTGGGGGAGCAGCTGATCAGGAGCACCAGGCTGCTGAC 2145
Db 2041 GTGCTGAGCTGGAGAGCAGCTAGGTGGAGCAGCTGATCAGGAGCCTCGCTGCTGCTG 2100
Qy 2146 TTCAGGACAGTACCAACACTGCGCTATCCATCCACGATGTCACGCTGCTGCTGCTGCTG 2205
Db 2101 TTCAGGACAGTACCAACACTGCTGCTTCCATCCACGAGCTGCTGCTGCTGCTGCTG 2160
Qy 2206 AAGAGTAAGCTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2265
Db 2161 AAGAGTAAGCTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2220
Qy 2266 CAGCGGTACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2325
Db 2221 CAGCAGTACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2280
Qy 2326 GCCTGCAAGCTGTGGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2385
Db 2281 GCCTGCAAGCTGTGGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2340
Qy 2386 AACATCAACAGGACACAAAGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2445
Db 2341 AACATCAACAGGACACAAAGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2400
Qy 2446 CCAGCCCTGTGGGCCCCAGTCCCTCAAGATCCCTTCCCTCAATTCGGGCAAGATTAAT 2505
Db 2401 CCAGCCCTGTGGGCCCCAGTCCCTCAAGATCCCTTCCCTCAATTCGGGCAAGATTAAT 2460
Qy 2506 TCAGAGCTGGACCCACCTGTAGCGGGGTGCGGCTGCGGCTGCTGCTGCTGCTGCTGCTG 2565
Db 2461 GCCAGTCTGGACCCACCTGTAGCGGGGTGCGGCTGCGGCTGCTGCTGCTGCTGCTGCTG 2520
Qy 2566 CACCTGGACAGCCATCTCAGCTCTTTTGCCTTCCAAAGCCCGAGCCCAAGCCATGATCCTC 2625
Db 2521 CACCTGGACAGCCATCTCAGCTCTTTTGCCTTCCAAAGCCCGAGCCCAAGCCATGATCCTC 2580

Qy 2626 AACCTGTGGAGCGCGGCACTTCCCAACCGCAACCTCAGCAGCTGGCTGCAAGAGTG 2685
Db 2581 AACCTATGGAGCGACGGCACTTCCCAACCGCAACCTCAGCAGCTGGCTGCAAGAGTG 2640
Qy 2686 GCTGGACTGGCCAGCAGCAGCTGGCTTCCACAGTGTGCGAGGCTGAGTGTGAGGC 2745
Db 2641 GCCGAGCTGGGCCAACCAAGATGCTGCGCTCTTACGGTGTGCGAGCCGAGTGTGAGAC 2700
Qy 2746 CGGCCAG 2752
Db 2701 CAGCCAG 2707

RESULT 9

US-10-240-154-15
; Sequence 15, Application US/10240154
; Publication No. US20030175741A1
; GENERAL INFORMATION:
; APPLICANT: Cochran et al.
; TITLE OF INVENTION: SCHIZOPHRENIA RELATED GENES
; FILE REFERENCE: CKFW-POI-006
; CURRENT APPLICATION NUMBER: US/10/240,154
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: PCT/GB01/01486
; PRIOR FILING DATE: 2001-04-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 2697
; TYPE: DNA
; ORGANISM: Rattus sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2697)
US-10-240-154-15

Query Match 81.8%; Score 2252.2; DB 16; Length 2697;

Best Local Similarity 89.7%; Pred. No. 0;
Matches 2419; Conservative 0; Mismatches 278; Indels 0; Gaps 0;

Qy 46 ATGCGCTCGCGCGCGCGCTGTGCGCAGCGCTCTCTGGGCATAGTCTCTCGCGCTTGGCTC 105
Db 1 ATGCGCTCGCGCGCGCGCTGTGCGCAGTGTCTCTGGGCATAGTCTCTCGCGCTTGGCTC 60
Qy 106 CGCGCTCGGGTCCCGCAGCAGAGTGCACCGTGGCCAAACCCAGTGTGTGCAACCCG 165
Db 61 CGTGGTTCGGTGTCCCGCAGCAGAGTGCACCGTGGCCAAACCCAGTGTGTGCAACCCG 120
Qy 166 GACTGCTTCCCACTTCTGTTGGAGCCCGAGATGTGTACATCTCAAGTCAACCGGAG 225
Db 121 GACTGCTTCCCACTTCTGTTGGAGCCCGAGATGTGTACATCTCAAGTCAACCGGAG 180
Qy 226 GTGCTGCTGTGCAAGCGCGCTGCGCCAGCAGATCTTCTCAAGTCAACCGGAG 285
Db 181 GTGTTGTTGTGCAAGCGCTGCTGCGCCAGCAGATCTTCTCAAGTCAACCGGAG 240
Qy 286 TGGGTGCGCAGTGGACCAACGTTGATCGAGCGCAGACAGACGCGGAGCTGGCTGCC 345
Db 241 TGGGTGCGCAGTGGACCAACGTTGATCGAGCGCAGACAGACGCGGAGCTGGCTGCC 300
Qy 346 ACCATGAGGTTCGCAATTAATGTCTCAAGCAGAGTTCGAGAGGTTCGGGCTGGAG 405
Db 301 ACCATGAGGTTCGCAATTAATGTCTCAAGCAGAGTTCGAGAGGTTCGGGCTGGAG 360
Qy 406 GAATACTGTCAGTGGTGGCATGGAGTCTCTCGGGCACCAACAGAGTTCAGAAAGGCC 465
Db 361 GAATACTGTCAGTGGTGGCATGGAGTCTCTCGGGCACCAACAGAGTTCAGAAAGGCC 420
Qy 466 TACATCCGATAGCCAGATTCGCAAGAACTTCAGCAGAGCGCTGTGGCCAGAGAGGTG 525
Db 421 TACATCCGATAGCCAGATTCGCAAGAACTTCAGCAGAGCGCTGTGGCCAGAGAGGTG 480

Qy 526 TCCCTGGAGCAGGCATCGTGTCTCCCTGCGTCCACCGGAGGCGATCCCTCCAGCCGAG 585
Db 481 TCACTGGAGCAAGCAATGTACTACCTTGTGCGCCCCCAGAGGAATCCCCCAGCTGAG 540
Qy 586 GTGAGTGGCTCCGGAACGAGGAACTGTGTGACCCGTCCTGTGGAACCCCAATGATATCATC 645
Db 541 GTGAGTGGCTTCGAAATGAGGAACTGTGTGACCCCTCCCTCGATCCCAATGTGTATCATC 600
Qy 646 ACGCGGAGCAGACGCTGTGTGTCGACAGSCCGCTTGTGTGACAGCGCCAACTACACC 705
Db 601 ACGCGGAGCAGACGCTGTGTGTCGACAGSCCGCTTGTGTGACAGCGCCAACTACACC 660
Qy 706 TGCCTGGCCAAAGAACTGTGTGTCGACGTCGCGCAGCGCTCCGCTGTGTATCATCGTCTAC 765
Db 661 TGTGTGCGCAAGAACATCGTAGCCGTCGCGCAAGCACCTCTGTGAGCGGTCATTGTTTAT 720
Qy 766 GTGAACGGTGGTGTGTCGACAGCGAGTGTGTCGTCGACGCGCAGCTGTGGGCGC 825
Db 721 GTGAACGGTGGTGTGTCGACAGCGAGTGTGTCGTCGACGCGCAGCTGTGGGCGT 780
Qy 826 GGCTGGCAGAAAACGAGCCGAGCTGCAACAAACCGCGCTCTCAACGGGGCGCTTTC 885
Db 781 GGCTGGCAGAAAACGAGCCGAGCTGCAACAAACCGCGCACTCTCAACGGGGCGCCTTC 840
Qy 886 TGTGAGGGGCAAGAAATGTCCAGAAACAGCCTGCGCCACCTGTGTCGCCAGTAGACGGCAGC 945
Db 841 TGTGAGGGGCAAGAAATGTCCAGAAACAGCCTGCGCCACCTGTGTCGCCAGTGGATGGAGC 900
Qy 946 TGGAGCCGTTGGAGCAAGTGTGCGGCTGTGGGCTGTGACTGTGACCCACTGCGGAGCCGT 1005
Db 901 TGGAGTTCGTGGAGTGTGTCAGCCTGTGGGCTGTGACTGTGACCCACTGCGGAGCCGC 960
Qy 1006 GAGTGTCTGACCCAGCAGCCCGCAACGAGGGGAGAGTGCAGGGCACTGTACCTGGAC 1065
Db 961 GAGTGTCTGACCCAGCAGCCCGCAATGAGAGTGTGAGAGTGTGCGGGTGTGACCTGGAC 1020
Qy 1066 ACCGCAACTGTACAGTACCTCTGTGTACACAGTGTCTTGTGCGCTGTGAGGACGTGGCC 1125
Db 1021 ACCGCAACTGTACAGTACCTCTGTGTGACACACCGCTTCTTGTGCGCGAGGAGTGGCT 1080
Qy 1126 CTCTATGTGGGCTCATCGCGTGGCGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTATC 1185
Db 1081 CTCTATCATCGGCTTGTGCTGTGGCTGTGTGCTCTTCTTGTGTGTGTGCTGGCCCTTGG 1140
Qy 1186 CTGTTTTATTGCGGAAGAGGGGCTGAGCTCAGATGTGGTGTGCTGTGCTGTGCTGTCTC 1245
Db 1141 CTCTATTTACTGTGCAAGAGGAGGGCTGAGCTTCCGATGTGGCGGACTGTCTCATCTCTC 1200
Qy 1246 ACCTCAGGCTTCCAGCCCGTCAGCATCAAGCCCAAGCAAGCAGCAACCCCACTCTGCTC 1305
Db 1201 ACCTCGGGCTTCCAGCCCTGTGAGCATCAAGCCCAAGCAAGCAGCAACCCCACTCTGCTC 1260
Qy 1306 ACCATCAGCGGACCTCAGGACACACACACACCTTACAGGGCAGTCTGTGTCGCCGG 1365
Db 1261 ACCATCAGCGGACCTCAGGACACACACACTACCACTTACAGGGCAGTCTGTGTTCGAGG 1320
Qy 1366 CAGATGGGCGCAGCCCAAGTTCCAGCTCACCATGGGCACTGTCTCAGCCCGCTGGGT 1425
Db 1321 CAGATGGACCCAGCCCAAGTTCCAGCTCTATATGTGTCACCTGTCTCAGCCCACTGGGG 1380
Qy 1426 GGGCGGCGCACACATGTCACCAAGCTCTCCACCTCTGTGAGGCGGAGGATTCGTCTCC 1485
Db 1381 AGTGGCGGCGCATAGTTGACCAAGCTCACCACCTCTGTGAGGCTGAGGACTTCGTCTCC 1440
Qy 1486 GGCCTCTCCACCGAAGACTATTCGCTCCGCTCCGCGGAGGCAACGACCAATGACCTAT 1545
Db 1441 GGCCTCTCCACCGAAGACTATTCGCTCCGCTCCGCGGAGGCAACGACCAATGACCTAT 1500
Qy 1546 GGGACCTTCACTTCTCGGGGCGGCTGTATGATCCCTAATACAGTATCAGCTCTCCTC 1605
Db 1501 GGGACCTTCACTTCTCGGGGCGGCTGTATGATCCCTAATACGGGGATCAGCCTCTCCT 1560
Qy 1606 ATCCCCCCAGATGCCATACCCCGAGGGAAGATCTATGAGATCTACCTCAGGCTGCAAG 1665

Db 1561 ATACCCCGGATGCCATCCCCCGAGGAAGATCTACGAGATCTACCTCAGACTGCACAAG 1620
Qy 1666 CCGAAGACGTGAGGTGCCCCCTAGCTGGCTGTGAGACCCCTGCTGAGTCCCATCTGTAGC 1725
Db 1621 CCAGAAGACGTGAGGTGCCCCCTAGCTGGCTGTGAGACCCCTGCTGAGTCCCATCTGTAGC 1680
Qy 1726 TGTGGACCCCTCGCGCTCTGCTCACCCGCGCAGTCACTCTGGCTATGAGCACTGTGGG 1785
Db 1681 TGTGGGCCCCCAGAGTCTCTGCTCACCCGCGCAGTCACTCTGCAATGGAACCTGTGGA 1740
Qy 1786 GAGCCACGCTCTGACAGCTGGAGCTGCGCTCAAAAGCAGTCTGTCGAGGGCAGCTGG 1845
Db 1741 GAGCCACGCTCTGACAGCTGGAGTGTGCGCTCAAAAGCAGTCTGCGAGGGCAGTGG 1800
Qy 1846 GAGGATGTGTCACCTGCGGAGGAGGCGCTTCCACCTCTACTACTGCGAGCTGGAG 1905
Db 1801 GAGGATGTGTCACCTTGTGTGAGGAGTCACTTCCACCTCTACTACTGCGAGCTGGAG 1860
Qy 1906 GCCAGTGCCTGCTACGCTTTCACCGAGCAGCTGGGCGCTTTGCGCTTGGTGGAGAGGCC 1965
Db 1861 GCCGGGCTGCTATGCTTTCACGAGCAGCTGGGCGCTTTGCGCTTGGTGGAGAGGCC 1920
Qy 1966 CTGAGGCTGCTGCCGCAAGCGCTCAAGCTGCTTCTGTTTGTGCGCGGTGGCTGCACC 2025
Db 1921 CTGAGGCTGCTGCCAAGCGCTCAGGCTCTCTTCTGTTTGTCTCCGTTGGCTGTACG 1980
Qy 2026 TCCTCTGAGTACAACTCCGGTCTACTGCTGATGACACCCACGATGCACTCAAGGAG 2085
Db 1981 TCCTTGTGATACAACTCCGAGTGTACTGCTTACAGACACCCACGAGCTCTCAAGGAG 2040
Qy 2086 GTGCTGAGCTGAGAGAGCAGCTGGGGGAGCAGCTGATCCAGAGGCCACGGCTCTGCAC 2145
Db 2041 GTGCTGAGCTGAGAGAGCAGCTGAGTGTGACAGCTGATCCAGAGGCTCTGCGTCTGCAC 2100
Qy 2146 TTCAAGGACAGTTACCAAACTGCGCTTATTCATCCAGATGTGCCAGCTCCCTGTGG 2205
Db 2101 TTCAAGACAGTTTACCACAACTACGCTCTCTCCATCCAGCAGCTGCCAGCTCCCTGTGG 2160
Qy 2206 AAGATGAGCTCTTGTGCTGACCTACAGGAGATCCCTTTTATCACATCTGGATGGCAGC 2265
Db 2161 AAGAGCAAGCTACTTGTGCTGACCTACAGGAGATCCCTTTTACCACTCTGGAAGGACCC 2220
Qy 2266 CAGCGTACTTGTGCTGACCTTTCACCTGAGCGTGTGAGCCAGCAGCTAGTGTAGCTG 2325
Db 2221 CAGCAGTATCTGACCTGTGACCTTCACTGAGAGGAGATCAAGCGCAGCAACAGGAGCTG 2280
Qy 2326 GCTGCAAGCTGTGGGTGTGGCAGGTGGAGGGGAGGCGAGAGCTTTCAGCATCAATTC 2385
Db 2281 GCCTGCAAGGTGTGGGTGTGGCAGGTGGAGGAGATGGGCGAGAGCTTCAACATCAATTC 2340
Qy 2386 AACATCAAGAGCAGCAAGGTTTGTGAGCTGTGCTGCTGCTGAGAGTGAAGCGGGGCTC 2445
Db 2341 AACATCAAGAGCAGCAAGGTTTGTGAAATTTGTGCTGCTGAGAGTGAAGCGGGGCTC 2400
Qy 2446 CCAGCCTGTGTGGGCGCCAGTGTCTCAAGATCCCTTCTCTTCTGCGCAGAGATATTT 2505
Db 2401 CCAGCCTGTGTGGGCGCCAGTGTCTCAAGATCCCTTCTCTTCTTCTGCGCAGAGATATTC 2460
Qy 2506 TCCAGCTGTGAACCCCTGTAGCGGGGTGCCAGCTGCGGAGCTCTGCGGCCAGAACTC 2565
Db 2461 GCCAGTCTGGAGCCACCCCTGACCGCGGGGCGAGCTGGAGAACTCTTAGCCAGAACTT 2520
Qy 2566 CACTGTGAGAGCCATCTCAGCTTCTTGTGCTTCAAGCCAGCCCAAGCAGCATGATCTC 2625
Db 2521 CACTGTGAGAGCCATCTTAGCTTCTTGTGCTTCAAGCCAGCCCAAGCAGCATGATCTC 2580
Qy 2626 AACCTGTGGAGGCGGCACTTCCCAACGGCAACTCAGCAGCTGGCTGAGCAGCTG 2685
Db 2581 AACCTATGGAGGCAAGGCACTTCCCAACGGCAACTCAGCAGCTGGCTGAGCAGCTG 2640
Qy 2686 GCTGTGAGCTGGGCGCAGCAGCTGCGCTTCTTCAAGTGTGCGAGGCTGAGTGTGA 2742

Db 958 CTCGAGTACAACTCCGGGTCTACTGCTGATGACACCCACGATGCACCTCAAGGAGTG 1017
Qy 2089 GTGAGCTGGAGAGAGCTGGGGGGACAGCTGATCCAGAGCCACGGGTCTCTGCATTC 2148
Db 1018 GTGAGCTGGAGAGAGCTGGGGGGACAGCTGATCCAGAGCCACGGGTCTCTGCATTC 1076
Qy 2149 AAGGACAGTTACCAACACCTTGGCCCTATCCATCCAGATGTCGCCAGCTCCCTGTGGAAG 2208
Db 1077 AAGGACAGTTACCAACACCTT - GCCCTATCATCCAGATGTCGCCAGCTCCCTGTGGAAG 1134
Qy 2209 AGTAAGCTCTTGTACCTACCAAGAGATCCCCCTTTTATCACATCTGGAATGCGACGCGAG 2268
Db 1135 AGTAAGCTCTTGTACCTACCAAGAGATCCCCCTTTTATCACATCTGGAATGCGACGCGAG 1194
Qy 2269 CGGTACTGTGACGACCTTCAACCTTGGAGCGTGTGAGCCCCAGCACTAGTGAACCTTGCC 2328
Db 1195 CGGTACTGTGACGACCTTCAACCTTGGAGCGTGTGAGCCCCAGCACTAGTGAACCTTGCC 1254
Qy 2329 TGCAGAGCTGTGGGTGTGGCAGGTGGAGGGGACGGGCGAGCTTCAGCATCAACTTCAAC 2388
Db 1255 TGCAGAGCTGTGGGTGTGGCAGGTGGAGGGGACGGGCGAGCTTCAGCATCAACTTCAAC 1314
Qy 2389 ATCAACAAGGACACAAAGTTTGTGAGCTGTGGCTCTGGAGAGTGAAGCGGGGTCCCA 2448
Db 1315 ATCAACAAGGACACAAAGTTTGTGAGCTGTGGCTCTGGAGAGTGAAGCGGGGTCCCA 1374
Qy 2449 GCCCTGTGGGCCCCAGTGCTTCAAGATCCCTTCTCATCTGGGCGAAGAGATAAATTTCC 2508
Db 1375 GCCCTGTGGGCCCCAGTGCTTCAAGATCCCTTCTCATCTGGGCGAAGAGATAAATTTCC 1434
Qy 2509 AGCTGGAACCCACCTCTAGCGGGGTGGCGACTGGCGGACTCTGGCCAGGAACCTCCAC 2568
Db 1435 AGCTGGAACCCACCTCTAGCGGGGTGGCGACTGGCGGACTCTGGCCAGGAACCTCCAC 1494
Qy 2569 CTGGACAGCCATCTCAGCTTCTTTGCTTCAAGCCAGCCAGCCAGCCATGATCCTCAAC 2628
Db 1495 CTGGACAGCCATCTCAGCTTCTTTGCTTCAAGCCAGCCAGCCAGCCATGATCCTCAAC 1554
Qy 2629 CTGTGGAGCGGGGCACTTCCCAACGGCAACTCAGCCAGCTGGCTGCGAGCAGTGCT 2688
Db 1555 CTGTGGAGCGGGGCACTTCCCAACGGCAACTCAGCCAGCTGGCTGCGAGCAGTGCT 1614
Qy 2689 GGACTGGCCAGCAGCAGCTGGCCCTC-TTCACAGTG-TGGAGGCTGAGTGTGAGGCC 2746
Db 1615 GGACTGGCCAGCAGCAGCTGGCTTCTTTTTCAGAGTTCGGAGGCTGAGTGTGAGGCC 1674
Qy 2747 GGCCAG 2752
Db 1675 GGCCAG 1680

RESULT 12

US-10-296-115-365
; Sequence 365, Application US/10296115
; Publication No. US20040053248A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: No. US20040053248A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 784PCT
; CURRENT APPLICATION NUMBER: US/10/296,115
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 1478
; SEQ ID NO 365
; LENGTH: 1321
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-296-115-365

Query Match

43.8%; Score 1206.6; DB 18; Length 1321;

Best Local Similarity 98.0%; Pred. No. 1.4e-299;
Matches 1295; Conservative 0; Mismatches 19; Indels 7; Gaps 7;
Qy 1435 CACACACTGCACACAGCTCTCCACCTCTGAGCCGAGAGTTCTGCTCCCGCTCTCC 1494
Db 1 CACACACTGCACACAGCTCTCCACCTCTGAGCCGAGAGTTCTGCTCCCGCTCTCC 60
Qy 1495 ACCAGAACTACTTCCGCTCCCTGCCCCGAGGCAACAGCAATGACCTTATGGACCTTC 1554
Db 61 ACCAGAACTACTTCCGCTCCCTGCCCCGAGGCAACAGCAATGACCTTATGGACCTTC 120
Qy 1555 AACTTCTCGGGGGCGGCTGATGATCCCTAATACAGGTTATCAGCTCTCATCCCCCA 1614
Db 121 AACTTCTCGGGGGCGGCTGATGATCCCTAATACAGGTTATCAGCTCTCATCCCCCA 180
Qy 1615 GATGCATACCCCGAGGGAAGATCTATGAGATCTAGCTCACGCTGCACAGCCGGAAGAC 1674
Db 181 GATGCATACCCCGAGGGAAGATCTATGAGATCTAGCTCACGCTGCACAGCCGGAAGAC 240
Qy 1675 GTGAGTTGCCCCCTAGCTGGCTGTGAGACCCCTGCTGAGTCCCATCGTTAGCTGTGACCC 1734
Db 241 GTGAGTTGCCCCCTAGCTGGCTGTGAGACCCCTGCTGAGTCCCATCGTTAGCTGTGACCC 300
Qy 1735 CCT-GGCGTCTGCTCACCGGCCAGTCACTCCT-GGCTATGGACCACTGT-GGCGAGCCC 1791
Db 301 CCTGGGCGTCTGCTTACCGGCCAGTCACTCCTGGGGTATGGAACCACTGTGGGGAGCCC 360
Qy 1792 AGCCCTGACAGCT-GGAGCCTGCGCTCAAAAAGCAGTCTGTCGAGGGCAGCTGGGAGGA 1850
Db 361 AGCCCTGACAGCTGGGAGCCTGCGCTCAAAAAGCAGTCTGTCGAGGGCAGCTGGGAGGA 420
Qy 1851 TGTGCTGCACTGGGGGAGAGCGCCCTCCCACTTACTACTGCGAGCTGAGGCGCAG 1910
Db 421 TGTGCTGCACTGGGGGAGAGCGCCCTCCCACTTACTACTGCGAGCTGAGGCGCAG 480
Qy 1911 TGCTCTGCTAGCTTTCACAGCAGCTGGGCGCTTTTGCCCTGCTGGGAGAGCCCTCAG 1970
Db 481 TGCTCTGCTAGCTTTCACAGCAGCTGAGCCCTATGCCCCCTGTTGGGAGAGCCCTCAG 540
Qy 1971 CGTGGCTGCGCCAAAGCGCTCAAGCTGCTTGTGTTTGGCCGGTGGCTGCACCTCCCT 2030
Db 541 CGTGGCTGCGCCAAAGCGCTCAAGCTGCTTGTGTTTGGCCGGTGGCTGCACCTCCCT 600
Qy 2031 CGAGTACACATCCGGGTCTACTGCTGATGACACCCAGATGCACTCAGAGAGTGGT 2090
Db 601 CGAGTACACATCCGGGTCTACTGCTGATGACACTCAGATGCACTCAACCTAGTGGT 660
Qy 2091 GCAGCTGGAGAGCAGCTGGGGGACAGCTGATCCAGGAGCCACCGGTCTCTGCACTTCAA 2150
Db 661 GCAGCTGGAGAGCAGCTGCGGGAACAGCTGATCCAGGAGCCACTGGTACTGCACTTCAA 720
Qy 2151 GGACAGTTACCAACACTCGGCTATCCATCCAGATGTGCCAGCTCTCTGTGGAAGAG 2210
Db 721 GGACAGTTACCAACACTCGGCTATCCATCCAGATGTGCCAGCTCTCTGTGGAAGAG 780
Qy 2211 TAGCTCTTGTGCTGCTGAGAGATCCCTTTTATCATCTGGAATGGCAAGCAGCG 2270
Db 781 TAGCTCTTGTGCTGCTGAGAGATCCCTTTTATCATCTGGAATGGCAAGCAGCG 840
Qy 2271 GTACTTGCACCTGCACTTCACTCGGAGGCTGTGAGCCCGCAGCACTAGTACCTGGCCTG 2330
Db 841 GTACTTGCACCTGCACTTCACTCGGAGGCTGTGAGCCCGCAGCACTAGTACCTGGCCTG 900
Qy 2331 CAAGCTGTGGGTGTGCGAGGTGAGGGGCGAGCGGGCAGAGCTTCAAGTCAACAT 2390
Db 901 CAAGCTGTGGGTGTGCGAGGTGAGGGGCGAGCGGGCAGAGCTTCAAGTCAACAT 960
Qy 2391 CACCAAGGACACAAAGTTTCTGAGCTGTGGCTCTGGAGAGTGAAGCGGGGTCCGAGC 2450
Db 961 CACCAAGGACACAAAGTTTCTGAGCTGTGGCTCTGGAGAGTGAAGCGGGGTCCGAGC 1020
Qy 2451 CTTGTGGGCGCCAGTGGCTTCAAGATCCCTTCTCATTTCGGCAGGAAGATAATTTCCAG 2510

Db 1021 CCTGGTGGCCCCAGTGCCTTCAAGATCCCTTCTCATTCGGCAGAGATAAATTTCCAG 1080
Qy 2511 CCTGACCCACCTGTAGGGGGGTGCGAGCTGCGGACTCTGSCCCAGAAACTCCACCT 2570
Db 1081 CCTGACCCACCTGTAGGGGGGTGCGAGCTGCGGACTCTGSCCCAGAAACTCCACCT 1140
Qy 2571 GGACAGCCATCTCAGCTTCTTTGCTCCAAAGCCAGCCCCACAGCCCATGATCTCTCAACCT 2630
Db 1141 GGACAGCCATCTCAGCTTCTTTGCTCCAAAGCCAGCCCCACAGCCCATGATCTCTCAACCT 1200
Qy 2631 GTGGAGGCGGGGACATCTCCCAAGCGCAACCTCAGCCAGTGGCTGCTCAGAGTGGCT-G 2689
Db 1201 GTGGAGGCGGGGACATCTCCCAAGCGCAACCTCAGCCAGTGGCTGCTCAGAGTGGCTGG 1260
Qy 2690 GACTGGGCGCAGCAGACGCTGGGCTC-TTACAGTG-TCCGAGGCTCAGTGGCTGAGGCCG 2747
Db 1261 GACTGGGCGCAGCAGAGGCTGGGCTTCTTTACAGTGTTCGAGGCTGAGTGGCTGAGGCCG 1320
Qy 2748 G 2748
Db 1321 G 1321

RESULT 13

us-10-087-684-1

; Sequence 1, Application US/10087684

; Publication No. US20040029116A1

GENERAL INFORMATION:

; APPLICANT: Edinger, Shlomit R.
; APPLICANT: MacDougall, John R.
; APPLICANT: Millet, Isabelle
; APPLICANT: Ellerman, Karen
; APPLICANT: Stone, David J.
; APPLICANT: Grosse, William M.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Casman, Stacie, J.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Baidog, Ferenc L.
; APPLICANT: Li, Li
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Mishra, Vishnu
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Rastelli, Luca
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Miller, Charles E.
; APPLICANT: Gangolli, Esha A.
; TITLE OF INVENTION: PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-214 CIP
; CURRENT APPLICATION NUMBER: US/10/087,684
; CURRENT FILING DATE: 2003-03-10
; PRIOR APPLICATION NUMBER: 60/253,834
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 60/250,926
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 60/264,180
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/274,194
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/313,656
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/327,456
; PRIOR FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 220
; SOFTWARE: Curaseqlist version 0.1
; SEQ ID NO 1
; LENGTH: 2860
; TYPE: DNA

; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (59)..(2857)
US-10-087-684-1

Query Match 34.0%; Score 936.2; DB 17; Length 2860;
Best Local Similarity 61.7%; Pred. No. 4.1e-230;
Matches 1662; Conservative 0; Mismatches 938; Indels 93; Gaps 7;

Qy 143 ACCAGTGCCTGTGTCACACCCCGAGACCTGTCTCCCACTCTCTGTTGGAGCCCGAGAGATG 202
Db 168 ACTCTCTCCGTCAGCGCCAGCAGAGCCGTGCGCTACTCTCTGCAAGAGCCACAGAGCG 227
Qy 203 TGTACATCGTCAAGAAACAAGCCAGTGTCTGTGTGCAAGGCCGTGSCCCGCCACAGAGA 262
Db 228 CCTACATTTGTAAGAAACAAGCCCTGTGAGCTTCGCTGCGCGGCTTCCCCGCCACACAGA 287
Qy 263 TCTTTCTCAAGTGCACACGGGGAGTGGGTGCGCCAGGTGGACCACTGATCGAGCGCAGCA 322
Db 288 TCTACTTCAAGTGCACACGGCGAGTGGGTGAGCCAGAACGACCAAGCTCACACAGAGGCC 347
Qy 323 CAGACGGAGCAGTGGGCTGCCCAACATGAGAGTCCGCATTAATGTCTCAAGCAGCAGG 382
Db 348 TGGATGAGGCCACCGGTCTGCGGGTGGCGAGGTGCAGATCGAGGTGTCGCGGCGAGCG 407
Qy 383 TCCAGAAGGTGTTCCGGGCTGGAGGAATACTGTGCCAGTCCGTGGCATGAGGTCTCTCGG 442
Db 408 TGGAGGAGCTCTTTGGGCTGGAGGAATACCTGTGCGCAGTCCGTGGCTTGGAGCTTCCGCG 467
Qy 443 GCACCAACAGAGTCAGAAAGCCCTACATCCGCATAGCCAGATTGCGCAAGAACTTCGAGC 502
Db 468 GCACCAACAGAGTCGCCGAGCTACGTCCGCATCGCTACCTGCGCAAGAACTTCGATC 527
Qy 503 AGGAGCGCTGGCCAAAGAGGTGTCTCTGAGCAGAGGAGCATCGTGTGCTGCTGCTGCTCAC 562
Db 528 AGGAGCTCTGGGCAAGAGAGGTGCCCTTGGACCATGAGGTCTCTCTGAGTGGCGCGCGC 587
Qy 563 CGGAGGGCATCCCTCCAGCCGGGTGGAGTGGGTCCGGAAACGAGGACCTGCTGTGACCCGT 622
Db 588 CGAGGGGGTGCCTGTGGCGAGTGGAAATGGCTCAAGAAATGAGGATGTTCATGACCCCA 647
Qy 623 CCTGACCCCAATGTATACATCACCGGGAGCAGACCTGTGTTGTCGACAGCCCGCGCC 682
Db 648 CCAGAGCACCACAACTTCTCTGCTCACCATCGACCAACCTCATCATCCGCGAGCGCGCC 707
Qy 683 TTGCTGACAGGCCAACTACACCTGCTGGCCAAAGAACATCGTGGCAGAGTGGCGCAGCG 742
Db 708 TGTGCGACACTGCCAACTATACCTGCGTGGCCAAAGAACATCGTGGCCAAACGCGGAGCA 767
Qy 743 CCTCCGCTGTGTCTACGTCTACGTGAAACGCTGGGTGGTCGACGTGACCGAGTGGTCCG 802
Db 768 CCACTGCCACCGTCATCGTCTAGTGAATGGCGGCTGGTCCAGCTGGGCAAGATGGTTCAC 827
Qy 803 TCTGACAGCCGACGTGTGGGCGCGGTGGCAGAAACGGAGCCGAGGTGCACCAACCCCG 862
Db 828 CCTGCTCCAAACCGCTGTGGCCGAGGCTGGCAGAAAGCGCACCCCGACCTGCAACACCCG 887
Qy 863 CGCTCTCAACCGGGGGCGCTTTCTGTGAGGGGGCAGAAATGTTCAGAAAAACAGCTTCGCCCA 922
Db 888 CTCACACTCAACGGAGGGGCGCTTCTGCGAGGGCCAGGCAATTCACAGAAAGACCGCTTGCA 947
Qy 923 CCCTGTGCCAGTAGACCGCAGCTGGAGCCCGTGGAGCAAGTGTGCTGGGCTGTGGGCTGG 982
Db 948 CCACTGCCCCAGTTCGATGGGGCGTGGAGTGGAGCAAGTGTGAGCTTCAGCTTCAGCACTG 1007
Qy 983 ACTGCACCCCACTGGCGAGCCGTGAGTGTCTGTACCCAGCACCCCGCAACGAGGGGAGG 1042
Db 1008 AGTGTGCCCACTGGCGTAGCCGCGAGTGCATGSCGCCGCCACCCCAAGAACGGAGGCGGTG 1067
Qy 1043 AGTGCAGGGGCACTGACCTTGGACACCCGCCAACTGTATCAGTGTACCTCTGTGTACACAGT 1102
Db 1068 ACTGCAGCGGACGCTGCTCGACTCTAAGAACTGCACAGATGGGCTGTGTCATGCAACTGG 1127

Query Match	34.0%;	Score 936.2;	DB 17;	Length 2860;
Best Local Similarity	61.7%;	Pred. No. 4.1e-230;		
Matches 1662;	Conservative 0;	Mismatches 938;	Indels 93;	Gaps 7;
QY	143	ACCCAGTGCCTGGTGCCAAACCGGACACTGCTTCCCCACTTCTCGTGGAGCCGAGATG	202	
DB	168	ACTCTTCCCGTCAGCGCCAGCAGCGCTGCCCTACTTCTCGAGGCCACAGACG	227	
QY	203	TGTATATCGTCAAGAAACAAGCAGTGCTGTTGTGTGCAAGCCGCTGCCCGCCACGAGA	262	
DB	228	CCTACATTGTGAAGAAACAAGCCTGTGAGCTTTCGTCGCGCGCTTCCCGCCACACAGA	287	
QY	263	TCTTCTTCAAGTGCAAACGGGAGTGGGTGCGCCAGGTGGACCACTGTCATCGAGCGCAGCA	322	
DB	288	TCTACTTCAAGTGCNAACGGCAGTGGGTGACGCAAGACCACTGTCACACAGGAAGGCC	347	
QY	323	CAGACGGAGCAGTGGGCTGCCACCATGAGGTCCGATTAAATGTTCTCAAGGCAGCAGG	382	
DB	348	TGGATGAGGCCACCGCGCTCGCGGTGCGCAGGTGCAGATCGAGGTGTCGCGGCAGCAGG	407	
QY	383	TCGAGAAGTGTTTCGGGCTCGAGGAATACTGGTGCACGTGGTGGCATGAGATCTCTCGG	442	
DB	408	TGAGGAGTCTTTGGGCTCGAGGATTTACTGGTGCCAGTGGTGGCTTGAGCTCCGACG	467	
QY	443	GCACCAACAAGAGTCAGAAGCGCTTACATCCGCATAGCCAGATTGCGCAAGAACTTCGAGC	502	
DB	468	GCACCAACAAGAGTCGCGGAGCCTTACGTCCGCATCGCCTACCTGCGCAAGAACTTCGATC	527	
QY	503	AGAGCCGCTGGCCCAAGGAGGTTCCTCTGAGCAGGGCATGTGCTCTCCCTCGCGTCCAC	562	
DB	528	AGAGCCTCTGGGCAAGGAGTGCCTTGACCAATGAGGTTCTCTCGAGTGGCGCCCGC	587	
QY	563	CGGAGGCATCCCTCCAGCCGAGTGGAGTGGCTCCGGAACGAGGACCTGGTGGACCCGT	622	
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QY	623	CCTTGAACCCCAATGTATACATACGCGGAGCAGACGCTGGTGGTGCAGACGCCCGCC	682	
DB	648	CCGAGGACACCAACTTCTCTGCTCACCATCGACACCAACCTCATCATCCGCAGGCCCGCC	707	
QY	683	TTGCTGACCGGCCCACTTACACCTGCTGGCCAGACATCGTGGCAGCTGCGCGCAGCG	742	
DB	708	TGTGGAACACTGCCAACTATACCTTGCCTGGCCAAAGAAACATCGTGGCCAAACCGCGGAGCA	767	
QY	743	CCTCCGCTGCTGTATCGTACGTGAACCGGTGGGTGGTGCAGTGTGACCGAGTGTGTCG	802	

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 Db 528 AGGAGCGCTGGCCAAAGAGGTGTCCTGGAGCAGGCGATCGTGTGCTCCCTGCGCTCCAC 587
 Qy 563 CGGAGGGCATCCCTCCAGCCGAGGTGAGTGGCTCCGGAACGAGGACCTGGTGACCCGT 622
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 Qy 1673 AGTGAGGTTGCCCTAGCTGCTGTCAGACCCCTGCTGAGTCCCATGCTTGTAGCTGTGGAC 1732
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 Db 1908 GTGCCGCTGACTGGATCTTTTCACTCAAGACCCAGGCCACACAGGGCCACTGGGAGGAG 1967
 Qy 1853 TGCTGACCTGGGCGAGGCGCCCTCCACCTCTACTACTGCTGCTGCTGAGGAGGAGG 1912
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 Job time : 2468 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 7, 2005, 11:56:52 ; Search time 13388 Seconds
(without alignments)
7824.385 Million cell updates/sec

Title: US-10-624-932C-1

Perfect score: 2752

Sequence: 1 ccgcggggcccccgcgcgg.....tgagtgctgagcggccag 2752

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1.*

2: gb_est2.*

3: gb_est3.*

4: gb_est4.*

5: gb_est5.*

6: gb_est6.*

7: gb_est7.*

8: gb_est8.*

9: gb_est9.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	960.2	34.9	2802	9 AY406491	AY406491 Homo sapi
2	950.4	34.5	2791	9 AY406493	AY406493 Mus muscu
3	923.4	33.6	3790	3 AK031655	AK031655 Mus muscu
4	884	32.1	1852	3 CR598115	CR598115 full-leng
5	872.4	31.7	3866	3 AK018177	AK018177 Mus muscu
6	814	29.6	2802	9 AY406492	AY406492 Pan trogl
7	810.4	29.4	2532	9 AY411747	AY411747 Homo sapi
8	780.4	28.4	2532	9 AY411749	AY411749 Mus muscu
9	768.6	27.9	1034	4 B1758231	B1758231 603029876
10	736.6	26.8	1532	3 BC033727	BC033727 Homo sapi
11	735.2	26.7	788	1 AI951556	AI951556 wv36f04.x
12	721.6	26.2	796	5 BX348193	BX348193 BX348193
13	716.4	26.0	818	4 B1818609	B1818609 603033362
14	692	25.1	853	5 BX364574	BX364574 BX364574
15	678.2	24.6	2532	9 AY411748	AY411748 Pan trogl
16	672.6	24.4	934	2 BF311804	BF311804 601897316
17	666	24.2	900	5 BX345406	BX345406 BX345406
18	665	24.2	859	2 BF311896	BF311896 601897733
19	645.2	23.4	977	5 BX345407	BX345407 BX345407
20	631.2	22.9	1072	5 BX422753	BX422753 BX422753
21	618.8	22.5	756	5 BU612387	BU612387 UI-M-BW0
22	613.2	22.3	874	5 BQ689148	BQ689148 AGENCOURT
23	610.2	22.2	2775	9 AY401471	AY401471 Mus muscu
24	607	22.1	889	5 BQ691915	BQ691915 AGENCOURT

25	599	21.8	2775	9 AY401469	AY401469 Homo sapi
26	595.2	21.6	601	1 AL516580	AL516580 AL516580
27	589.4	21.4	604	2 BE314370	BE314370 601147261
28	586.6	20.6	678	6 CA749784	CA749784 UI-M-FD0-
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32	494.2	18.0	499	7 CR747398	CR747398 CR747398
33	486.2	17.7	548	5 BX452510	BX452510 BX452510
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38	433	15.7	471	5 BX282095	BX282095 BX282095
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40	424	15.4	843	4 EG913440	EG913440 602811321
41	417.8	15.2	856	7 CN164143	CN164143 994266 MA
42	411.8	15.0	749	7 CF735417	CF735417 UI-M-HB0-
43	410.6	14.9	1111	4 BG298307	BG298307 602397080
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ALIGNMENTS

RESULT 1	AY406491	2802 bp	DNA	linear	GSS 15-DEC-2003
LOCUS	AY406491	Homo sapiens UNC5C gene, genomic survey sequence.			
DEFINITION	AY406491.1	GI:39762465			
ACCESSION	AY406491				
VERSION	AY406491.1				
KEYWORDS	GSS.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 2802)				
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.				
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios				
JOURNAL	Science 302 (5652), 1960-1963 (2003)				
PUBMED	14671302				
REFERENCE	2 (bases 1 to 2802)				
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.				
TITLE	Direct Submission				
JOURNAL	Rockville, MD 20850, USA				
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment.				
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	/db_xref="taxon:9606"				
	<1..>2802				
	/gene="UNC5C"				
	/locus_tag="HMC2575"				
ORIGIN					
Query Match	34.9%	Score 960.2;	DB 9;	Length 2802;	
Best Local Similarity	61.3%	Pred. No. 6.4e-192;			
Matches 1682;	Conservative	0; Mismatches 995;	Indels 69;	Gaps 6;	
QY	57	GCCTGGCGCTGTGCGCAGCGCTCTCGGCGATAGTCTCGCGCTTGGCTCGCGCTCGGG	116		

Db 66 GCTCGTGTACTGCCCTGCTCAGCGCCAGCGGCACCTGGCTCCGCCGCCAAGA 125
Qy 117 TGCCACGAGTGCCACCGTGGCCAAACCAGTGCTGTGTGCCAA CCCGACCTGCTTCC 176
Db 126 TGATGACTTTTTCATGAACCTCCAGAAACTTTTCTCTGTGATCCACCTGAGCGCTCGCC 185
Qy 177 CCACTTCCTGGTGAGGCCGAGGATGTATCATGCTCAAGAAACAAGCCAGTGTCTGTGT 236
Db 186 ACATTTCTTATTGAGCTGAGAGGCTTATATTTGTGAGAAATAGCTGTGAACCTGTGA 245
Qy 237 GTGCAAGCCGCTGCCGCCACGAGATCTTTCTTCAAGTGCAACGGGAGTGGGTGGCCCA 296
Db 246 CTGTAAAGCAAGCCCTGCCACCAGATCTATTTCAAGTGTAATAGTGAATGGGTTCATCA 305
Qy 297 GGTGGACCACTGATCGAGCGCAGCACAGACGGGAGCGTGGGCTGCCACCACTGAGGT 356
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Db 366 GAGCATTGAGATTTCCGCCCAGACAGTGGGAAGAACTCTTTGGACCTGAAGATTACTGGTG 425
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VERSION AY406493.1 GI:39762467
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 2791)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 2791)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
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RESULT 3
AK031655
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DEFINITION
AK031655 3790 bp mRNA linear HTC 03-APR-2004
Mus musculus 13 days embryo male testis cDNA, RIKEN full-length
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elegans) 3, full insert sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
AK031655 GI:26327502
HTC; CAP trapper.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)

JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,

Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Wataniki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Murakami, M., Inoue, Y., Kira, A., and Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
 Genome Res. 10 (11), 1757-1771 (2000)
 20530913
 11076861

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

4 The RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium.

Functional annotation of a full-length mouse cDNA collection
 Nature 409, 685-690 (2001)

5 The PANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)

6 (bases 1 to 3790)

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, P., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, P., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tonaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

Direct Submission

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@ac.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.
 URL: http://genome.gsc.riken.jp/
 URL: http://fantom.gsc.riken.jp/.

Location/Qualifiers

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ORIGIN

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Db	2906	CCGTCTTGG	AAGAAATGG	GGAAGACATG	AGACAGTGGTGT	TACTTTGGCAGCAGAAAGGACAGT	2965	
Qy	2738	GCTGA	2742					
Db	2966	ATTGA	2970					
RESULT 4								
CR598115								
LOCUS								
DEFINITION								
ACCESSION								
VERSION								
KEYWORDS								
SOURCE								
ORGANISM								
REFERENCE								
AUTHORS								

RESULT 4	CR598115	1852 bp	mrna	linear	HTC 21-JUL-2004
LOCUS	CR598115	full-length cDNA clone CS0DA006XG16 of Neuroblastoma of Homo sapiens (human).			
DEFINITION					
ACCESSION	CR598115				
VERSION	CR598115.1	GI:50478922			
KEYWORDS	HTC; CNSLT_cDNA.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1 (bases 1 to 1852)				
AUTHORS	Li, W.B., Gruber, C., Jesse, J. and Polayes, D.				

TITLE
JOURNAL
REMARK

Full-length cDNA libraries and normalization
Unpublished
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paraday Avenue
2 (bases 1 to 1852)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segre@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
Location/Qualifiers
source
1..1852
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODA006YG16"
/tissue_type="Neuroblastoma"
/plasmid="pCMVSPORT_6"

ORIGIN

Query Match 32.1%; Score 884; DB 3; Length 1852;
Best Local Similarity 100.0%; Pred. No. 7.5e-176; Mismatches 0; Indels 0; Gaps 0;
Matches 884; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1869 GGAGCGCCCTCCACCTTACTACTGCGAGTGGAGGCGAGTGCCTGCTACGTTCTTAC 1928
Db 1 GGAGCGCCCTCCACCTTACTACTGCGAGTGGAGGCGAGTGCCTGCTACGTTCTTAC 60

Qy 1929 CGACAGCTGGCGCTTGGCCCTGTGGAGAGGCGCTCAGCTGGTGGCGCAAGCG 1988
Db 61 CGACAGCTGGCGCTTGGCCCTGTGGAGAGGCGCTCAGCTGGTGGCGCAAGCG 120

Qy 1989 CCTCAAGCTGCTTCTGTTGGCGCGTGGCTGCGACCTCCCTCGAGTACACATCCGGT 2048
Db 121 CCTCAAGCTGCTTCTGTTGGCGCGTGGCTGCGACCTCCCTCGAGTACACATCCGGT 180

Qy 2049 CTACTGCTGCATGACACCCACGATGCACTCAAGGAGTGTGTGCGCTGGAGAGCAGCT 2108
Db 181 CTACTGCTGCATGACACCCACGATGCACTCAAGGAGTGTGTGCGCTGGAGAGCAGCT 240

Qy 2109 GGGGGGACGTGATCAGAGGCCACGGTCTCTGCACTTCAAGACAGTTACCAACCT 2168
Db 241 GGGGGGACGTGATCAGAGGCCACGGTCTCTGCACTTCAAGACAGTTACCAACCT 300

Qy 2169 GCGCTATCCATCCACGATGCGCCAGCTCCCTGTGGAAGTAAAGCTCTTGTGAGCTA 2228
Db 301 GCGCTATCCATCCACGATGCGCCAGCTCCCTGTGGAAGTAAAGCTCTTGTGAGCTA 360

Qy 2229 CCAGGAGATCCCTTTTATCACAFTCTGGAATGGCAGCGGCTGCTGCACTGCACTT 2288
Db 361 CCAGGAGATCCCTTTTATCACAFTCTGGAATGGCAGCGGCTGCTGCACTGCACTT 420

Qy 2289 CACCTGAGGCTGTACGCCCCAGCACTAGTGACCTGGCTGCAAGCTGTGGTGTGGCA 2348
Db 421 CACCTGAGGCTGTACGCCCCAGCACTAGTGACCTGGCTGCAAGCTGTGGTGTGGCA 480

Qy 2349 GGTGGAGGGGACGGGACAGCTTTCAGTCATCACTCAACATCAACGACGACAGGTT 2408
Db 481 GGTGGAGGGGACGGGACAGCTTTCAGTCATCACTCAACATCAACGACGACAGGTT 540

Qy 2409 TGCTGAGCTGTGCTCTGGAGAGTGAAGCGGGGCTCCAGCCCTGCTGGGCCCGAGTGC 2468
Db 541 TGCTGAGCTGTGCTCTGGAGAGTGAAGCGGGGCTCCAGCCCTGCTGGGCCCGAGTGC 600

Qy 2469 CTTCAAGATCCCTTCTCTATTCGGCAGAGATAAATTTTCAGCTGGACCCAGCTGTAG 2528
Db 601 CTTCAAGATCCCTTCTCTATTCGGCAGAGATAAATTTTCAGCTGGACCCAGCTGTAG 660

Qy 2529 GCGGGTGGCAGCTGGCGGACTCTGGCCCGAGAACTCCACTGGACGCCATCTCAGCTT 2588
Db 661 GCGGGTGGCAGCTGGCGGACTCTGGCCCGAGAACTCCACTGGACGCCATCTCAGCTT 720

Qy 2589 CTTTGCCTCCAAAGCCCGAGCCCGACAGCATGATCCTCAACCTGTGGAGGCGCGCACTT 2648
Db 721 CTTTGCCTCCAAAGCCCGAGCCCGACAGCATGATCCTCAACCTGTGGAGGCGCGCACTT 780

Qy 2649 CCCCAAGCGGACCTCAGCCAGCGTGGCTGCGAGCTGGTGGCTGCGAGCCAGCAGCGC 2708
Db 781 CCCCAAGCGGACCTCAGCCAGCGTGGCTGCGAGCTGGTGGCTGCGAGCCAGCAGCGC 840

Qy 2709 TGGCTCTTCCACAGTTCGAGGCGTGTGCTGAGGCGCGCCAG 2752
Db 841 TGGCTCTTCCACAGTTCGAGGCGTGTGCTGAGGCGCGCCAG 884

RESULT 5
AK018177
LOCUS
DEFINITION
Mus musculus adult male medulla oblongata cDNA, RIKEN full-length
enriched library, clone:630415B02 product:TRANSMEMBRANE RECEPTOR
UNC5H2 homolog [Rattus norvegicus], full insert sequence.
ACCESSION
AK018177
VERSION
AK018177.1 GI:12857775
KEYWORDS
HTC; CAP trapper.
SOURCE
Mus musculus
ORGANISM
Mus musculus
REFERENCE
1
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
PUBMED
10349636
2
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20493174
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11042159
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Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kiteunai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamanoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
PUBMED
11078861
4
The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
5
The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 3866)
Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H.,
Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y.,
Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K.,

1560	Db	GTGCGCGTCTTTGTGGTGTAGCGGTTCTCATGCGCGAGGAGTGATCGTATACCGAGA	1619
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1620	Db	AATCGCGGAGTTCGACACGGACATCACCGACTCTCTGCGGCCCTCATCTGGTGGCTTC	1679
1258	Qy	CAGCCGTCAGCATCAAGCCGAGCAAGCAGACAAACCCCATTTGCT-----CACATC	1311
1680	Db	CACCTGTCAACTTCAAGACTGCAAGGCCCAACAAACCCGAGCTCTCTGCACCCGTCGCGC	1739
1312	Qy	CAGCGGACCTCAGCACCAACACACCTTACCAGGGCAGTCTCTGTCTCCCGGACAGA-	1370
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1371	Qy	-----TGGGCCCCAGGCCCAAG	1386
1800	Db	TCCGCCCAAGATCCCACATGACTAATTGCCCCCTGTGTGATCCCCCTGCCAGCCTCAAG	1859
1387	Qy	TTCCAGCTCACCAATGGGCACTGCTCAG-----C	1416
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1477	Qy	TTGCTCTCCGCGCTCTCACCC-----AGAACTACTTTCGCTCCCTGCCCCGAGGCACC	1530
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2100	Db	GGGCTCAGCCTGTTGGTATCAAAATGGAGCCATTTCCCCAGGGCGAAGTTCTATGACCTGTAT	2159
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1831	Qy	TGCGAGGGCAGCTGGGAGGATGTCTCACTTGGCGGAGAGGGCGCCCTCCCACTCTAC	1890
2340	Db	CATCAGGGCCACTGGGAGAGGTGTGACCTTGTATGAGGAGACCTTCAACACACCTCTGC	2399
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1951	Qy	CTGGTGGGAGGGCCCTCAGGGTGGCTGCGGCCAGCGCCTCAAGCTGCTTCTGTTTGGC	2010
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2011	Qy	CCGGTGGCTGCACCTCCCTCGAGTACAAATCCGGGTCTACTCGCTGATGACACCCAC	2070
2520	Db	CCAGCCTCTGCACCTCCCTGGAGTATAGCCTCAGGGTCTACTGTCTGGAGGACACACCT	2579
2071	Qy	GATGCACTCAAGGAGGTGTGCAGCTGGAGAAGCAGCTGGGGGACAGCTGATCCAGGAG	2130
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Db	2640	CCCAAGCCTTTGTCTTTTAAAGACAGTTACCAACAACCTACGCTCTCCCTTCCATGACATC	2699
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Qy	2311	AGCACTAGTACCTTGGCTCCAGACTGTGGTGTGGCAGGTGGAGGCGGACGGCAGCAGC	2370
Db	2820	GCCTCCACGAGATTACCTCTTAAGGCTGTGGTGGCGAGGTCTGAAGGGGAAGGCCAGATT	2879
Qy	2371	TTCAGCATCAACTTCAACATCACCC--AAGGACACAAGGTTTGTGTAGCTGTGGCTCTG	2427
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Qy	2608	CCACAGCCATGATCTCAACCTGTGGAGGCGCGGACCTTCCCAACGCAACCTCAGC	2667
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Qy	2668	CAGCTGGCTGCACAGTGGCTGCACTGGGCGCCAGCAGCGCTGGCTCTTTCACAGTGTG	2727
Db	3180	AGCTTGGCCAGTGCCTTGGAGGAGATGGGCAAGTGAAGTGTGGTAGCCATGGCCACA	3239
Qy	2728	GAGGCTGAGTGTGAG	2743
Db	3240	GATGGCGATTGTGAG	3255
RESULT 6	AY406492	2802 bp DNA linear	GSS 15-DEC-2003
LOCUS	Pan troglodytes UNC5C gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.		
DEFINITION	AY406492		
ACCESSION	AY406492.1 GI:39762466		
VERSION	GSS.		
KEYWORDS	Pan troglodytes (chimpanzee)		
SOURCE	Pan troglodytes		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.		
REFERENCE	1 (bases 1 to 2802)		
AUTHORS	Clark,A.G., Glanowski,S., Nielsen,R., Thomas,P., Kejarawal,A., Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B., Ferreria,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.		
TITLE	Inferred nonneutral evolution from human-chimp-mouse orthologous gene trios		
JOURNAL	Science 302 (5652), 1960-1963 (2003)		
PUBMED	14671302		
REFERENCE	2 (bases 1 to 2802)		
AUTHORS	Clark,A.G., Glanowski,S., Nielsen,R., Thomas,P., Kejarawal,A., Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B., Ferreria,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.		
TITLE	Direct Submission		
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA		
COMMENT	This sequence was made by sequencing genomic exons and ordering		

FEATURES		them based on alignment.	Location/Qualifiers	
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Best Local Similarity 53.8%; Pred. No. 4.7e-161;				
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Qy	237	GTGCAAGGCC-----GTGCCGCCACGCGAGATCTTCTTCAAGTGCAACGGGAGTGGGT	290	
Db	246	CTGTAAAGCAAGCCCTGNN	305	
Qy	291	GCGCCAGGTGGACCACTGATCGAGCGCAGCAGCAGCGGAGCAGTGGGCTGCCACCAT	350	
Db	306	NN	365	
Qy	351	GGAGGTCCGCATTAAATGTCTCAAGGACGAGGTGAGAGGTGTTTCGGGCTGGAGGAATA	410	
Db	366	NN	425	
Qy	411	CTGGTGCCAGTGGTGGCATGAGTCTCTCGGCAACCAAGAGTCAGAAAGCCTACAT	470	
Db	426	NN	485	
Qy	471	CCGCATAGCCAGATTGCGCAAGAACTTCAGCAGGAGCGCTGGCCAAAGAGGTGTCCT	530	
Db	486	NN	545	
Qy	531	GGAGCAGGGCATCGTGTCTCCCTCGCGTCCACCGAGGGCATTCCTCCAGCCGAGGTGGA	590	
Db	546	GGAAACAGGAAGTCTTACTCCAGTGTGGCCACCTGAAAGGATCCAGTGGCTGAGNNNN	605	
Qy	591	GTGGCTCCGGAACGAGAACCTGGTGGACCGCTCCCTGGACCCCAATGTATACATCAGCG	650	
Db	606	NNNNNGAATAATGAAAGATAATTTGATCCCGCTTGAAGATCGGAATTTTATATTACTAT	665	
Qy	651	GGAGCAGCCTGGTGGCGAGCGCCGCTGTCTGACAGCGCCAACTACACCTCGT	710	
Db	666	TGATCAAACTCATATAAGCAGGCGCCGACTCTCTGATCTGCAATTTATACCTGTGT	725	
Qy	711	GGCCAAAGAAACATCGTGCGACGTCGCGCGCAGCGCTCCGCTGTGTCTGTCATCGTCACTGAA	770	
Db	726	TGCCAAAACATTTGTTGCCAAGAGGAAGTAACTGCCACTGTCTATGTCTATGTCAA	785	
Qy	771	CGGTGGTGGTGCAGCTGACCGATGTGTCGTCGAGCGCGCAGCTGTGGGCGCGGTG	830	
Db	786	CGGTGGCTGTGTCACCTGGAACGAGGTGTGTGTGTGTAACAGCGCTGTGGACAGGGTA	845	
Qy	831	GCAGAAACGAGCGGAGCTGCACCAACCGCGCGCTCTCAACGGGGCGCTTTCTGTGA	890	
Db	846	TCAGAAACGTAACAGGACTTTGTATCAACCCCGCACCACTCAATGGGGGTGCTTCTGTGA	905	
Qy	891	GGGGCAGAAATGTCAGAAACAGCCTGCGGCCACCTGTGTCCTGAGTACAGCGCAGCTGGAG	950	
Db				
906	AGGGCAGAGTGTGCAGAAAATAGCCTGTACTACTGTTATGCCCACTGGATGGCAGGTGGAC	965		
Qy	951	CCCGTGGAGCAAGTGTGTGGCTCGGCTGCACTGCCCTGAGAGTGGCCCTCTAGATG	1010	
Db	966	GCCATGGAGCAAGTGTGTACTTGTGGAACTGAGTGCACCCACTGGCGCAGGAGGAGTG	1025	
Qy	1011	CTCTGACCCAGCACCCCGCAACGGAGGGAGGAGTGCAGGGGACATGACCTGGGACACCG	1070	
Db	1026	CACGGCGCCAGCCCCCAAGAAATGGAGGCAAGGACTGCGATGGCCCTGCTTGTGCAATCCAA	1085	
Qy	1071	CAACTGTACCAGTACCTCTGTGTACACAGTGTCTTGGCCCTGAGAGCTGGCCCTCTTA	1130	
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Qy	1131	TGTGGG---CCTCATCGCGGTGGCCCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1187	
Db	1146	TGTTGGGATTTGATAGCAGTGTATCTTTGCTGGCGATCTCTGTAGTTGTGGCCTTGT	1205	
Qy	1188	CGTTTATTCGGGAAGAGAGGGGCTGGACTCAGATGTGGCTGACTGCTGCTCAATTTCTCAC	1247	
Db	1206	TGTGTATCGGAAGAATCATCTGTAATTTGAGTCTGATATTTGACTCTTTCGGCACTCAA	1265	
Qy	1248	CTCAGGCTTCCAGCCGTCAGCATCAAGCCAGCAAGAGCAGCAACCCCATCTGTCTCAC	1307	
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Qy	1368	GGATG-----GGCCAGCCCAAGTTCAGCTCACCCTGCTGCTGCTGCTGCTGCTGCTGCT	1418	
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Qy	1737	TGGCGTCTGTCTACCCGCGCAGTCACTCTGGCTATGGAACACTGTGGGAGGCCAGGCC	1796	
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Qy	1857	GCACCTGGCGCAGGAGGCGCCTCCCACTCTACTACTGCTGCTGAGGCGCAGTGGCTG	1916	
Db	1917	GGTGTGGGAGGAGAAAACCTTCAACACCCCTGCTACATTCAGCTGGATGACAGAGCCTG	1976	
Qy	1917	CTACGCTTTCAACGAGCAGCTGGGCGCGCTTTGCCCTGGTGGGAGAGGCCCTCAGCGTGGC	1976	
Db	1977	CCACATCTCTCACAGAGAACCTCAGCACCTACGCGCTTGGTAGGACATTCACCAACCAAGC	2036	

Qy 1977 TGCGCCAAAGCGCCTCAAGCTGCTTCTGTTTGGCGCGTGCCCTGCACCTCCCTCGAGTA 2036
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Qy 2157 TGAGAGACAGATGGAGACAGCTCTTGAAGAACCCTAAGGCTCTTATTTAAAGGAC 2216
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Qy 2337 GCATGACCTTCACTCTGGAAGATTTAGCCTGAACACAGTGGAGCTGGTTTGCAAACT 2396
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Qy 2337 GTGGGTGTGGCAGGTGGAGGCGGACGGCAGAGCTTCAGCATCAACTTCAACATCACAA 2396
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Qy 2457 GGAACCTACTGGCATGATTTGGCGCTGTGATCTCGGAACACCATCAACCGGTAC 2516
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Qy 2637 GTACTTGAATTAATTTGCCACCAATCCAGCCCACTGGCGTAATCTGGATCTTTGGGA 2696
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Qy 2637 GGGCGGCACTTCCCAACGCGACCTCAGCCAGCTGGCTGCAGCACTGGCTGAGCTGGG 2696
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Qy 2697 AGCAGAGAACTTCCAGATGGAACCTGAGCATCTGGCAGCTGTCTTGAAGAAATGGG 2756
Db |||
Qy 2697 CCAGCCAGAGCTGGCCTCTTCAAGTGTGGAGGCTGAGTGCTGA 2742
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Db |||

RESULT 7
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LOCUS 2532 bp DNA linear GSS 12-DEC-2003
DEFINITION Homo sapiens HCM4327 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION AY411747
VERSION AY411747.1 GI:39767715
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2532)
REFERENCE
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 2532)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
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source 1..2532
/organism="Homo sapiens"
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Qy 412 TGGTGCAGTGCCTGGCATGGAGCTCTCTCGGGCACCACCAAGAGTTCAGAGGCTTACATC 471
Db |||
Qy 73 TGGTGCAGTGCCTGGCTGGAGCTTCGGCGGCGCACCACCAAGAGTTCGCCGAGCTACGTC 132
Db |||
Qy 472 CGCATAGCAGATTGCGCAAGAACTTCGACAGAGCGCTGGCCAAAGAGGTGTCCCTG 531
Db |||
Qy 133 CGCATGCGCTTACCTGCGCAAGAACTTCGATCAGAGGCTCTGGGCAAGAGGTTGCCCTG 192
Db |||
Qy 532 GAGCAGGGCATCTGTGCTGCTCCCTGCTCCACCGAGGGCATCCCTCCAGCGAGGTGGAG 591
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Qy 193 GACCATGAGTTCTCTGTCAGTGCCTCCCGCGGAGGGGTGCTGTGGCGAGGTGGAA 252
Db |||
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Db |||
Qy 253 TGGCTCAAGAAATGAGGATGTCATCGACCCCAACCGAGACCACTTCTCTGCTCACCATC 312
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Qy 313 GACCAACAACCTCATCTATCCGCGAGGCGCCCTGTGCGACACTGCCAACTATACCTGCTG 372
Db |||
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Db |||
Qy 373 GCCAAGAAACATCTGTGTCAGAAACCGCGGAGACCACTGCCACCTGCTATGCTAGCTGAAT 432
Db |||
Qy 772 GGTGGGTGTGTCAGCTGGACCCGAGTGGTCCGTCTGTCAGCGCCAGCTGTGGCGCGCTGG 831
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Qy 433 GGGCGGTGGTCCAGCTGGGCGAGTGTGTCACTCCCTGCTCCAAACCGCTGTGGCGGAGCTGG 492
Db |||
Qy 832 CAGAAACGAGCGCGAGCTGCACCAACCGCGCGCTCTCAACGGGGCGCTTTCTGTGAG 891
Db |||
Qy 493 CAGAAAGCGACCGCGAGCTGCACCAACCGCGCTCCACTCAACGGAGGGGCTTTCTGCGAG 552
Db |||
Qy 892 GGGCAGAAATGTCCAGAAAAACAGCTTCGCCCAACCTGTGCGCCAGTAGACGCGCAGCTGGAGC 951
Db |||
Qy 553 GGCAGGCAATTCAGAAAGACCGCTGCACCACTCTGCCAGTTCGATGGGGGTGGACG 612
Db |||
Qy 952 CCCTGGAGCAAGGTGGCTGGCTGTGGGCTGGAGCTGCACCACTGGCGGAGCCGTGAGTGC 1011
Db |||
Qy 613 GAGTGGAGCAAGTGGTTCAGCTTCAGCACTGAGTGTGCCCACTGGGCTAGCCGCGAGTGC 672
Db |||
Qy 1012 TCTGACCCAGCACCCCGCAACGAGGGGAGTGTGCAGGGCACTGACCTTGAGACACCCGC 1071
Db |||
Qy 673 ATGGCGCCCCCAACCCAGAAACGAGGCGGTGACTGTGAGCGGAGCGCTGCTCGACTCTTAAG 732
Db |||

Db 777 GTCCAGTGGACGGCAGCTGTAGCACGTGGAGCCAGCTGTGGCTGTGGCTTGGCTT 836
 Qy 986 GCACCCACT--GGCGAGCCGTGAGTGTCTGTGACCCAGCACCCCGACGAGGGGAGGA 1043
 Db 837 GCACCCACTTGGGCGAGCCGAGTGTCTGTGACCCAGCACCCCGACGAGGGGAG 896
 Qy 1044 GTG---CGAGGCACTGACCTGGACACCCGCAACTGTACCACTGACCTCTGTGTACACAG 1100
 Db 897 GTGTGCCAGGTCACTGGACCTGGACCCCGGA-TGGTCCAGTGAAGTCTGTGT-CCAC 954
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 Db 955 GGGTCTGGCCCTGAGGACTTGGCTCTGTGTGGGCTCATCCCG 1001

RESULT 10

BC033727
 LOCUS
 DEFINITION Homo sapiens unc-5 homolog A (C. elegans), mRNA (cDNA clone IMAGE:5166762), containing frame-shift errors.
 ACCESSION BC033727
 VERSION
 KEYWORDS
 SOURCE Homo sapiens (human)

ORGANISM
 HTc
 GI:21707230

REFERENCE
 AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1532)
 Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haie, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.P., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Umedin, T.B., Toshikiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A.C., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalek, U., Snailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
 Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

TITLE
 JOURNAL
 PUBMED
 REPECE
 AUTHORS
 TITLE
 JOURNAL

2 (bases 1 to 1532)

Strausberg, R.
 Direct Submission
 Submitted (02-JUL-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK
 COMMENT

NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgabs-x@mail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NIISC),
 Gaithersburg, Maryland;
 Web site: <http://www.nisic.nih.gov/>
 Contact: nisc_mgc@hgr.nih.gov

Akhter, N., Ayele, K., Beckett, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Green, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,

McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W., Taurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAK Plate: 68 Row: i Column: 2
 This clone was selected for full length sequencing because it passed the following selection criteria: Genomescan gene prediction
 This clone has the following problem: frame shifted.

FEATURES

source

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 /mol_type="mRNA"
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Query Match 26.8%; Score 736.6; DB 3; Length 1532;
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 Qy 637 GTATACATCACCGGGAGACACGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 696
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 Qy 757 ATCGTCTAGCTGAACGTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 816
 Db 1032 ATCGTCTAGCTG----- 1043
 Qy 817 TGTGGGCGGCGGTGGCAGAAACGAGCCGAGAGTGCACCAACCCGGCGCTCTCTCAACGGG 876
 Db 1044 ----- 1043
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QY 1117 GACGTGGCCCTCTATGTGGGCTCATCGCGTGGCGCTGCTGCTGCTGCTGCTGCTGCT 1176
Db 1224 GACGTGGCCCTCTATGTGGGCTCATCGCGTGGCGCTGCTGCTGCTGCTGCTGCTGCT 1283
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LOCUS
DEFINITION
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similar to TR:008721 008721 TRANSMEMBRANE RECEPTOR UNC5H1. ;, mRNA
sequence.

AI951556

AI951556.1 GI:5743866

EST.

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Db 301 CTATGACCACTGTGTGGGAGCCAGCCCTGACAGCTGGAGCTTGCCTCAAAAAGCAGT 360
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Db 601 ACAGTCACTCAAGGAGTGGTGCAGCTGGAGAGCAGCTGGAGGAGCAGCTGATCCAGG 660
QY 2129 AGCCAGGCTCTGCACTTCAAGGAGCAGTTACAAACCTGCGCCCTATCCATCCAGATG 2188
Db 661 AGCCAGTGGTACTGCACTTCAAGGAGCAGTTACCAACCTGCGCCCTATTCATCCAGATG 720
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RESULT 12

BX348193/c

LOCUS

DEFINITION

AI951556

AI951556

AI951556

AI951556

AI951556

AI951556

AI951556

AI951556

AI951556

BX348193 796 bp mRNA linear EST 08-APR-2004
BX348193 Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED Homo sapiens
cDNA clone CS00B008YE02 5-PRIME, mRNA sequence.
BX348193
ACCESSION
BX348193
VERSION
BX348193.2
KEYWORDS
EST.

SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 796)
Li, W.B., Gruber, C., Jesse, J., and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 5, 2003 this sequence version replaced gi:30367258.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
3239.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0BAF0042D01_AF00293_1&c=3239.r

FEATURES
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/mol_type="mRNA"
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/clone="CS0DR008YE02"
/tissue_type="NEUROBLASTOMA COT 10-NORMALIZED"
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primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
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Query Match
Best Local Similarity 96.4%; Pred. No. 1.3e-141;
Matches 758; Conservative 0; Mismatches 26; Indels 2; Gaps 2;

ORIGIN
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1739 GCCTCTGCTCACCGCCAGTCTCTGCTATGACCACTCTGGAGCCAGCCCTG 1798
1799 ACAGCTGGAGCCTCGCCCTC-AAAAAGCAGTCTGCGAGGCGCAGCTGGAGGATGTGCTG 1857
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1918 TAGCTCTTACCGAGCAGCTGGGCGCTTTGCTGCTGGAGAGCCCTCAGCGTGGCT 1977
1978 GCCGCCAAGCGCTCAAGCTGCTTCTGTTGCGCGGCTGCTGCTCCCTCCAGGTAC 2037
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2218 CTTGTAGCTACAGAGATGCCCTTTTATCATCTGGAATGCGAGCGGTACTTG 2277
256 CTTGTAGCTACAGAGATGCCCTTTTATCATCTGGAATGCGAGCGGTACTTG 197
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196 CACTGCACCTTACACCTGGAGCGTGTACGCCCGCAGCACTAGTACCTGGCCTGCAAGCTG 137
2338 TGGGTGTGGCAGGTGGAGGCGCAGCGGCGAGAGCTTCAGCATCACTTCAACATCACCAAG 2397
136 TGGGTGTGGCAGGTGGAGGCGCAGCGGCGAGAGCTTCAGCATCACTTCAACATCACCAAG 77
2398 GACACAAAGTTTGTCTAGCTGCTGCTGGAGAGTGAAGCGGGGCTCCAGGCGCTGCTG 2457
76 GACACAAAGTTTGTCTAGCTGCTGCTGGAGAGTGAAGCGGGGCTCCAGGCGCTGCTG 17
2458 GGCCCC 2463
16 GGCCCC 11

RESULT 13
BI818609
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DEFINITION 818 bp mRNA linear EST 04-OCT-2001
60303362F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5174559 5',
mRNA sequence.
BI818609
VERSION
BI818609.1 GI:15929902
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
DNA Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLML1434 row: 1 column: 16
High quality sequence stop: 744.
Location/Qualifiers
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pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dr primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."

ORIGIN
Query Match 26.0%; Score 716.4; DB 4; Length 818;
Best Local Similarity 97.7%; Pred. No. 1.7e-140;


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RESULT 15
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DEFINITION Pan troglodytes HCM4327 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence..
ACCESSION AY4111748
VERSION AY4111748.1 GI:39767716
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzees)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
1 (bases 1 to 2532)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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Db 13 GAGGTGCAGATCGAGGTGTCCGCGCAGCAGGTGAGGAGCTTTTGGGCTGGAGATTAC 72

Qy 412 TGGTCCAGTCGTGGATGAGTCTCTCGGGCAACACAGAGTCAAGAGCCCTACATC 471
Db 73 TGGTCCAGTCGTGGGCTTGGAGTCTCTCGGGCAACACAGAGTTCGCGAGCCTACGTC 132

Qy 472 CGCATAGCCAGATTGCGCAAGAACTTCGACGAGGCGGCTGGCCAAGAGGTGTCCTG 531
Db 133 CGCATCGCTTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 192

Qy 532 GAGCAGGCGCATCGTGTGCTCCGTCGCGTCCACCGAGGCGCATCCCTCCAGCGAGTGGAG 591
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Qy 592 TGGTCCGGAACGAGGACTGGTGGACCGGTCTCTGACCCCAATGTATACATCACGCGG 651
Db 253 TGGTCAAGATGAGGATGTATCGACCCCAACCCAGGACACCAACTTCTCTGCTCACCATC 312

Qy 652 GAGCAGACCTGGTGGTGGCAGGCGGCTTCTGACACGGCAACTACCTGGGTG 711
Db 313 GACCACAACTCATATCCCGCAGGCGGCTGTGCGACACTGCGCAACTATACCTGGGTG 372

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Qy 712 GCCAAGAACATCGTGGCAGCGTCCGCCAGCGCCTCCGCTGTGTCTCATCTCTACGTGAAC 771
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Qy 772 GGTGGGTGGTGCAGCTGGGAACGAGTGTCTCTGACAGCGCAGCTGTGGGCGCGGCTGG 831
Db 433 GGCCTGGTGGTCCAGTGGCAGAGTGGTGGCCTCTGCTCCAAACCGCTGTGGNNGANNCTGG 492

Qy 832 CAGAAAACGAGCGGAGTGCACCAACCGCGGCTCTCAACGGGGGCGCTTCTCTGTGAG 891
Db 493 CAGAAAGCGCACCGCGAGCTGCACCAACCGCGGCTCTCAACGGAGGNNNNNTCTGCGAG 552

Qy 892 GGCAGAAATGTCCAGAAAAACAGCCTGCGCCACCCCTGTGCCCCAGTAGACGAGCTGGAGC 951
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Qy 952 CCCTGGAGCAAGTGGTGGGCTGTGGGCTGAGCTGCAACCACTGCGGAGCGGTGAGTGC 1011
Db 613 GAGTGGAGCAAGTGGTGGGCTGTGGGCTGAGCTGAGTGTGCCACTGCGCGTAGCGGAGTGC 672

Qy 1012 TCTGACCCAGCACCCCGCAACGAGGAGGAGTGCAGGCGCACTGACCTCGACACCCGCG 1071
Db 673 ATGGCGCCCCACCCAGAACGGAGGCGGTGACTGACGCGGAGCGCTGCTCGACTCTAAG 732

Qy 1072 AACTGTACCACTGACCTCTGTGTACACAGTCTTCT----- 1107
Db 733 AACTGCACAGATGGCTGTGCATGCAAAATAAGAAACTCTAAGCGACCCCAACAGCCAC 792

Qy 1108 -----GGCCCTGAGAGCGTGGCCCTCTATATGGGCTC-----ATGCGCGTGGCGTCC 1155
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Qy 1216 GACTCAGATGTGGCTGACTCTGCTCCATT---CTACCTCAGCTTTCAGCGCGCTCAGCATC 1272
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Qy 1375 -----CCAGCGCCCAAGTTCACAGCTCACCA-- 1399
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Qy 1400 -----ATGGGCACTCTCAGCCCTCTGGGTGGCGCGCC-----ACACA 1440
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Qy 1441 CTGCACACAGCTCTCCACTCTGAGCGCGAGAGTTCCTCCCGCTCTCCACCCAG 1500
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Qy 1546 GGGACCTTCAACTTCTCTCGGGGCGCGGCTGATGATCCCTAATACAGGTATCAGCTCTCTC 1605
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Qy 1606 ATCCCCCAGATGCCATACCCCGAGGAGATCTATGAGATCTACTCAGCTGCAAG 1665
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Job time : 13411 secs

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Qy      1906 GCCAGTGCCTGTACGCTTTTCA CCGAGACAGCTGGCGCGCTTTGCCCTGTGGGAGAGGCC 1965
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Qy      1966 CTGAGCGTGGCTGCGGCCAAGCGCCT CAAGCTGTTCTGTTGGCGGGTGGCCTGCACC 2025
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Qy      2386 AACATCACCAAG---GACACAAGTTT GCTGAGCTGTGGCTCTGGAGAGTGAAGCGGGG 2442
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Qy      2443 GTCCAGCCCTGTGGGCCCAAGTGCTT CAAGATCCCTTCTCATTTGGGCAGAAAGATA 2502
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Search completed: August 7, 2005, 22:20:45

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: August 7, 2005, 22:31:25 ; Search time 14556 Seconds
(without alignments)
2989.337 Million cell updates/sec

Title: US-10-624-932C-2

Perfect score: 4791

Sequence: 1 MAVRPGWLPALLGIVLAWL.....AVAGLGQDPAGLFTVSAEC 898

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=GenEmbl -QWITS=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl.*

1: gb_ba.*

2: gb_hgt.*

3: gb_in.*

4: gb_cm.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_ets.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4791	100.0	2752	6	AX449572 Sequence
2	4781	99.8	2697	6	AX451652 Sequence
3	4698.5	98.1	2881	6	AX527916 Sequence
4	4685	97.8	3992	10	MMU487852

5	4645.5	97.0	2784	6	CQ730306
6	4638	96.8	2697	6	AX268596 Sequence
7	4638	96.8	2697	10	U87305 Rattus norv
8	4638	96.8	3014	6	BD057524 Netrin re
9	4413	92.1	3580	6	AX367094 Sequence
10	4312	90.0	3844	10	BC058084 Mus muscu
11	3107	64.9	4294	10	AK122575 Mus muscu
12	2845	59.4	2688	9	BC009333 Homo sapi
13	2787	58.2	9299	10	MMU72634
14	2770	57.8	9328	10	AB118026
15	2761	57.6	2962	5	AY187310 Gallus ga
16	2755	57.5	3646	6	CQ881060 Sequence
17	2755	57.5	3646	9	AF055634 Homo sapi
18	2745.5	57.3	242128	2	AC123700 Mus muscu
19	2736	57.1	2986	6	CQ881052 Sequence
20	2710	56.6	1787	6	BD057525 Netrin re
21	2646.5	55.2	2832	5	AY099459 xenopus l
22	2585	54.0	3672	10	BC048162 Mus muscu
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24	2578.5	53.8	2838	10	RNU87306
25	2578.5	53.8	3788	10	MMU487853
26	2568	53.6	3770	9	AY126437
27	2563.5	53.5	2860	6	AX686445
28	2563.5	53.5	2860	6	AX686447
29	2558.5	53.4	3884	6	AR528525 Sequence
30	2558.5	53.4	3884	6	AX464012 Sequence
31	2558.5	53.4	3884	6	AY358351
32	2558.5	53.4	3933	6	CQ850929 Sequence
33	2558.5	53.4	3933	9	AK128132 Homo sapi
34	2558.5	53.4	3935	9	AB096256 Homo sapi
35	2553	53.3	166534	2	AC034209 Homo sapi
36	2551.5	53.3	2895	6	AX512281 Sequence
37	2544.5	53.1	2831	6	BD057526 Netrin re
38	2544	53.1	2995	6	AX497288 Sequence
39	2526.5	52.7	2612	6	CQ881064 Sequence
40	2503.5	52.3	2780	6	CQ881054 Sequence
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42	2420.5	50.5	121282	9	AC027318 Homo sapi
43	2384	49.8	4330	5	AY744919 Petromyzo
44	2300	48.0	2625	6	CQ721377 Sequence
45	2287	47.7	9700	6	AX054976 Sequence

ALIGNMENTS

RESULT 1

AX449572

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

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ORIGIN

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Pred. No.:

Score:

9.92e-278

4791.00

Length:

2752

Matches:

898

DNA

linear

PAT 03-JUL-2002

Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
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QY	21	ArgGlySerGlyAlaGlnSerAlaThrValAlaAsnProValProGlyAlaAsnPro	40
DB	106	CGGGCTCGGGTGCCCAAGAGTGCACCGTGGCCAAACAGTGGCTGTGTGCACACCG	165
QY	41	AspLeuLeuProHisPheLeuValGluProGluAspValTyrIleValLysAsnLysPro	60
DB	166	GACCTGCTTCCCCACTTCTCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGACAGCCA	225
QY	61	ValLeuLeuValCysLysAlaValProAlaThrGlnIlePhePheLysCysAsnGlyGlu	80
DB	226	GTGCTGCTGTGTGCAAGGCGGTGCCCGCCACGCGATCTTCAAGTGCACCGGGAG	285
QY	81	TrpValArgGlnValAspHisValIleGluArgSerThrAspGlySerSerGlyLeuPro	100
DB	286	TGGGTGCCCGAGGTGGACCACTGATCGAGCGCAGCACACGGGAGCAGTGGGCTGCC	345
QY	101	ThrMetGluValArgIleAsnValSerArgGlnGlnValGluLysValPheGlyLeuGlu	120
DB	346	ACCATGGAGTCCGCATTATGCTCAAGCGCAGCAGTCCGAGAAGGTGTTCCGGCTGGAG	405
QY	121	GluTyrTrpCysGlnCysValAlaIaTrpSerSerSerGlyThrThrLysSerGlnLysAla	140
DB	406	GAATACTGTGTGCCAGTGCCTGGATGGAGTCTCTCGGGCACCAACCAAGAGTCAAGAGGCC	465
QY	141	TyrIleArgIleAlaArgLeuArgLysAsnPheGluGlnGluProLeuAlaLysGluVal	160
DB	466	TACATCCGCAATAGCCAGATTGCGCAGAACTTTCAGCAGGAGCGCTGGCCAAAGAGGTG	525
QY	161	SerLeuGluGlnGlyIleValLeuProCysArgProProGluGlyIleProProAlaGlu	180
DB	526	TCCTCGAGCAGGATCGTGTGCTGCCCTGCCCTCCACCGGAGGCATCCCTCCAGCCGAG	585
QY	181	ValGluTrpLeuArgAsnGluAspLeuValAspProSerLeuAspProAsnValTyrIle	200
DB	586	GTGGAGTGGCTCCGGAAACGAGGACCTGGTGGACCCGCTCCCTGGACCCCAATGTATACATC	645
QY	201	ThrArgGluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThr	220
DB	646	ACGGGGAGCAGACCTGGTGGTGGCAGAGCCCGCTTGTCTGACACGGCCAACTACACC	705
QY	221	CysValAlaLysAsnIleValAlaArgArgSerAlaSerAlaAlaValIleValTyr	240
DB	706	TGCGTGGCCAAACAATCGTGGCAGCTGCGCGCAGCGCTCCGCTGCTGTCTATCGTCTAC	765
QY	241	ValAsnGlyIlyTrpSerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArg	260
DB	766	GTGAACGGTGGGTGGTGGACCTGGACCGAGTGGTCTGTCAGCGCCAGCTGTGGCGGC	825
QY	261	GlyTrpGlnLysArgSerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPhe	280
DB	826	GGCTGGCAGAAACGGAGCCGAGCTGCACCAACCCGGCGCTCTCAACGGGGCGCTTTC	885
QY	281	CysGluGlyGlnAsnValGlnLysThrAlaCysAlaThrLeuLeuCysProValAspGlySer	300
DB	886	TGTAGGGGCGAGAAATGTCCAGAAAAACAGCTCGCCACCTGTGCCAGTAGACGCGAGC	945
QY	301	TrpSerProTrpSerLysTrpSerAlaCysGlyLeuAspCysThrHisTrpArgSerArg	320
DB	946	TGAGGCCGCGGAGCAAGTGGTGGGCTGTGGACTGCACCCACCTGGCGGAGCCGT	1005
QY	321	GluCysSerAspProAlaProArgAsnGlyGlyGluCysGlnGlyThrAspLeuAsp	340
DB			

1006	GAGTGTCTGACCCAGCAGACCCCCCAACGAGGAGGGAGGTGCCAGGGCACTGACCTGGAC	1065
341	ThrArgAsnCysThrSerAspLeuCysValHisSerAlaSerGlyProGluAspValAla	360
1066	ACCGCAACTGTACCACTGACCTCTGTGTACACAGTGTCTTGGCCCTGAGGACGTGGCC	1125
361	LeuTyrValGlyLeuIleAlaValAlaValCysLeuValLeuLeuLeuValLeuIle	380
1126	CTCTATGTGGCCCTCATCGCCGTGGCGCTGTGCTGTGCTGTGCTGTGCTGTGCTCATC	1185
381	LeuValTyrCysArgLysLysGlyLeuAspSerAspValAlaAspSerSerIleLeu	400
1186	CTCGTTTATTTCCGGAAGAGAGGGGGCTGGACTCAGATGTGCTGACTGCTCATTC	1245
401	ThrSerGlyPheGlnProValSerIleLysProSerLysAlaAspAsnProHisLeuLeu	420
1246	ACCTCAGGCTTCCAGCCCGCTCAGCATCAAGCCAGCAAGAGCAGCAACCCCATCTGCTC	1305
421	ThrIleGlnProAspLeuSerThrThrThrThrThrThrThrThrThrThrThrThrThr	440
1306	ACCATCCAGCGGACCTCAGCACCAACACCTACACAGGGCAGTCTCTGTGCCCGG	1365
441	GlnAspGlyProSerProLysPheGlnLeuThrAsnGlyHisLeuLeuSerProLeuGly	460
1366	CAGGATGGGCCAGCCCAAGTTCCAGCTCACCAATGGGCACCTGCTCAGCCCTGGGT	1425
461	GlyGlyArgHisThrLeuHisHisSerSerProThrSerGluAlaGluGluPheValSer	480
1426	GGCGGCGCCACACACTGCACCAACAGCTCTCCACCTCTGAGGCCGAGGAGTTCTGCTCC	1485
481	ArgLeuSerThrGlnAsnTyrPheArgSerLeuProArgGlyThrSerAsnMetThrTyr	500
1486	CGCTCTCCACCCAGAACTACTTCCGCTCCCTGCCCGAGGCCACCAACATGACCTAT	1545
501	GlyThrPheAsnPheLeuGlyArgLeuMetIleProAsnThrGlyIleSerLeuLeu	520
1546	GGGACCTTCAACTTCTCGGGGCGGCTGATGATCCCTTAATACAGGTATCAGCTTCTC	1605
521	IleProProAspAlaIleProArgGlyLysIleTyrGluIleTyrLeuThrLeuHisLys	540
1606	ATCCCCCAGATGCCATACCCCGAGGGAAGATCATGAGATCTATCCTACGCTGCACAG	1665
541	ProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeuLeuSerProIleValSer	560
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DEFINITION Sequence 1 from Patent WO0233080.
ACCESSION AX451652
VERSION AX451652.1 GI:21698587

KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Koehler, R.H.
TITLE Regulation of human netrin binding membrane receptor unc5h-1
JOURNAL Patent: WO 0233080-A 1 25-APR-2002;
Bayer Aktiengesellschaft (DE)

FEATURES
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Percent Similarity: 99.89%
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Best Local Similarity: 99.78% Mismatches: 1
Query Match: 99.79% Indels: 0
DB: 6 Gaps: 0

US-10-624-932C-2 (1-898) x AX451652 (1-2697)

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REFERENCE 1			
Engelkamp,D.			
AUTHORS Cloning of three mouse Unc5 genes and their expression patterns at mid-gestation			
JOURNAL Mech. Dev. 118 (1-2), 191-197 (2002)			
MEDLINE 22239710			
PUBMED 12351186			
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(bases 1 to 3992)			
AUTHORS Engelkamp,D.			
TITLE Direct Submission			
JOURNAL Submitted (15-MAY-2002) Neuroanatomy, Max Planck Institute for Brain Research, Deutscherordenstrasse 46, Frankfurt 60528, GERMANY			
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CQ730306
LOCUS 2784 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 16240 from Patent WO02068579.
ACCESSION CQ730306
VERSION CQ730306.1 GI:42303801
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
TITLE Kits, such as nucleic acid arrays, comprising a majority of human exons or transcripts, for detecting expression and other uses thereof

JOURNAL Patent: WO 02068579-A 16240 06-SEP-2002;

PE Corporation. (NY) (US)

FEATURES Location/Qualifiers

source

1. .2784

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

ORIGIN

Alignment Scores:

Pred. No.: 5,28e-269 Length: 2784

Score: 4645.50 Matches: 881

Percent Similarity: 93.63% Conservativeness: 1

Best Local Similarity: 93.52% Mismatches: 1

Query Match: 96.96% Indels: 59

DB: 6 Gaps: 3

US-10-624-932C-2 (1-898) x CQ730306 (1-2784)

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DB 61 CGGGCTCGGGTCCCGCAGCAGAGTGCCACCGTGGCCNACCAGTGCCTGGTGCAACCCG 120
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RESULT 6
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DEFINITION Sequence 15 from Patent WO0175440.
ACCESSION AX268596
VERSION AX268596.1 GI:16541710
KEYWORDS
SOURCE Rattus sp.

ORGANISM Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
AUTHORS Cochran, S.W., Paterson, G.Y., Ohashi, Y.W., Morris, B.Y. and
Pratt, J.Y.
TITLE Schizophrenia related genes
JOURNAL Patent: WO 0175440-A 15 11-OCT-2001;
WELFIDE CORPORATION (JP)
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DEFINITION U87305
ACCESSION U87305.1 GI:2055391
VERSION
KEYWORDS Rattus norvegicus (Norway rat)
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Rattus.

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REFERENCE 1 (bases 1 to 2697)
AUTHORS Leonardo, E.D., Hincin, L., Masu, M., Keino-Masu, K., Ackerman, S.L. and Tessier-Lavigne, M.
TITLE Vertebrate homologues of C. elegans UNC-5 are candidate netrin receptors
JOURNAL Nature 386 (6627), 833-838 (1997)
MEDLINE 97271897
PUBMED 9126742
REFERENCE 2 (bases 1 to 2697)
AUTHORS Leonardo, E.D., Hincin, L., Masu, M., Keino-Masu, K. and Tessier-Lavigne, M.
TITLE Direct Submission
JOURNAL Submitted (28-JAN-1997) Anatomy, UCSF, 513 Parnassus, San Francisco, CA 94143-0452, USA
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DEFINITION Netrin receptors.
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VERSION BD057524.1 GI:22603130
KEYWORDS JP 2001505062-A/1.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 3014)
AUTHORS Lavigne,M.T., Leonardo,D.E., Hinck,L., Masu,M. and Masu,K.K.
TITLE Netrin receptors
JOURNAL Patent: JP 2001505062-A 1 17-APR-2001;
THE REGENTS OF THE UNIV OF CALIFORNIA
COMMENT PN JP 2001505062-A/1
PD 17-APR-2001
PF 19-FEB-1998 JP 1998536840
PR 19-FEB-1997 US 08/808982
PI MARC TESSIER LAVIGNE, DAVID E LEONARDO, LINDSAY HINCK, MASAYUKI
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Db 2101 TTCAAAGACAGTATCCACCACTTACGCTCTCTCATCCACGACGCTGCCAGCTCTCTGTTG 2160
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RESULT 9
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LOCUS Sequence 13 from Patent WO0198354.
DEFINITION AX367094
ACCESSION AX367094
VERSION AX367094.1 GI:188955296
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Griffin,J.A., Kallick,D.A., Tribouley,C.M., Yue,H., Nguyen,D.B.,
Tang,Y.T., Lal,P., Policky,J.L., Azimzai,Y., Lu,D.A., Graul,R.,
Yao,M.G., Burford,N., Hafalia,A.J., Baughn,M.R., Bandman,O.,
Patterson,C., Yang,J., Xu,Y., Warren,B.A., Ding,L. and
Sanjanwala,M.S.
TITLE Receptors
JOURNAL Patent: WO 0198354-A 13 27-DEC-2001;
INCYTE Genomics, Inc. (US)
FEATURES
source 1. 3580
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/notes="Incyte ID No: 6052371CB1"

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US-10-624-932C-2 (1-898) x AX367094 (1-3580)
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Qy      21  ArgGlySerGlyAlaGlnGlnSerAlaThrValAlaAsnProValProGlyAlaAsnPro 40
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Qy      41  AspLeuLeuProHisPheLeuValGluProGluAspValTyrIleValLysAsnLysPro 60
Db      124  GACTTGCTTCCCCACTTCTTGGTGGAGCCGAGGATGTGTACATCGTCAAGAACAGCCCA 183
Qy      61  ValLeuLeuValCysLysAlaValProAlaThrGlnIlePhePheLysCysAsnGlyGlu 80
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Qy      101  ThrMetGluValArgIleAsnValSerArgGlnGlnValGlnLysValPheGlyLeuGlu 120
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Qy      381  LeuValTyrCysArgGlyLysGluGlyLeuAspSerAspValAlaAspSerIleLeu 400
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DEFINITION MGC:66671 IMAGE:6813463), complete cds.
VERSION BC058084
ACCESSION BC058084.1 GI:34784158
KEYWORDS MGC.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 3844)
AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heide, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toehiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McSwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.C., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smal, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
JOURNAL MEDLINE 22388257
PUBMED 12477932
REFERENCE 2 (bases 1 to 3844)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (08-SEP-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
COMMENT Contact: MGC help desk
Email: cgapsb@mail.nih.gov
cdna Library Preparation: M. Bento Soares, University of Iowa
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@cgsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Leticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo

Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Ana-Liisa Prabhu, Parvaneh Saedi, Jacqueline Schein, Duane Smalius, Michael Smith, Lorraine Spence, Jeff Scott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAK Plate: 136 Row: b Column: 11
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 23346570.

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Query Match:	90.00%	Indels:	56
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LOCUS Mus musculus mRNA for mKIAA1976 protein.
DEFINITION AK122575
ACCESSION AK122575.1 GI:28972881
VERSION FLI CDNA.
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM
REFERENCE
AUTHORS Okazaki,N., Kikuno,R., Ohara,R., Inamoto,S., Aizawa,H., Yuasa,S., Nakajima,D., Nagase,T., Ohara,O. and Koga,H.
TITLE Prediction of the coding sequences of mouse homologues of KIAA gene: II. The complete nucleotide sequences of 400 mouse KIAA-homologous cDNAs identified by screening of terminal sequences of cDNA clones randomly sampled from size-fractionated libraries
JOURNAL DNA Res. 10, 35-48 (2003)
REFERENCE 2 (bases 1 to 4294)
AUTHORS Okazaki,N., Kikuno,R., Nagase,T., Ohara,O. and Koga,H.
TITLE Direct Submission
JOURNAL Submitted (07-FEB-2003) Hisashi Koga, Kazusa DNA Research Institute, Laboratory for Genome Informatics, 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan (E-mail:mouse@kazusa.or.jp, Tel:81-438-52-3919, Fax:81-438-52-3918)
COMMENT The CREATE program supported by Japan science and technology corporation; cDNA full insert sequencing; Kazusa DNA Research Institute; cDNA library construction, clone selection and 5'- & 3'-end one pass sequencing.

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Percent Similarity:	49.77%	Conservative:	13
Best Local Similarity:	48.78%	Mismatches:	8
Query Match:	64.85%	Indels:	654
DB:	10	Gaps:	2
US-10-624-932c-2 (1-898) x AK122575 (1-4294)			
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DB	2	GCCTGCGGCGCGGCTGTGGCAGCGCTCTGGCATAGTCTCCTACTGCTGCTTCGT	61
QY	22	GlySerGlyValGlnGlnSerAlaThrValAlaAsnProValProGlyAlaAsnProAsp	41
DB	62	GGTTGGGTGCCCAGCAGAGTGCCACAGTGGCCACCCAGTGCCTGGTCCAAACCCGGAC	121
QY	42	LeuLeuProHisPheLeuValGluProGluAspValTyrIleValLysAsnLysProVal	61
DB	122	CTGCTGCCCCACATCTCTGGTAGAGCGGAGGAGCTGTACATTGTCAAGAACAAAGCCGGT	181
QY	62	LeuLeuValCysLysAlaValProAlaThrGlnIlePhePheLysCysAsnGlyGluTrp	81
DB	182	CTGCTGGTGTGCAAGGCTGTGCGCGCCACCCAGATCTTCTCAAGTGCAAACGGGAATGG	241
QY	82	ValArgGlnValAspHisValIleGluArgSerThrAspGlySerSerGlyLeuProThr	101
DB	242	GTTTGGCAGGTGATCAGCTCATTTGAACGAGCAGCTGACGCGCAGCGAGGATGGCAACC	301
QY	102	MetGluValArgIleAsnValSerArgGlnValGluLysValPheGlyLeuGluGlu	121
DB	302	ATGGAGGTCCGGATCAACGTATCAAGCAGCAGGTTCGAGAAAGTGTGGCTGGAGGAG	361
QY	122	TyrTrpCysGlnCysValAlaTrpSerSerSerGlyThrThrLysSerGlnLysAlaTyr	141
DB	362	TACTGTGCCAGTGTGTGGCATGGAGCTCTCAGGAACACCACCAAAAGCCAGAAGGCTAC	421
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DB	602	CGGAGACACAGCTTAGTGTGGCGCAGGCCCTGGCCGACACTGCCAACTACACCTGC	661
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DB	962	TGCTCGACCCAGCGCCCGCAACGAGGTGAGGAGTGC CGGGTGCTGACCTGGACACC	1021
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QY 353 ----- 353
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QY 354 ----- SerGlyProGluAspValAlaLeuTyr 362
Db 2281 ATTCTAAGACCACTTTCTCTCGCAGCTCTTCCGGCCCCGAGGAGCTGTCTCTAC 2340
QY 363 ValGlyLeuIleAlaValAlaValCysLeuValLeuLeuLeuValLeuIleLeuVal 382
Db 2341 ATCGGCTCTGTCGCGGTGGCGGTGTGCTCATCTTGTGCTGTGCTCTCGTCTCATC 2400
QY 383 TyrCysArgLysLysGluGlyLeuAspSerAspValAlaAspSerSerIleLeuThrSer 402
Db 2401 TACTGCCGCAAGGAAGGAGCTGGACTCAGATGTGGCTGACTCATCATCTTACCTCA 2460
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RESULT 12

LOCUS BC009333

DEFINITION Homo sapiens unc-5 homolog A (C. elegans), mRNA (cDNA clone IMAGE:4126760), partial cds.

ACCESSION BC009333

VERSION

KEYWORDS

SOURCE BC009333.2 GI:40226527

ORGANISM Homo sapiens (human)

REFERENCE 1 (bases 1 to 2688)

AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klatschke, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zebberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullany, S.J., Bosak, S.A., McSwain, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Greenchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Shreen, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalusz, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

PUBMED 12477932

REFERENCE 2 (bases 1 to 2688)

AUTHORS Strausberg, R.

TITLE Direct Submission

JOURNAL Submitted (12-JUN-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>

COMMENT On Dec 19, 2003 this sequence version replaced gi:14424611.

Contact: MGC help desk

Email: cgabbs-remail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Rubin Laboratory

DNA Sequencing by: The I.M.A.G.E. Consortium (LNL)

Sequencing Center (NISC), Gaithersburg, Maryland;

Web site: <http://www.nisc.nih.gov/>

Contact: nisc_mgc@hghri.nih.gov

Blakesley, R.W., Bouffard, G.G., Green, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Lari, P., Legaapi, R., Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W., Tsougeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>

Series: IRAL Plate: 26 Row: g Column: 22.

Location/Qualifiers

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413..724

/gene="UNC5A"

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1343..1594

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/note="DEATH; Region: DEATH domain, found in proteins involved in cell death (apoptosis). Alpha-helical domain present in a variety of proteins with apoptotic functions. Some (but not all) of these domains form homotypic and heterotypic dimers"

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ORIGIN

Alignment Scores:

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Score: 2845.00 Matches: 541

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Best Local Similarity: 100.00% Mismatches: 0

Query Match: 59.38% Indels: 0

DB: 9 Gaps: 0

US-10-624-932C-2 (1-898) x BC009333 (1-2688)

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Db 2 GACGTGGCCCTCTATGTGGCGCTCATCGCGCGCTGCTGCTGCTGCTGCT 61
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QY 378 ValLeulleLeuValTyrrCysArgLysLysGluGlyLeuAspSerValAlaAspSer 397
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Db 62 GTCCTCATCTCTGTTATTTCGCGAGAGAGAGGGGCTGGACTCAGATGTGCTGACTCG 121
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QY 398 SerilleLeuthrSerGlyPheGlnProValSerilleLysProSerLysAlaAspAenPro 417
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Db 122 TCCATTCTCACCTCAGGCTTCCAGGCCCGCTCAGCATCAGCCAGCAAGCAGACACCCC 181
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ORIGIN

Alignment Scores:

Pred. No.:	5,918-157	Length:	9299
Score:	2787.00	Matches:	522
Percent Similarity:	74.0%	Conservative:	153
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US-10-624-932C-2 (1-898) x MMU72634 (1-9299)

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Qy	29	Ala-----ThrValAlaAsnProValProGlyAlaAsnProAspLeuLeuProHis	45
Db	280	GAATTTTTTCAGAACTCCAGAAACCTTTCCATCTGACCCCACTGTAGCCATTCGCCACAC	339
Qy	46	PheLeuValGluProGluAspValTyrIleValLysAsnLysProValLeuLeuValCys	65
Db	340	TTCTCTCATTTGAGCCCGAGGAAGCTTTACATTTGTGAAGAACAAAGCCCTGTGAACCTGTATTGT	399
Qy	66	LysAlaValProAlaThrClnIlePhePheLysCysAsnGlyGluTrpValArgInVal	85
Db	400	AAAGCCAGCCCTGCCACCCAGATCTACTTCAAGTGCACACGAGTGGGTTTCATCAGAAAG	459
Qy	86	AspHisValIleGluArgSerThrAspGlySerSerGlyLeuProThrMetGluValArg	105
Db	460	GACCACGTAGTAGACGAGAGAGTAGATGAACCTCTGGTCTAATTGTGAGAGAAGTGAGC	519
Qy	106	IleAsnValSerArgGlnInValGlnLysValPheGlyLeuGluGluTyrTrpCysGln	125
Db	520	ATTGAGATTTCACGCCAGCAGGTGAGGAACCTGTTTGGGCCTGGAAGATTACTGGTGGCAG	579
Qy	126	CysValAlaTrpSerSerGlyThrThrLysSerGlnLysAlaTyrIleArgIleAla	145
Db	580	TGTTGTCCTGCAGCTCAGCGGCACACGAAAGAGTCGGAAGGCATACGTGCGCATTTGCG	639
Qy	146	ArgLeuArgLysAsnPheGluGlnGluProLeuAlaLysGluValSerLeuGluGlnGly	165
Db	640	TATCTCGGAAGACATTCAGAGCAGAAACCCCTTGGGAAAGGAAGTGTCTCTTGGAGCAGAA	699
Qy	166	IleValLeuProCysArgProGluGlyIleProAlaGluValGluTrpLeuArg	185
Db	700	GTCTTACTCAGTGTGCGGCACCTGAAAGGATCCAGTGGCTGAGGTGGATGGCTTAAAG	759
Qy	186	AsnGluAspLeuValAspProSerLeuAspProAsnValTyrIleThrArgGluHisSer	205
Db	760	AATGAAGACATAATTGATCCTCTGCAAGATCGGAACCTTTTATATTACTATTCGATCATCAAC	819
Qy	206	LeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysValAlaLysAsn	225
Db	820	CTGATCATCAAGCAAGCCCGATCTCCAGATACAGCAAAATTACTGTGTTGGCCAAAAT	879
Qy	226	IleValAlaArgArgSerAlaSerAlaAlaValIleValTyrValAsnGlyGlyTrp	245
Db	880	ATTGTTTGCCAAGAGAAAGACACCAAGCCACTGTCTCATGTTATGTTTAATGTTGGCTGG	939

Qy	246	SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg	265
Db	940	TCACACCTGGACAGAGTGTCTGTGTAAACAGCCGCTGTGGCGGAGATATCAGAAACGC	999
Qy	266	SerArgSerCysThrAsnProAlaProLeuAsnGlnGlyAlaPheCysGluGlyGlnAsn	285
Db	1000	ACAGAAGACCTGCACCAACCCAGCCCCACTCAATGTTGGGGCCCTTCTGTGAGGGGCAGAGT	1059
Qy	286	ValGlnLysThrAlaCysAlaThrLeuCysProValaspGlySerTrpSerProTrpSer	305
Db	1060	GTGCAGAAAAATAGCATGCACCTAGCTTATGTATGCCAGTGGATGGTAGTGGAATCTCATGTGAGC	1119
Qy	306	LysTrpSerAlaCysGlyLeuAspCysThrHisTrpArgSerArgGluCysSerAspPro	325
Db	1120	AAATGGTCAACCTGTGGAGCTGAATGCACCCACTGGCGCAGGAGGAGTGTACAGACCA	1179
Qy	326	AlaProArgAsnGlyGlyGluGluCysGlnGlyThrAspLeuAspThrArgAsnCysThr	345
Db	1180	GCCCCCAAGAACGGGGTAAGGACTGTGATGGCTGTGTCTCCAAATCCAGAAGACTGCACCT	1239
Qy	346	SerAspLeuCysValHisSerAlaSerGlyProGluLaspValAlaLeuTyrValGlyLeu	365
Db	1240	GATGGGCTGTGCATGACGAGCTGCTCTCGACTCAGATGATGTGCTCTCTACGTGGGGAT	1299
Qy	366	--IleAlaValAlaValCysLeuValLeuLeuLeuValLeuLeuValTyrCys	384
Db	1300	GTGATCGCTGTACAGCTGTCTGGCGACTCAGTGTGTGGTGGCCCTGTTGTGTATCGG	1359
Qy	385	ArgLysLysGluGlyLeuAspSerAspValAlaAspSerSerIleLeuThrSerGlyPhe	404
Db	1360	AAGAACCCCGTGACTTTTGAGTCTGACATCATTTGACTCTCTCAGCACTCAATGGCGGCTTT	1419
Qy	405	GlnProValSerIleLysProSerLysAlaAspAsnProHisLeuLeuThrIleGlnPro	424
Db	1420	CAGCCTGTGAACATCAAGGCTGCCAGACAAGAT-----CTCCCTGGCTGTCCCCCCT	1470
Qy	425	AspLeuSerThrThrThrThrThrGlnGlySerLeuCysProArgGlnAspGlyPro	444
Db	1471	GACCTCACCTCAGTCGACGCATGTACAGGGAGCCTGTCTATGCTCTGTCATGAT--GTC	1527
Qy	445	SerProLysPheGlnLeuThrAsnGlyHisLeuLeuSerProLeuGlyGlyArgHis	464
Db	1528	TCAGACAAAATCCCAATGACCAACTCTCCAAATTTCTGGACCCACTACCCAACTTGA	1587
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Qy	481	ArgLeuSer-----ThrGlnAsnTyrPhe-----	488
Db	1648	AAACTGTACCCCGCAGATGACCCAGCTCTCTCTAGAGAATGAGGCCCTTAACCTGAAGA	1707
Qy	489	ArgSerLeuProArgGlyThr-----SerAsnMetThrTyrGlyThrPheAsnPheLeu	506
Db	1708	CAGAGCCTCGCAGACAGACATGACCCCATCTCGACAGCATTTGGTACTTCACTCTCT	1767
Qy	507	GlyGlyArgLeuMetIleProAsnThrGlyIleSerLeuLeuIleProProAspAlaIle	526
Db	1768	GGGGTCACTCATCTTCTTAATTCAGGAGTAAGCTTGTGATTCCTCCGCTGGGGCCATT	1827
Qy	527	ProArgGlyLysIleTyrGluIleTyrLeuThrLeuHisLysProGluAspValArgLeu	546
Db	1828	CCTCAGGGGAGAGTCTATGAATATGATGTACATGTACACAGGAAGAAAAATATAGAGCC	1887
Qy	547	ProLeuAlaGlyCysGlnThrLeuLeuSerProIleValSerCysGlyProProGlyVal	566
Db	1888	CCCATGAAGACTCTAGACCTTACTTACCCCTGTGTGTAGCTGTGGCCCTCTGGAGCT	1947
Qy	567	LeuLeuThrArgProValIleLeuAlaMetAspHisCysGlyGluProSerProAspSer	586
Db	1948	CTGTGACCGCCCTGTCACTCTCACTCTGCATCTCAGTGTACAGACCCCGACGCGAGC	2007


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Qy 587 TrpSerLeuArgLeuLysLysGlnSerCysGluGlySerTrpGluAspValLeuHisLeu 606
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Qy 607 GlyGluAlaProSerHisLeuTyrCysGlnLeuGluAlaSerAlaCysTyrVal 626
Db 2068 GGGAGAGAGAACTTCAACAACCCCTGTTACATTCAGCTGATGCAGAGGCTGCATATC 2127
Qy 627 PheThrGluGlnLeuGlyArgPheAlaLeuValGlyGluAlaLeuSerValAlaAla 646
Db 2128 CTCACAGAGAACCTCAGTACTATGCTGCTGTTGGCGATCCACCAAGAGCAGTGC 2187
Qy 647 LysArgLeuLysLeuLeuPheAlaProValAlaCysThrSerLeuGluTyrAsnIle 666
Db 2188 AAGCGTCTTAACTGGCCATCTTTGGGCCCTCTGCTGCTCTTCCCTGGAGTACAGCAT 2247
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Qy 687 GlnLeuGlyGlnLeuLysGlnProArgValLeuHisPheLysAspSerTyrHis 706
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Qy 707 AsnLeuArgLeuSerIleHisAspValProSerSerLeuTyrLysSerLysLeuVal 726
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AB118026
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ACCESSION AB118026
VERSION AB118026.1 GI:40217509
KEYWORDS Rattus norvegicus (Norway rat)
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus
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REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

1 Kuramoto, T., Kuwamura, M. and Serikawa, T.
Rat neurological mutations cerebellar vermis defect and hobble are caused by mutations in the netrin-1 receptor gene Unc5h3
Brain Res. Mol. Brain Res. 122 (2), 103-108 (2004)
15010202

2 (bases 1 to 9328)
Kuramoto, T. and Serikawa, T.
Direct Submission
Submitted (22-AUG-2003) Takashi Kuramoto, Institute of Laboratory Animals, Graduate School of Medicine, Kyoto University;
Yoshidakono-cho, Sakyo-ku, Kyoto 606-8501, Japan
(E-mail:tkuramoto@anim.med.kyoto-u.ac.jp, Tel:81-75-753-4494, URL:www.anim.med.kyoto-u.ac.jp, Fax:81-75-753-4409)

FEATURES
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ORIGIN

Alignment Scores:
Pred. No.: 6,2e-156 Length: 9328
Score: 2770.00 Matches: 519
Percent Similarity: 73.87% Conservative: 154
Best Local Similarity: 56.97% Mismatches: 210
Query Match: 57.82% Indels: 28
DB: 10 Gaps: 9

US-10-624-932C-2 (1-898) x AB118026 (1-9328)

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QY 146 ArgLeuArgLysAsnPheGluGlnGluProLeuAlaLysGluValSerLeuGluGlnGly 165
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QY 166 IleValLeuProCysArgProGluGlyIleProProAlaGluValGluTrpLeuArg 185
Db 700 GTGTACTCCAGTCGCGCGGCACCTGAAGGGATCCCAATGGCTGAGGTGGCTAAAG 759
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QY 465 ThrLeuHisHisSerSer-----ProThrSerGluAlaGluGluPheValSer 480
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QY 489 ArgSerLeuProArgGlyThr-----SerAsnMetThrTyrGlyThrPheAsnPheLeu 506
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QY 507 GlyGlyArgLeuMetIleProAsnThrGlyIleSerLeuLeuIleProProAspAlaIle 526
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Db      850  ACAAAGACCTGCACTAACCCCTGCCCACTCAATGGGGGGCCCTCTGCGAGGGGCAAAAT 909
Qy      286  ValGlnLysThrAlaCysAlaThrLeuLysCysProValAspGlySerTrpSerProTrpSer 305
Db      910  GTTCAGAAATAGCTTTGCACCAACCCCTGTGTCCAGTGGATGGCAAAATGGAGCTCTCGAGC 969
Qy      306  LysTrpSerAlaCysGlyLeuAspCysThrHisTrpArgSerArgGluCysSerAspPro 325
Db      970  AAGTGTCTCACTTGTGGCAGAGTGTACCACTGGCGCGGAGGAGTGCACAGCTCCG 1029
Qy      326  AlaProArgAsnGlyGlyGluGluCysGlnGlyThrAspLeuAspThrArgAsnCysThr 345
Db      1030  GCCCCGAAGAAATGGAGCAAGACTGTGAGGAACTGGTGTGCTGAGTCTAAGAACTGCAC 1089
Qy      346  SerAspLeuCysValHisSerAlaSerGlyProGluAspValAlaLeuTyrValGlyLeu 365
Db      1090  GATGGGCTCTGCATGCAAGGCTGCACCTGACTCGGATGATGTTGCTCTCTACGTGGGAT 1149
Qy      366  ---IleAlaValAlaValCysLeuValLeuLeuLeuValLeuLeuLeuValTyrCys 384
Db      1150  GTCAITGCTGTGATGTGTGCTGCGCTATTCTGTGTTGTGGCCCTGTTTGTCTATCGC 1209
Qy      385  ArgLysLysGluGlyLeuAspSerAspValAlaAspSerSerIleLeuThrSerGlyPhe 404
Db      1210  AAGAACCCCGTCACTTTGAGTCAGATATATTCGACTCATCGCGCTAAATGGGGATTT 1269
Qy      405  GlnProValSerIleLysProSerLysAlaAspAsnProHisLeuLeuThrIleGlnPro 424
Db      1270  CAGCCTGTTAAATCAAGCTGCAAGACAAAGAC-----CTCTTGGCAGTGCACCA 1320
Qy      425  AspLeuSerThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThr 444
Db      1321  GACCTCACTCTGCTGCGCCATGTACAGGGGGCCTGTGTATGCCCTTGATGAT---GTC 1377
Qy      445  SerProLysPheGlnLeuLeuAsnGlyHisLeuLeuSerProLeuGlyGlyArgHis 464
Db      1378  TCTGATAAATCCCATGACCAATCTCCGATCCTGGACCACTGCCCATCTGAAGATT 1437
Qy      465  ThrLeuHisHisSerSer-----ProThrSerGluAlaGluGluPheValSer 480
Db      1438  AAGTTTATAACACCTCTGGAGCAGTCAACCCCGCAGGATGAACTCTCTGACTTCTCTCC 1497
Qy      481  ArgLeuSer-----ThrGlnAsnTyrPhe----- 488
Db      1498  AAGCTGTCCCAACAGATTACCCAGTCTCTGTGGAGAAATGAGACTCTGAACGTGAAGAAC 1557
Qy      489  ArgSerLeuProArgGlyThr-----SerAsnMetThrTyrGlyThrPheAsnPheLeu 506
Db      1558  CAAAGCCTTGACGGCAACAGACCCATCTGTGCACCTGCATTTGGGACCTTCAACTCGTTA 1617
Qy      507  GlyGlyArgLeuMetIleProAsnThrGlyIleSerLeuLeuIleProAspAlaIle 526
Db      1618  GGGGGCCACCTAGTAATTCCTAATTCAGGAGTGTGCTGATCCAGCGGGGCTGT 1677
Qy      527  ProArgGlyLysIleTyrGluIleTyrLeuLeuHisLysProGluAspValArgLeu 546
Db      1678  CCCAAGGAAGAGTCTATGAATATGATGACAGTCCACAGGAAGGGGCGCATGAGACCA 1737
Qy      547  ProLeuAlaGlyCysGlnThrLeuLeuSerProIleValSerCysGlyProProGlyVal 566
Db      1738  CCTGTAGAGACACGACGAGCTGCTGCACACAGTGTGTGAGCTGTGGCCACCGAGCG 1797
Qy      567  LeuLeuThrArgProValIleLeuAlaMetAspHisCysGlyGluProSerProAspSer 586
Db      1798  CTGCTGACCCGACCCGCTGTGTGTGACCATGACCACTGTGCTGAGCCCAACATGGATGAC 1857
Qy      587  TrpSerLeuArgLeuLysLysGlnSerCysGluGlySerTrpGluAspValLeuHisLeu 606
Db      1858  TGGACATCCAGCTCAAGCAACCGAGGACCGCCAGGACCATGGGAGATGTAGTGGTGGTC 1917
Qy      607  GlyGluGluAlaProSerHisLeuTyrTyrCysGlnLeuAlaSerAlaCysTyrVal 626
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Db      1918  GGGGAGGAAAACTTACCACTCCATCCAGCTGGACCCAGAGGCGCTGTCTATATC 1977
Qy      627  PheThrGluGlnLeuGlyArgPheAlaLeuValGlyGluAlaLeuSerValAlaAla 646
Db      1978  CTGACGGAGACCTCAGCAGCTACGCTTGGTGGGCAATCCATCACCAGGAGCAGCC 2037
Qy      647  LysArgLeuLysLeuLeuLeuPheAlaProValAlaCysThrSerLeuGluTyrAsnIle 666
Db      2038  AAAACGCTCAAAATTTGGCCATCTTGGACCACTGTCTGTCTCTCACTGAGTAGCAGATC 2097
Qy      667  ArgValTyrCysLeuHisAspThrHisAspAlaLeuLysGluValValGlnLeuGluLys 686
Db      2098  CGGCTCTACTGCTCGATGCACACAGGATGCCTGAAAGAGGTCTCCAGCTTGAGCGG 2157
Qy      687  GlnLeuGlyGlyGlnLeuLeuGlnGluProArgValLeuHisPheLysAspSerTyrHis 706
Db      2158  CAGATGGGTGGGCGAGCTGTGGAGGAACCCAAAACCTTTCATTTTAAAGGAAGTACCCAC 2217
Qy      707  AsnLeuArgLeuSerIleHisAspValProSerSerLeuTrpLysSerLysLeuVal 726
Db      2218  AACCTGCGCTTATCCATTCATGACATTCGCCACTCTCTCTGGAAGAGCAAACTGCCGGCT 2277
Qy      727  SerTyrGlnGluIleProPheTyrHisIleTyrAsnGlyThrGlnArgTyrLeuHisCys 746
Db      2278  AAATACCAAGAGATTCCTTTTACCACTCTGGAGTGGTCCAGAGGAACTTGCACTGC 2337
Qy      747  ThrPheThrLeuGluArgValSerProSerThrSerAspLeuAlaCysLysLeuTrpVal 766
Db      2338  ACCTTCACGCTCGAACGATTCAGTCTCAATACCTCGGAGCTGCTCTGCAAACTCTGTGTG 2397
Qy      767  TrpGlnValGluGlyAspGlyGlnSerPheSerIleAsnPheAsnIleThrLysAspThr 786
Db      2398  CGGCAAGTCGAAGGAGAGGGCAGATCTTCAGCTGAACCTGCTCAGTATCAGAGGAACCC 2457
Qy      787  ArgPheAlaGluLeuAlaLeuGluSerGluAlaGlyValProAlaLeuValGlyPro 806
Db      2458  ACTGGCATTTGATTATCCCATCATGGATTTCAGCAGCGCAGCATCACACGATAGTTGGGCC 2517
Qy      807  SerAlaPheLysIleProPheLeuIleArgGlnLysIleIleSerSerLeuAspProPro 826
Db      2518  AACGCTTTTCAGCATCCCTCCCAATAAGGCAGAGCTCTGCAGCAGCCTGGATGCACCC 2577
Qy      827  CysArgArgGlyValAspTrpArgThrLeuAlaGlnLysLeuHisLeuAspSerHisLeu 846
Db      2578  CAGACCCGGGGCCATGACTGGAGAGTCTGGCCCAACAGCTGAATTTGACAGGATACCTA 2637
Qy      847  SerPhePheAlaSerLysProSerProThrAlaMetIleLeuAsnLeuTrpGluAlaArg 866
Db      2638  AATTATTTTGTACGAAGTCGAGTCCACTGGGGTGTATCTCTGGGAAGCCAG 2697
Qy      867  HisPheProAsnGlyAsnLeuSerGlnLeuAlaAlaAlaValAlaGlyLeuGlnPro 886
Db      2698  AATTTCCCTGTATGGCAACCTGAGCATGTGGCAGCAGTGTCTGGAAGAAATGGGACGACAT 2757
Qy      887  AspAlaGlyLeuPheThrValSerGlu 895
Db      2758  GAAACGTTGTTTCTTTGTCAGCAGAA 2784
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Search completed: August 8, 2005, 09:12:00.
Job time : 14684 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 7, 2005, 22:20:50 ; Search time 1654 seconds
(without alignments)
3213.983 Million cell updates/sec

Title: US-10-624-932C-2

Perfect score: 4791

Sequence: 1 MAVRPGIWPALLGIVLAAML.....AVAGLGQPDAGLFTVSEAC 898

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgn2_1/USPTO_spool_p/US10624932/runat_03082005_110053_3194/app_query.fasta_1.1095
-DB=N Geneseq 16Dec04 -QFMT=fastap -SUFFIX=ring -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10624932@cgn_1.1.708 @runat_03082005_110053_3194 -NCPUP=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N Geneseq 16Dec04.*
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4: Geneseqn2001as.*
5: Geneseqn2001bs.*
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8: Geneseqn2003as.*
9: Geneseqn2003bs.*
10: Geneseqn2003cs.*
11: Geneseqn2003ds.*
12: Geneseqn2004as.*
13: Geneseqn2004bs.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4791	100.0	2752	6	ABK37922
2	4791	100.0	2752	12	ADH71617
3	4781	99.8	2697	6	ABK52891
4	4698.5	98.1	2881	6	ABK49422
5	4698.5	98.1	2881	12	ADH71609

6	4698.5	98.1	2881	12	ADH71627
7	4697.5	98.0	2881	12	ADH71635
8	4695.5	98.0	2881	12	ADH71641
9	4695.5	98.0	2881	12	ADH71639
10	4694.5	98.0	2881	12	ADH71637
11	4694.5	98.0	2881	12	ADH71631
12	4693.5	98.0	2880	12	ADH71633
13	4691.5	97.9	2881	12	ADH71629
14	4691.5	97.9	2881	12	ADH71643
15	4691.5	97.9	2881	12	ADH71647
16	4690.5	97.9	2881	10	ADG42568
17	4689.5	97.9	2881	12	ADH71625
18	4686.5	97.8	2881	12	ADH71645
19	4684.5	97.8	2881	12	ADH71649
20	4638	96.8	2697	6	AA516843
21	4638	96.8	3014	2	AAV52940
22	4526.5	94.5	2907	4	AAK52261
23	4413	92.1	3561	12	ADL06497
24	4413	92.1	3580	6	ABK15169
25	4360	91.0	2575	12	ADH71621
26	4282	89.4	2463	12	ADH71623
27	2845	59.4	2635	11	ADN95100
28	2755	57.5	2796	10	AAU56266
29	2755	57.5	3646	5	AA575738
30	2755	57.5	3646	13	ADR99257
31	2736	57.1	2986	13	ADR99249
32	2710	56.6	1787	2	AAV52941
33	2578.5	53.8	2838	12	ADO09501
34	2563.5	53.5	2860	6	ABT06279
35	2563.5	53.5	2860	6	ABT06280
36	2558.5	53.4	3884	4	AA521316
37	2558.5	53.4	3884	8	ACA03675
38	2558.5	53.4	3884	8	ABX89213
39	2558.5	53.4	3884	8	ACD41867
40	2558.5	53.4	3884	8	ACA04096
41	2558.5	53.4	3884	9	ADA45664
42	2558.5	53.4	3884	9	ADA76095
43	2558.5	53.4	3884	9	ADA18745
44	2558.5	53.4	3884	9	ADA61368
45	2558.5	53.4	3884	9	ADB19153

ALIGNMENTS

RESULT 1
ABK37922
ID ABK37922 standard; cDNA; 2752 BP.
XX
AC ABK37922;
XX
DT 21-MAY-2002 (first entry)
XX
DE cDNA encoding Human protein NOV1.

Human; NOVX; ss; gene; cardiomyopathy; atherosclerosis; diabetes;
cell signal processing disorder; metabolic disorder; obesity; infection;
anorexia; cancer-associated cachexia; cancer; neurodegenerative disorder;
Alzheimer's disease; Parkinson's disease; immune disorder;
haematopoietic disorders; dyslipidaemia; pain; asthma; hypertension;
osteoporosis; Crohn's disease; multiple sclerosis; angina pectoris;
myocardial infarction; ulcer; allergy; benign prostatic hypertrophy;
psychosis; neurological disorder; anxiety; schizophrenia;
manic depression; dementia; dyskinesia; Huntington's disease;
Gilles de la Tourette's syndrome; gene therapy.

XX Homo sapiens.
XX
XX WO200210216-A2.
XX
XX 07-FEB-2002.
XX
XX 30-JUL-2001; 2001WO-US024225.
XX

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PR 28-JUL-2000; 2000US-0221409P.
PR 04-AUG-2000; 2000US-0222840P.
PR 04-AUG-2000; 2000US-0223752P.
PR 04-AUG-2000; 2000US-0223752P.
PR 04-AUG-2000; 2000US-0223769P.
PR 04-AUG-2000; 2000US-0223770P.
PR 14-AUG-2000; 2000US-0225146P.
PR 15-AUG-2000; 2000US-0225392P.
PR 15-AUG-2000; 2000US-0225470P.
PR 16-AUG-2000; 2000US-0225697P.
PR 01-FEB-2001; 2001US-0263662P.
PR 05-APR-2001; 2001US-0281645P.
XX (CURA-) CURAGEN CORP.
PA
XX
PI Padigar M, Mezes P, Mishra V, Burgess C, Caaman S, Grosse WM;
PI Alsobrook JP, Lepley DM, Gerlach VL, Macdougall JR, Smithson G;
XX
DR WPI: 2002-180074/23.
DR P-PSDB; ANU85403.
XX
XX New isolated cytoplasmic, nuclear, membrane bound, or secreted
PT polypeptide, useful for treating cardiomyopathy, atherosclerosis,
PT infections, cancer, neurodegenerative, metabolic, hematopoietic and
PT immune disorders.
XX
XX Claim 9; Page 9-10; 213pp; English.
XX
XX The invention relates to an isolated cytoplasmic, nuclear, membrane
CC bound, or secreted polypeptide (NOVX, x= 1-14) their variants or mature
CC form. Also included are the nucleic acids encoding the NOVX proteins, a
CC vector comprising the nucleic acid, a cell comprising the vector, an anti
CC -NOVX antibody and modulators of NOVX. NOVX, the nucleic acid and the
CC antibody are useful for treating or preventing a NOVX-associated
CC disorder, where the disorder is selected from cardiomyopathy,
CC atherosclerosis, diabetes, a disorder related to cell signal processing
CC and metabolic pathway modulation, metabolic disorders, obesity,
CC infectious disease, anorexia, cancer-associated cachexia, cancer,
CC neurodegenerative disorders, Alzheimer's disease, Parkinson's disease,
CC immune disorders, haematopoietic disorders, and the various
CC dyslipidaemias, metabolic disturbances associated with obesity, the
CC metabolic syndrome X and wasting disorders associated with chronic
CC diseases, bacterial, fungal, protozoal and viral infections, pain,
CC bulimia, asthma, hypertension, urinary retention, osteoporosis, Crohn's
CC disease, multiple sclerosis, Albrit Hereditary Osteodystrophy, angina
CC pectoris, myocardial infarction, ulcer, allergy, benign prostatic
CC hypertrophy, and psychotic and neurological disorders, including anxiety,
CC schizophrenia, manic depression, delirium, dementia, and dyskinesias,
CC such as Huntington's disease and Gilles de la Tourette's syndrome. The
CC nucleic acid is useful in gene therapy. The present sequence encodes a
CC NOVX protein
XX
SQ Sequence 2752 BP; 505 A; 937 C; 829 G; 481 T; 0 U; 0 Other;

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Alignment Scores:

Pred. No.:	1 91e-304	Length:	2752
Score:	4791.00	Matches:	896
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-10-624-932c-2 (1-898) x ABK37922 (1-2752)

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QY 1 MetAlaValArgProGlyLeuTrpProAlaLeuLeuGlyIleValLeuAlaAlaTrpLeu 20
DB 46 ATGGCGCTCCGGCCGCGCTGTGGCCAGCGCTCTGGGCATAGTCTCTCGCGCTTGGCTC 105
QY 21 ArgGlySerGlyIaGlnGlnSerAlaThrValAlaAsnProValProGlyAlaAsnPro 40
DB 106 CGCGGCTCGGGTGCCCGAGAGAGTGCACCGTGGCCAAACCCAGTGCCTGTGCAACCCG 165
QY 41 AspLeuLeuProHisPheLeuValGluProGluAspValTyrIleValLysAsnLysPro 60

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DB 166 GACCTGCTTCCCACATCTCTGTGGAGCCCGAGGATGTGTACATCTGTCAAGAAACAGCCA 225
QY 61 ValLeuLeuValCysLysAlaValProAlaThrGlnIlePhePheLysCysAsnGlyGlu 80
DB 226 GTGCTGCTTGTGTCAAGGCGGTGCGCCGCCACCGAGATCTTCTCAAGTGCACGGGGAG 285
QY 81 TrpValArgGlnValAspHisValIleGluAArgSerThrAspGlySerSerGlyLeuPro 100
DB 286 TGGGTGCGCCAGGTGCACCGATCGAGCGCAGCACAGACGGAGCAGTGGGCTGCC 345
QY 101 ThrMetGluValArgIleAsnValSerArgGlnGlnValGluLysValPheGlyLeuGlu 120
DB 346 ACCATGGAGGTCCGCATTAAATGTCTCAGAGCAGCGGTGAGAGAGGTGTTCGGGCTGGAG 405
QY 121 GluTyrTrpCysGlnCysValAlaTrpSerSerSerGlyThrThrLysSerGlnLysAla 140
DB 406 GAATACTGCTGCCAGTGCCTGGCATGGAGCTCTCGGGCACCCACCAGAGTCAAGAGGCC 465
QY 141 TyrIleArgIleAlaArgLeuArgLysAsnPheGluGlnGluProLeuAlaLysGluVal 160
DB 466 TACATCCGATAGCCAGATTGGCGAAGAACTTCGAGCAGAGCGCTGGCCCAAGGAGTG 525
QY 161 SerLeuGluGlnGlyIleValLeuProCysArgProProGluGlyIleProProAlaGlu 180
DB 526 TCCCTGGAGCAGGGCATCTGCTGCCCTCCGTCACCGAGGCGATCCCTCCAGCCGAG 585
QY 181 ValGluTrpLeuArgAsnGluAspLeuValAspProSerLeuAspProAsnValTyrIle 200
DB 586 GTGGAGTGGCTCCGGAACGAGGACCTGTGTGGACCCGCTCTCGACCCCAATGTATACATC 645
QY 201 ThrArgGluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThr 220
DB 646 ACGCGGGAGCAGACGCTGTGTGGCAGAGCGCGCTTGTGTCACAGCGCCCACTACAC 705
QY 221 CysValAlaLysAsnIleValAlaArgArgArgSerAlaSerAlaAlaValIleValTyr 240
DB 706 TCGTGGCCCAAGAACATCTGGCAGCTGCCCGAGCGCTCCGCTCTGTATCTGTCTAC 765
QY 241 ValAsnGlyGlyTrpSerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArg 260
DB 766 GTGAACGGTGGGTGGTTCGACGTGGACCGAGTGGTCTGTGACGAGCCAGCTGTGGCGC 825
QY 261 GlyTrpGlnLysArgSerArgSerCysThrAnProAlaProLeuAsnGlyGlyAlaPhe 280
DB 826 GGTGTGCAAAACGGAGCGGAGCTGCACCAACCGCGCGCTCTCAACGGGGCGCTTTC 885
QY 281 CysGluGlyGlnAsnValGlnLysThrAlaCysAlaThrLeuCysProValAspGlySer 300
DB 886 TGTGAGGGGCGAGATGTCCAGAAAACAGCTGGGCCACCTGTGCCAGTAGACGGCAGC 945
QY 301 TrpSerProTrpSerIleTrpSerAlaCysGlyLeuAspCysThrHisTrpArgSerArg 320
DB 946 TGGAGCCCGTGAGCAAGTGGTCCGCTGTGGCTGGACTGCACCCACCTGGCGGAGCCGT 1005
QY 321 GluCysSerAspProAlaProArgAsnGlyGlyGluCysGlnClyThrAspLeuAsp 340
DB 1006 GAGTGTCTTCAGCCACGACCCCGCAACCGAGGGGAGGAGTGCACGGGCGCTGACCTGGAC 1065
QY 341 ThrArgAsnCysThrSerAspLeuCysValHisSerAlaSerGlyProGluAspValAla 360
DB 1066 ACCCGCACTGTACCACTGACCTCTGTGTACACAGTGTCTTGGCCCTGAGGAGCTGGCC 1125
QY 361 LeuTyrValGlyLeuIleAlaValAlaValCysLeuValLeuLeuLeuValLeuIle 380
DB 1126 CTCTATGTGGGCTCATCGCGTGGCGCTGCTGGTCTGCTGCTGTGCTGTCTCATC 1185
QY 381 LeuValTyrCysArgLysGlyLeuAspSerAspValAlaAspSerIleLeu 400
DB 1186 CTCGTTTATGTCCGAAGAAGAGGGGCTGGACTCAGATGTGGCTGACTCGCTCATTC 1245
QY 401 ThrSerGlyPheGlnProValSerIleLysProSerLysAlaAspAsnProHisLeuLeu 420

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Db	1246	ACCTCAGCGTTCACGCCGTCAGCATCAAGCCGACGAAGCAGACAACCCCATCTGCTC	1305
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Db	1306	ACCATCCAGCCGGAGCCTCAGCACCAACACCACTACCAAGGCAGTCTCTGTCCCCGG	1365
Qy	441	GlnAspGlyProSerProIysPheGlnLeuThrAsnGlyHisLeuLeuSerProLeuGly	460
Db	1366	CAGGATGGCCCGCAGCCCAAGTTCAGCTCAACCAATGGCAACCTGTCTCAGCCCCCTGGT	1425
Qy	461	GlyGlyArgHisThrLeuHisHisSerSerProThrSerGluAlaGluPheValSer	480
Db	1426	GGCGGCCGCCACACACTGCACACAGCTTCTCCACCTCTGAGGCCGAGAGTTCGTCTCC	1485
Qy	481	ArgLeuSerThrGlnAsnTyrPheArgSerLeuProArgGlyThrSerAsnMetThrTyr	500
Db	1486	CGCCTCTCACCCAGAACTACTTCGGCTCCCTGCCCCGAGGCACCAATGACCTAT	1545
Qy	501	GlyThrPheAsnPheLeuGlyGlyArgLeuMetIleProAsnThrGlyIleSerLeuLeu	520
Db	1546	GGGACCTTCAACTTCTCGGGGGCGGGTGATGATCCCTTAATCAGGTATCAGCTCCTC	1605
Qy	521	IleProProAspAlaIleProArgGlyIleTyrGluIleTyrLeuThrLeuHisLys	540
Db	1606	ATCCCCCAGATGCCATACCCCGAGGGAAAGATCATGAGATCTACCTCAGCTGCACAAG	1665
Qy	541	ProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeuLeuSerProIleValSer	560
Db	1666	CCGGAAGAGTGGAGTTGCCCTAGCTGGCTGTCCAGACCCCTGCTGAGTCCCATCGTTAGC	1725
Qy	561	CysGlyProProGlyValLeuLeuThrArgProValIleLeuAlaMetAspHisCysGly	580
Db	1726	TGTGGACCCCTGGCGTCTCTCACCGCGCAGTCATCTTGGCTATGGACCACCTGTGGG	1785
Qy	581	GluProSerProAspSerTrpSerLeuArgLeuIlysGlnSerCysGluGlySerTrp	600
Db	1786	GAGCCCAAGCCCTGCAGCTGGAGCCTGCGCTCAAAAAGCAGTCTGTCGAGGGCGAGCTGG	1845
Qy	601	GluAspValLeuHisLeuGlyGluGluAlaProSerHisLeuTyrTyrCysGlnLeuGlu	620
Db	1846	GAGGATGTCTGCACCTGGGCGAGGAGGGCGCCTCCCACTTACTACTGCCAGCTGGAG	1905
Qy	621	AlaSerAlaCysTrpValPheThrGluGlnLeuGlyArgPheAlaLeuValGlyGluAla	640
Db	1906	GCCAGTGCCTCTACGCTCTTCAACGAGCAGCTGGCGCGCTTGGCCCTGGTGGGAGAGGCC	1965
Qy	641	LeuSerValAlaAlaAlaLysArgLeuIlysLeuLeuPheAlaProValAlaCysThr	660
Db	1966	CTCAGCGTGGCTGCGCCCAAGCGCTCAAGCTGCTTCTGTGTGCGCGGTGGCTGTCACC	2025
Qy	661	SerLeuGluTyrAsnIleArgValTyrCysLeuHisAspThrHisAspAlaLeuLysGlu	680
Db	2026	TCCCTCGAGTACAACATCCGGGTCTACTGCTTGATGACACCCACGATGCATCAAGGAG	2085
Qy	681	ValValGlnLeuGluLysGlnLeuGlyGlyGlnLeuIleGlnGluProArgValLeuHis	700
Db	2086	GTGCTGCAGCTGGAGAAGCAGCTGGGGGAGCAGCTGATCCAGGAGCCAAGGCTCTGCAC	2145
Qy	701	PhelyAspSerTyrHisAsnLeuArgLeuSerIleHisAspValProSerSerLeuTrp	720
Db	2146	TTCAAGGACAGTTACCAACACTCGCGCTATCCATCCACGATGTGCGCCAGCTCCCTGTGG	2205
Qy	721	LysSerLysLeuLeuValSerTyrGlnGluIleProPheTyrHisIleTrpAsnGlyThr	740
Db	2206	AAGAGTAAGCTCTCTGTGAGCTACAGAGATCCCTTTTATACATCTCGAATGGCAGC	2265
Qy	741	GlnArgTyrLeuHisCysThrPheThrLeuGluArgValSerProSerThrSerAspLeu	760
Db	2266	CAGCGGTACTTGCACTGCACCTTCAACCTGGAGCGTGTCCAGCCCCCAGCACTAGTAGCTG	2325
Qy	761	AlaCysLysLeuTrpValTrpGlnValGluGlyAspGlyGlnSerPheSerIleAsnPhe	780
Db	2326	GCCTGCAAGCTGTGGGTGTGCGAGTGGAGGGCCAGCGGAGAGCTTTCAGCATCAACTTC	2385

Qy	781	AsnIleThrIysAspThrArgPheAlaGluLeuLeuAlaLeuGluSerGluAlaGlyVal	800
Db	2386	AACATCACCAAGGACACAAGGTTTGGCTGTGAGCTGTGGAGAGTGAAGCGGGGTC	2445
Qy	801	ProAlaLeuValGlyProSerAlaPheLysIleProPheLeuIleArgGlnLysIleIle	820
Db	2446	CCAGCCTTGGTGGGCCCCAGTGCCCTTCAAGATCCCTTCTCATTCGGCAGAAGATAAAT	2505
Qy	821	SerSerLeuAspProProCysArgArgGlyAlaAspTrpArgThrLeuAlaGlnLysLeu	840
Db	2506	TCCAGCCTGGAGCCACCCTGTAGGCGGGTGGCGACTGGCGGACTCTGGCCACAGAACTC	2565
Qy	841	HisLeuAspSerHisLeuSerPhePheAlaSerIysProSerProThrAlaMetIleLeu	860
Db	2566	CACCTGACAGCCCATCTCAGCTTCTTTTGGCCTCCAAGCCCAAGCCCAAGCCCATGATCCTC	2625
Qy	861	AsnLeuTrpGluAlaArgHisPheProAsnGlyAsnLeuSerGlnLeuAlaAlaVal	880
Db	2626	AACCTGTGGGAGGCGCGGCACTTCCCCAAGCGGCAACCTCAGCCAGCTGGCTGCAGCAGTG	2685
Qy	881	AlaGlyLeuGlyGlnProAspAlaGlyLeuPheThrValSerGluAlaGluCys	898
Db	2686	GCTGGACTGTGGCCACGACGACGCTGGGCTCTTACAGTGTCGGAGGCTGAGTGC	2739
RESULT 2			
ADH71617			
ID	ADH71617 standard; DNA; 2752 BP.		
XX			
AC	ADH71617;		
XX			
DT	25-MAR-2004 (first entry)		
XX			
DE	Human gene of the invention NOV21e SEQ ID NO:513.		
XX			
KW	ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;		
KW	anorectic; antidiabetic; antimicrobial; antilipemic; gene therapy;		
KW	vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;		
KW	obesity; diabetes; infectious disease; metabolic syndrome X;		
XX	dyslipidaemia.		
OS	Homo sapiens.		
XX			
PN	WO2003102155-A2.		
XX			
PD	11-DEC-2003.		
XX			
PF	03-JUN-2003; 2003WO-US017430.		
XX			
PR	03-JUN-2002; 2002US-0385120P.		
PR	04-JUN-2002; 2002US-0385784P.		
PR	05-JUN-2002; 2002US-0386041P.		
PR	06-JUN-2002; 2002US-0386047P.		
PR	06-JUN-2002; 2002US-0386376P.		
PR	06-JUN-2002; 2002US-0386453P.		
PR	06-JUN-2002; 2002US-0386864P.		
PR	06-JUN-2002; 2002US-0387016P.		
PR	07-JUN-2002; 2002US-0386796P.		
PR	07-JUN-2002; 2002US-0386816P.		
PR	07-JUN-2002; 2002US-0386931P.		
PR	07-JUN-2002; 2002US-0386942P.		
PR	07-JUN-2002; 2002US-0386971P.		
PR	08-JUN-2002; 2002US-0387262P.		
PR	08-JUN-2002; 2002US-0296960P.		
PR	10-JUN-2002; 2002US-0387400P.		
PR	10-JUN-2002; 2002US-0387535P.		
PR	11-JUN-2002; 2002US-0387610P.		
PR	11-JUN-2002; 2002US-0387625P.		
PR	11-JUN-2002; 2002US-0387634P.		
PR	11-JUN-2002; 2002US-0387688P.		
PR	11-JUN-2002; 2002US-0387696P.		
PR	11-JUN-2002; 2002US-0387702P.		
PR	11-JUN-2002; 2002US-0387836P.		

PR	11-JUN-2002;	2002US-0387859P.
PR	12-JUN-2002;	2002US-0387933P.
PR	12-JUN-2002;	2002US-0387934P.
PR	12-JUN-2002;	2002US-0387960P.
PR	12-JUN-2002;	2002US-0388022P.
PR	12-JUN-2002;	2002US-0388096P.
PR	13-JUN-2002;	2002US-0389123P.
PR	14-JUN-2002;	2002US-0389118P.
PR	14-JUN-2002;	2002US-0389120P.
PR	14-JUN-2002;	2002US-0389144P.
PR	14-JUN-2002;	2002US-0389146P.
PR	17-JUN-2002;	2002US-0389729P.
PR	17-JUN-2002;	2002US-0389742P.
PR	18-JUN-2002;	2002US-0389884P.
PR	18-JUN-2002;	2002US-0390006P.
PR	19-JUN-2002;	2002US-0390209P.
PR	21-JUN-2002;	2002US-0390763P.
PR	17-JUL-2002;	2002US-0396706P.
PR	06-AUG-2002;	2002US-0401628P.
PR	09-AUG-2002;	2002US-0402156P.
PR	09-AUG-2002;	2002US-040256P.
PR	09-AUG-2002;	2002US-0402389P.
PR	12-AUG-2002;	2002US-0402786P.
PR	12-AUG-2002;	2002US-0402816P.
PR	12-AUG-2002;	2002US-0402821P.
PR	12-AUG-2002;	2002US-0402832P.
PR	13-AUG-2002;	2002US-0403448P.
PR	13-AUG-2002;	2002US-0403459P.
PR	13-AUG-2002;	2002US-0403531P.
PR	13-AUG-2002;	2002US-0403532P.
PR	13-AUG-2002;	2002US-0403563P.
PR	13-AUG-2002;	2002US-0406317P.
PR	15-AUG-2002;	2002US-0406316P.
PR	26-AUG-2002;	2002US-0406182P.
PR	26-AUG-2002;	2002US-0406355P.
PR	21-AUG-2002;	2002US-0406240P.
PR	12-SEP-2002;	2002US-0410084P.
PR	20-SEP-2002;	2002US-0412528P.
PR	23-SEP-2002;	2002US-0412731P.
PR	30-SEP-2002;	2002US-0414801P.
PR	30-SEP-2002;	2002US-0414839P.
PR	30-SEP-2002;	2002US-0414840P.
PR	30-SEP-2002;	2002US-0414954P.
PR	09-OCT-2002;	2002US-0417186P.
PR	09-OCT-2002;	2002US-0417406P.
PR	23-OCT-2002;	2002US-0420639P.
PR	28-OCT-2002;	2002US-0421156P.
PR	31-OCT-2002;	2002US-0422690P.
PR	01-NOV-2002;	2002US-0423130P.
PR	03-NOV-2002;	2002US-0042379P.
PR	05-NOV-2002;	2002US-0423798P.
PR	12-NOV-2002;	2002US-0425453P.
XX	(CURA-) CURAGEN CORP.	
PA		
XX		
PI	Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ; Catterton E, Chapoval A, Crabtree-Boker JR, Edinger SR, Ellerman K; Ettenberg S, Gargoli EA, Gerlach VL, Gorman L, Gunther E, Guo X; Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR; MacLachlan T, Mallyankar UM, Mezick AJ, Millet I, Mishra VS; Padigarau M, Patturajan M, Pena CEA, Peyman JA, Raha D, Rastelli L; Rieger DK, Rothenberger ME, Sciore P, Shenoy SG, Shinkets RA; Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M; Zhong H;	
XX		
DR	WPI; 2004-081935/08.	
DR	P-PSDB; ADH71618.	
XX		
PT	New NOVX polypeptides and nucleic acid molecules useful for preventing or treating NOVX-associated disorders, e.g. cancer, diabetes, infection or obesity, and in chromosome mapping, tissue typing or pharmacogenomics.	
XX		
PS	Example 21; SEQ ID NO 513; 1880pp; English.	

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XX  The invention relates to a novel isolated polypeptide (NOVX). A
CC  polypeptide of the invention has cytostatic, immunomodulator,
CC  neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
CC  antilipaeamic activity, and may have a use in gene therapy, and as a
CC  vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
CC  any of the 303 fully defined nucleotide sequences given in the
CC  specification. The polypeptide is useful in the manufacture of a
CC  medicament for treating a syndrome associated with a human disease. The
CC  polypeptide, polynucleotide and antibody are useful in diagnosing,
CC  treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
CC  Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
CC  diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
CC  further used as hybridisation probes, in chromosome mapping, tissue
CC  typing, preventive medicine, and pharmacogenomics. The present sequence
CC  encodes a NOVX polypeptide of the invention.
XX
SQ  Sequence 2752 BP; 505 A; 937 C; 829 G; 481 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:          1,91e-304          Length:          2752
Score:              4,791.00           Matches:          898
Percent Similarity: 100.00%            Conservative:    0
Best Local Similarity: 100.00%          Mismatches:     0
Query Match:        100.00%            Indels:         0
DB:                  12                 Gaps:           0

```

QY 221 CysValAlaIysAenIleValAlaArgArgSerAlaSerAlaValIleValTyr 240
DB TCGTGGCCAAAGACATCGTGGCAGCTCGCGCAGCGCCTCCGCTGCTGTCATGCTAC 765
QY 241 ValAenGlyGlyTyrSerThrTyrThrGluTyrSerValCysSerAlaSerCysGlyArg 260
DB GTGAACGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 825
QY 261 GlyTyrGlnIysArgSerArgSerCysThrAsnProAlaProLeuAenGlyGlyAlaPhe 280
DB GGCTGGCAGAAACGGAGCGGAGCTGCACCAACCCGGGCTCTCAACGGGGGGCGCTTC 885
QY 281 CysGluGlyGlnAenValGlnIysThrAlaCysAlaThrLeuCysProValAspGlySer 300
DB TGTGAGGGGAGAAATGTCAGAAACAGCCCTGGCCACCCTGTGCCCCAGTAGAGCGCAGC 945
QY 301 TrpSerProTyrSerIleTyrSerAlaCysGlyLeuAspCysThrHisTyrArgSerArg 320
DB TGGAGCCCGTGGAGCAAGTGGTGGCTGTGGGCTGGACTGCACCCACTGGCGGAGCGGT 1005
QY 321 GluCysSerAspProAlaProArgAsnGlyGlyGluCysGlnGlyThrAspLeuAsp 340
DB GAGTGTCTGACCCAGCAGACCCCGCAGCGAGGGAGAGGTGCCAGGGCACTGACTGGAC 1065
QY 341 ThrArgAenCysThrSerAspLeuCysValHisSerAlaSerGlyProGluAspValAla 360
DB ACCCGCAACTGATACAGTACCTCTGTGTATACACAGTGTCTTGGCCCTGAGGAGCTGGCC 1125
QY 361 LeuTyrValGlyLeuIleAlaValAlaValCysLeuValIleLeuLeuValIle 380
DB CTCTATGTGGGCTCAATCGCGCTGGCGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 1185
QY 381 LeuValTyrCysArgIysGlyGlyLeuAspSerAspValAlaAspSerSerIleLeu 400
DB CTGTTTATTTGCCGGAAGAGGGGCTGGACTCAGATGGTGGTGGTGGTGGTGGTGGTGG 1245
QY 401 ThrSerGlyPheGlnProValSerIleLysProSerLysAlaAspAenProHisLeuLeu 420
DB ACCTCAGGCTTCCAGCCCGTCAGCATCAAGCCAGCAAGCAAGCAAGCAAGCAAGCAAG 1305
QY 421 ThrIleGlnProAspLeuSerThrThrThrThrThrThrThrThrThrThrThrThrThr 440
DB ACCATCCAGCCGAGCCTCAGCACCACCACCACCACCACCACCACCACCACCACCACCACC 1365
QY 441 GlnAspGlyProSerProLysPheGlnLeuThrAsnGlyHisLeuLeuSerProLeuGly 460
DB CAGATGGGCGCAGCCCAAGTTCAGCTCACCNAATGGGCACTGTCTCAGCCCTCTGGGT 1425
QY 461 GlyGlyArgHisThrLeuHisHisSerSerProThrSerGluAlaGluGluPheValSer 480
DB GCGGGCGCCACACACTGCACACACAGCTCTCCACCTCTGAGCGCGAGGAGTTCTGCTCC 1485
QY 481 ArgLeuSerThrGlnAenTyrPheArgSerLeuProArgGlyThrSerAenMetThrTyr 500
DB CGCTCTCCACCCAGAACTACTTCGCTCCCTGCGCCGAGGCCACCAGCAACATGACCTAT 1545
QY 501 GlyThrPheAenPheLeuGlyGlyArgLeuMetIleProAenThrGlyIleSerLeuLeu 520
DB GGAACCTTCAACTCTCTCGGGGGCGGCTGATGATCCCTAATACAGGTATCAGCCCTCTC 1605
QY 521 IleProProAspAlaIleProArgGlyIleIleTyrGluIleTyrLeuThrLeuHisLys 540
DB ATCCCCCAGATGCCATACCCGAGGGAAGATCTATGAGATCTACCTCAGCTGCACAAG 1665
QY 541 ProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeuLeuSerProIleValSer 560
DB CCGGAAGACGTGAGGTTGGCCCTAGCTGGCTGTGAGACCCCTGCTGAGTCCCATCGTTAGC 1725
QY 561 CysGlyProProGlyValLeuLeuThrArgProValIleLeuAlaMetAspHisCysGly 580
DB TGTGAGCCCCCTGGCGTCTGCTCACCAGGCGAGTCACTCTGGCTATGGACCACTGTGGG 1785
QY 581 GluProSerProAspSerTrpSerLeuArgLeuLysLysGlnSerCysGluGlySerTrp 600

DB 1786 GAGCCAGCCCTGACAGCTGGAGCCTGGCGCTCAAAAAGCAGTCGTGGAGGGCAGCTGG 1845
QY 601 GluAspValIleHisLeuGlyGluAlaProSerHisLeuTyrTyrCysGlnLeuGlu 620
DB GAGATGTGTGCTGACCTGGCGGAGGAGCGCCCTCCACCTCTACTACTCCAGCTGGAG 1905
QY 621 AlaSerAlaCysTyrValPheThrGluGlnLeuGlyArgPheAlaLeuValGlyGluAla 640
DB GCCAGTGGCTGCTACGCTTTCACCGAGCAGCTGGCGCGCTTTGCCCTGGTGGAGAGGCC 1965
QY 641 LeuSerValAlaAlaAlaIysArgLeuLysLeuLeuLeuPheAlaProValAlaCysThr 660
DB CTGAGCGTGGCTGGCCCAAGCGCTCAAGCTGCTTCTGTTTGGCGCGTGGCTGCACC 2025
QY 661 SerLeuGluTyrHisIleArgValTyrCysLeuHisAspThrHisAspAlaLeuLysGlu 680
DB TCCCTCGAGTACAACTCCGGGTCTACTGCTCGATGACACCCACGATGACCTCAAGGAG 2085
QY 681 ValValGlnLeuLysGlnLeuGlyGlyGlnLeuIleGlnGluProArgValLeuHis 700
DB GTGGTGCAGCTGGAGAAAGCAGCTGGGGGAGCAGCTGATCCAGGAGCCACGGGTCTGCAC 2145
QY 701 PheLysAspSerTyrHisAenLeuArgLeuSerIleHisAspValProSerSerLeuTrp 720
DB TTCAGGACAGATTACCAACACCTGGCGCTATCCATCCACGATGTGCCAGCTCCCTCTGG 2205
QY 721 LysSerLysLeuLeuValSerTyrGlnGluIleProPheTyrHisIleTyrAsnGlyThr 740
DB AAGATTAAGTCTCTGTGAGTACCAAGGAGATCCCCCTTTTATCACATCTGGAATGGCAGC 2265
QY 741 GlnArgTyrLeuHisCysThrPheThrLeuGluArgValSerProSerThrSerAspLeu 760
DB CAGCGGTACTTGCACCTTCACTGGAGCGGTGTCAGCCCGCAGCAGCTAGTGACCTG 2325
QY 761 AlaCysLysLeuTrpValTrpGlnValGluGlyAspGlyGlnSerPheSerIleAsnPhe 780
DB GCCTGCAAGCTGTGGGTGTGGCAGGTGGAGGCGCAGGGCAGAGCTTCAGCATCAACTTC 2385
QY 781 AsnIleThrLysAspThrArgPheAlaGluLeuLeuAlaLeuGluSerGluAlaGlyVal 800
DB AACATCACAAGGACACAAGGTTTGTGAGCTCTGCTCTGGAGAGTGAAGCGGGGGTCT 2445
QY 801 ProAlaLeuValGlyProSerAlaPheValIleProPheLeuIleArgGlnLysIle 820
DB CAGCCCTCTGGTGGGCCCCAGTGGCTTCAAGATCCCTCTCTCATTCGGCAGAGATTAAT 2505
QY 821 SerSerLeuAspProProCysArgArgGlyAlaAspTrpArgThrLeuAlaGlnLysLeu 840
DB TCCAGCTGGACCCACCTGTAGCGGGGTGCGAGCTGGCGGAGCTCTGGCCAGAAACTC 2565
QY 841 HisLeuAspSerHisLeuSerPhePheAlaSerLysProSerProThrAlaMetIleLeu 860
DB CACCTGGACAGCCATCTCAGCTTCTTGGCTCCAAAGCCAGCCCGCAGCATGATCTCTC 2625
QY 861 AsnLeuTrpGluAlaArgHisPheProAsnGlyAsnLeuSerGlnLeuAlaAlaVal 880
DB AACCTGTGGAGGGCGGCACTTCCCCACAGGCAACTCAGCCAGCTGGCTGGCAGCAGTG 2685
QY 881 AlaGlyLeuGlyGlnProAspAlaGlyLeuPheThrValSerGluAlaGluCys 898
DB GCTGGAGTGGGCCAGCAGCAGCTGGCGCTCTTCAAGTGTGGAGGCTGAGTGC 2739
RESULT 3
ABK52891
ID ABK52891 standard; DNA; 2697 BP.
XX
AC ABK52891;
XX
DT 27-AUG-2002 (first entry)
XX
DE Human netrin binding membrane receptor UNC5H-1 DNA sequence #1.
XX

KW Netrin binding membrane receptor; receptor; UNC5H-1; gene; ds; human;
 KW neotropic; neuroprotective; cytoskeletal; antiparkinsonian;
 KW cerebroprotective; cancer; central nervous system; CNS; stroke;
 KW Parkinson's disease; multiple sclerosis; Alzheimer's disease.

XX Homo sapiens.

XX Key Location/Qualifiers
 XX CDS 1..2697
 XX /*tag= a
 XX /product= "Netrin binding membrane receptor UNC5H-1"

XX WO20233080-A2.

XX 25-APR-2002.

XX 15-OCT-2001; 2001WO-EP011891.

XX 16-OCT-2000; 2000US-0240061P.

XX (FARB) BAYER AG.

XX Koehler RH;

XX WPI; 2002-463314/49.

XX P-PSDB; AAU97899.

XX Novel human netrin binding membrane receptor polypeptide and
 PT polynucleotides for identifying modulating agents useful in treating
 PT diseases e.g. Parkinson's disease, multiple sclerosis, stroke,
 PT Alzheimer's disease.

XX Claim 1; Fig 1; 94pp; English.

XX This invention relates to the DNA and protein sequences of a novel
 CC purified human netrin binding membrane receptor, UNC5H-1. The DNA
 CC sequence of the invention is useful as a probe for detecting a nucleic
 CC acid encoding the UNC5H-1 protein in a biological sample. The sequences
 CC of the invention are useful to screen for agents which decrease the
 CC activity of the UNC5H-1 protein. The sequences are also useful for
 CC screening agents which regulate (modulate) the activity of the protein of
 CC the invention. A pharmaceutical composition containing the protein of the
 CC invention or a reagent that modulates the activity of the UNC5H-1 protein
 CC may be useful for treating a UNC5H-1 dysfunction related disease such as
 CC cancer or a central nervous system (CNS) disorders (e.g. Parkinson's
 CC disease, multiple sclerosis, stroke and Alzheimer's disease). Fusion
 CC proteins comprising the UNC5H-1 protein are useful for generating
 CC antibodies and for in various assay systems, and the protein can be used
 CC as a bait protein in a two-hybrid assay or three-hybrid assay. The method
 CC of the invention is useful for detecting a coding sequence for the UNC5H-
 CC 1 protein. The present sequence represents a DNA sequence encoding the
 CC human netrin binding membrane receptor UNC5H-1 protein of the invention

XX Sequence 2697 BP; 503 A; 906 C; 807 G; 481 T; 0 U; 0 Other;

XX Alignment Scores:

Pred. No.:	8,43e-304	Length:	2697
Score:	4781.00	Matches:	896
Percent Similarity:	99.89%	Conservative:	1
Best Local Similarity:	99.78%	Mismatches:	0
Query Match:	99.79%	Indels:	0
DB:	6	Gaps:	0

US-10-624-932C-2 (1-898) x ABK52891 (1-2697)

QY	1	MetAlaValArgProGlyLeuTTPProAlaLeuLeuGlyTleValLeuAlaAATpLeu	20
DB	1	ATGGCCGTCCGGCCCGCCCTGTGGCCAGCGCTCTCTGGGCATAGTCTCTGCCCGTTGGCTC	60
QY	21	ArgGlySerGlyAlaGlnGlnSerAlaThrValAlaAsnProValProGlyAlaAlaAsnPro	40
DB	61	CGCGGCTCGGGTCCCGCAGCAGAGTGCACCGTGGCCAAACCCAGTGGCTGGTGCACCCG	120

QY	41	AspLeuLeuProHisPheLeuValGluProGluAspValTyrIleValLysAsnLysPro	60
DB	121	GACCTGCTCCCCACTTCTCGTGGAGCCGCGAGATGTGTACATCGTCAAGAAACAAGCCA	180
QY	61	ValLeuLeuValCysLysAlaValProAlaThrGlnIlePhePheLysCysAsnGlyGlu	80
DB	181	GTGCTGCTTGTGTGCAAGCCGTCGCCGCCACACAGATCTTCTCAAGTCAACGGGGAG	240
QY	81	TTPValArgGlnValAspHisValIleGluArgSerThrAspGlySerSerGlyLeuPro	100
DB	241	TGGGTGGCCAGGTGGACACCGTGTATCGAGCGCAGCACAGCGGAGCAGTGGGCTGCC	300
QY	101	ThrMetGluValArgIleAsnValSerArgGlnGlnValGlnLysValPheGlyLeuGlu	120
DB	301	ACCATGGAGGTCCGCATTAAATGTCTCAAGCAGCAGGTCCAGAAAGGTGTTCGGGCTGG	360
QY	121	GluTyrTrpCysGlnCysValAlaThrSerSerGlyThrThrLysSerGlnLysAla	140
DB	361	GAATCTGGTGCAGTGGCTGGCATGGAGCTCTCCGGGCACCAAGAGTCAAGAGGCC	420
QY	141	TyrIleArgIleAlaArgLeuArgLysAsnPheGluGlnGluProLeuAlaLysGluVal	160
DB	421	TACATCCGCATAGCCTATTTCGCAAGAACTTCGAGCAGAGCGCTGGCCAGGAGGTG	480
QY	161	SerLeuGluGlnGlyIleValLeuProCysArgProProGluGlyIleProAlaGlu	180
DB	481	TCCCTGGAGCAGGGCATCGTGTGCTGCTCCGCTCCACCGAGGCGCATCCCTCCAGCCG	540
QY	181	ValGluTrpLeuArgAsnGluAspLeuValAspProSerLeuAspProAsnValTyrIle	200
DB	541	GTGGAGTGGCTCCGGAAACGAGGACCTGTGTGGACCCCTCTGGACCCCAATGTATCATC	600
QY	201	ThrArgGluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThr	220
DB	601	ACGCGGGAGCACACGCTGTGTGTGTCACAGGCCCGCTTGTGTGACACGCGCAACTACAC	660
QY	221	CysValAlaIysAsnIleValAlaArgArgArgSerAlaSerAlaAlaValIleValTyr	240
DB	661	TGCGTGGCCCAAGAACATCGTGCACGTCCGCGCAGCGCTCCGCTCTGTCACTGCTAC	720
QY	241	ValAsnGlyGlyTrpSerThrTrpTrpTrpSerValCysSerAlaSerCysGlyArg	260
DB	721	GTGACGCTGGTGGTGTGTCAGCTGGACCGAGTGGTCTGTGACGCGCCAGCTGTGGGCGC	780
QY	261	GlyTrpGlnLysArgSerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPhe	280
DB	781	GGCTGGCAGAAACGGAGCCGAGCTGCACCAACCCGCGCTCTCAACGGGGCGCTTTC	840
QY	281	CysGluGlyGlnAsnValGlnLysThrAlaCysAlaThrIleuCysProValAspGlySer	300
DB	841	TGTGAGGGGCGAATGTCCAGAAACAGCTTGGCCACCTGTGCGCAGTGGACGGCAGC	900
QY	301	TrpSerProTrpSerLysTrpSerAlaCysGlyLeuAspCysThrHisTrpArgSerArg	320
DB	901	TGGAGCCCGTGGAGCAAGTGTGCTGGCTGTGGCTGGACTGCACCCACTGGCGGAGCCGT	960
QY	321	GluCysSerAspProAlaProArgAsnGlyGlyGluCysGlnGlyThrAspLeuAsp	340
DB	961	GAGTGTCTTGACCCAGCACCCCGCAACGGAGGGGAGGAGTGGCCAGGCGCATGACCTGG	1020
QY	341	ThrArgAsnCysThrSerAspLeuCysValHisSerAlaSerGlyProGluAspValAla	360
DB	1021	ACCCGCAACTGTACCACTGCTGTGTGTACACACTGTCTGTGGCCCTTGGAGCAGTGGCC	1080
QY	361	LeuTyrValGlyLeuIleAlaValAlaValCysLeuValLeuLeuLeuValLeuIle	380
DB	1081	CTCTATGTGGGCTCATCGCCGTGGCCGCTGTGCTGTGCTGTGCTGTGCTGTGCTCATC	1140
QY	381	LeuValTyrCysArgLysLysGluGlyLeuAspSerAspValAlaAspSerSerIleLeu	400
DB	1141	CTCGTTTATTGGCGGAAGAGGGGCTGGACTCAGATGTGGCTGACTGCTCATTTCTC	1200
QY	401	ThrSerGlyPheGlnProValSerIleLysProSerLysAlaAspAsnProHisLeuLeu	420

[illegible]

Db	2281	GCCTGCAAGCTGTGGGTGTGGCAGGTGGAGGGCGACGGCAGAGCTTTCAGCATCAACTTC	2340
Qy	781	AenileThrLysAspThrArgPheAlaGluLeuAlaLeuGluSerGluAlaGlyVal	800
Db	2341	AACATCACAAGGACACAGAGTTTGTCTGAGCTGTGGCTCTGGAGAGTGAAGCGGGGTC	2400
Qy	801	ProAlaLeuValGlyProSerAlaPheLysIleProPheLeuIleArgGlnLysIle	820
Db	2401	CCAGCCCTGGTGGGCCCGCTTCAAGATCCCTTCCTCATTCGCGAGAGATAATT	2460
Qy	821	SerSerIeuAapProProCysArgArgGlyAlaAspTrpArgThrLeuAlaGlnLysLeu	840
Db	2461	TCCAGCCTGGAGCCACCCCTGTGAGCGGGGTGCCGACTCTGGCGGACTCTGGCCCAAGAACTC	2520
Qy	841	HisLeuAepSerHisLeuSerPhePheAlaSerLysProSerProThrAlaMetIleLeu	860
Db	2521	CACCTGGACACGCATCTCAGCTTCTTGGCTTCCAGGCCAGCCACGACCATGATCTCTC	2580
Qy	861	AsnLeuTrpGluAlaArgHisPheProAsnGlyAsnLeuSerGlnLeuAlaAlaVal	880
Db	2581	AACCTGTGGAGGCGCGCACTTCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTG	2640
Qy	881	AlaGlyLeuGlyGlnProAspAlaGlyIlePheThrValSerGluAlaGluCys	898
Db	2641	GCTGGACTGGGCCAGCCAGCGCTGGCTCTTTCACAGTGTGGAGGCTGAGTGC	2694
RESULT 4			
ABK49422			
ID	ABK49422	standard; DNA; 2881 BP.	
XX	AC	ABK49422;	
XX	DT	15-JUL-2002 (first entry)	
XX	DE	DNA encoding human UNC5-like protein NOV1.	
KW	Human; NOVX polypeptide; cardiomyopathy; atherosclerosis; cancer;		
KW	cell signal processing; metabolic pathway modulation; cancerous tissue;		
KW	antibody; diabetes; transgenic animal; UNC5-like protein; NOV1;		
KW	chromosome 13; gene; ds.		
OS	Homo sapiens.		
FH	Key	Location/Qualifiers	
FT	CDS	87..2786	
FT		/*tag= a	
FT		/product= "Human UNC5-like protein NOV1"	
XX	WO200229038-A2.		
PN	11-APR-2002.		
XX	04-OCT-2001; 2001WO-US031377.		
XX	04-OCT-2000; 2000US-0237862P.		
PA	(CURA-) CURAGEN CORP.		
PI	Herrmann JL, Rastelli L, Shimkets RA;		
XX	WPI; 2002-340104/37.		
DR	P-PSDB; RAU79939.		
XX	Novel isolated NOVX polypeptide, and encoded polynucleotide, useful for		
PT	treating cardiomyopathy, atherosclerosis, and cancer.		
XX	Claim 8; Page 7-8; 180pp; English.		
XX	The present invention relates to a new NOVX polypeptide having a 900		
CC	(NOV1, 4349 (NOV2), 940 (NOV3), 798 (NOV4), 865 (NOV5), or 331 (NOV6)		
CC	residue amino acid sequence, as given in the specification. The novel		
CC	polypeptide, and its encoding polynucleotide, are used to treat		
CC	cardiomyopathy, atherosclerosis, cancer or a disease related to cell		


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PR 09-OCT-2002; 2002US-0417406P.
PR 23-OCT-2002; 2002US-0420639P.
PR 28-OCT-2002; 2002US-0421156P.
PR 31-OCT-2002; 2002US-0422690P.
PR 01-NOV-2002; 2002US-0423130P.
PR 05-NOV-2002; 2002US-00423798.
PR 05-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.
XX
PA (CURA-) CURAGEN CORP.
XX
XX Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
PI Catterton E, Chapoval A, Crabtree-Bokor JR, Bainger SR, Elleman K;
PI Ectenberg S, Gangoli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
PI Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
PI MacLachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;
PI Padigaru M, Patturajan M, Pena CE, Peyman JA, Raha D, Rastelli L;
PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shinkete RA;
PI Smithson G, Spytek KA, Stone DJ, Vernet CM, Voss EZ, Zhong M;
PI Zhong H;
XX
XX WPI; 2004-081935/08.
DR P-PSDB; ADH71610.
XX
XX New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.
XX
XX Example 21; SEQ ID NO 505; 1880pp; English.
XX
XX The invention relates to a novel isolated polypeptide (NOVX). A
CC polypeptide of the invention has cytostatic, immunomodulator,
CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
CC antilipase activity, and may have a use in gene therapy, and as a
CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
CC any of the 303 fully defined nucleotide sequences given in the
CC specification. The polypeptide is useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease. The
CC polypeptide, polynucleotide and antibody are useful in diagnosing,
CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
CC further used as hybridisation probes, in chromosome mapping, tissue
CC typing, preventive medicine, and pharmacogenomics. The present sequence
CC encodes a NOVX polypeptide of the invention.
XX
XX Sequence 2881 BP; 526 A; 985 C; 868 G; 502 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 2,36e-298 Length: 2881
Score: 4698.50 Matches: 888
Percent Similarity: 98.89% Conservative: 2
Best Local Similarity: 98.67% Mismatches: 7
Query Match: 98.07% Indels: 3
DB: 12 Gaps: 3
XX
US-10-624-932C-2 (1-898) x ADH71609 (1-2881)
QY 1 MetAlaValArgProGlyLeuTrpProAlaLeuLeuGlyIleValLeuAlaAlaTrpLeu 20
DB 87 ATGGCCGTCCGGCCGGCCGTGTGGCCAGCGCTCTGGGCATAGTCTCTGCCGCTTGGCTC 146
QY 21 ArgGlySerGlyAlaGlnGlnSerAlaThrValAlaAsnProValProGlyAlaAsnPro 40
DB 147 CGCGGCTCGGGTGCAGCAGAGTGCACCGCTGGCCAAACCCAGTGCCTGGTGCACCCCG 206
QY 41 AspLeuLeuProHisPheLeuValGluProGluAspValTyrIleValIysAsnLysPro 60
DB 207 GACCTGCTTCCCCACATCTCTCTGGTGGAGCCCGAGAGTGTACATCTGTCAGAAACAAGCCA 266
QY 61 ValLeuLeuValCysLysAlaValProAlaThrGlnIlePhePheLysCysAsnGlyGlu 80
DB 267 GTGCTGCTGTGTGCAAGGCCGTGCCGCCACGACGATCTTCTTCAAGTGCACAGGGGAG 326

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Qy 440 ArgGlnAspGlyProSerProLysPheGlnLeuThrAsnGlyHisLeuLeuSerProLeu 459
Db 1404 CGGCAGGATGGGCCCCAGCCCAAGTTCAGCTCACCAATGGGACACTGCTCAGCCCCCTG 1463
Qy 460 GlyGlyArgHisThrLeuHisHisSerSerProThrSerGluAlaGluGluPheVal 479
Db 1464 GGTGGCGGCGCCACACACTGCACACACAGCTCTCCACCTCTGAGGGCCGAGGATTGCTC 1523
Qy 480 SerArgLeuSerThrGlnAsnTyrPheArgSerLeuProArgGlyThrSerAsnMetThr 499
Db 1524 TCCCGCTCTCCACCCAGAACTACTTCGGCTCCCTGCGCCGAGGACACAGCAATGACC 1583
Qy 500 TyrGlyThrPheAsnPheLeuGlyGlyArgLeuMetIleProAsnThrGlyIleSerLeu 519
Db 1584 TATGGGACCTTCAACTTCTCGGGGGCGGGCTGATGATCCCTAATACAGGTATCAGCCTC 1643
Qy 520 LeuIleProProAspAlaIleProArgGlyLysIleTyrGluIleTyrLeuThrLeuHis 539
Db 1644 CTATCCCGCCAGATGCCATACCCCGAGGGAAGATCTATGAGATCTACCTCAGCTGCAC 1703
Qy 540 LysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeuLeuSerProIleVal 559
Db 1704 AGCCGGAAGACGTGAGGTGCCCCCTAGCTGGCTGTGAGACCCCTGCTGAGTCCCATCGTT 1763
Qy 560 SerCysGlyProProGlyValLeuLeuThrArgProValIleLeuAlaMetAspHisCys 579
Db 1764 AGCTGTGACCCCTGGGCTCTGTCTACCCGGCCAGTCTATCTGGCTATGGACCACTGT 1823
Qy 580 GlyGluProSerProAspSerTrpSerLeuArgLeuLysLysGlnSerCysGluGlySer 599
Db 1824 GGGAGGCCAGCCCTGACAGCTGGAGCTCGCGCTCAAAAGACAGTCTGCGAGGGCAGC 1883
Qy 600 TrpGlu---AspValLeuHisLeuGlyGluAlaProSerHisLeuTyrTyrCysGln 618
Db 1884 TGGAGCAGGATGTGCTGACCTGGCGAGAGCGCCCTCCCACTCTACTACTGCGAG 1943
Qy 619 LeuGluAlaSerAlaCysTyrValPheThrGluGlnLeuGlyArgPheAlaLeuValGly 638
Db 1944 CTGGAGCCAGTGCTGCTGCTAGCTCTTCACCGAGCAGCTGGCGCGCTTTGGCCCTGGTGGGA 2003
Qy 639 GluAlaLeuSerValAlaAlaLysArgLeuLysLeuLeuPheAlaProValAla 658
Db 2004 GAGGCCCTCAGCGTGGCTGGCGCAGCGCTCAAGCTGCTTCTGTTGGCGCGGTGGCC 2063
Qy 659 CysThrSerLeuGluTyrAsnIleArgValTyrCysLeuHisAspThrHisAspAlaLeu 678
Db 2064 TGCACTCCCTCGAGTACAACTCCGGGTCTACTGCTGTGATGACACCCACGATGCACTC 2123
Qy 679 LysGluValValGlnLeuGluLysGlnLeuGlyGlnLeuIleGlnGluProArgVal 698
Db 2124 AAGGAGTGTGCTGGAGAGCAGCTGGGGGACAGCTGATCCAGGAGCCACGGGTC 2183
Qy 699 LeuHisPheLysAspSerTyrHisAsnLeuArgLeuSerIleHisAspValProSerSer 718
Db 2184 CTGCACCTTCAAGGACAGTACCAACCTCGCGCTATCCATCCAGATGTGCCAGCTCC 2243
Qy 719 LeuTrpLysSerLysLeuLeuValSerTyrGlnIleProPheTyrHisIleTrpAsn 738
Db 2244 CTGTGGAAGAGTAACTGCTTGTGCTGACGAGATCCCTTTTATCATCATCTGGAAT 2303
Qy 739 GlyThrGlnArgTyrLeuHisCysThrPheThrLeuGluArgValSerProSerThrSer 758
Db 2304 GGCACGCGGGTACTTGGACTGACCTTCACTGAGGAGTGTGACGCGCCAGCACTAGT 2363
Qy 759 AspLeuAlaCysLysLeuTrpValTrpGlnValGluGlyAspGlyGlnSerPheSerIle 778
Db 2364 GACCTGGCTCGAAGCTGTGGGTGTGGAGTGGAGGGCGAGCGGACAGCTTCAGCATC 2423
Qy 779 AsnPheAsnIleThrLysAspThrArgPheAlaGluLeuLeuAlaLeuSerGluAla 798
Db 2424 AACTTCAACATCACCAAGGACACAAGGTTTGTGCTGAGCTGTGGCTCTGGAGAGTGAAGCG 2483
Qy 799 GlyValProAlaLeuValGlyProSerAlaPheLysIleProPheLeuIleArgGlnLys 818

Db 2484 GGGGTCCAGCCCTGGTGGGCCCCAGTGCCTTCAAGATCCCTTCTCATTTGGSCAAG 2543
Qy 819 IleIleSerSerLeuAspProProCysArgArgGlyAlaAspTrpArgThrLeuAlaGln 838
Db 2544 ATAATTTCCAGCCTGGACCCACCTGTAGGCGGGGTGCCACTGGCGGACTCTGGCCAG 2603
Qy 839 LysLeuHisLeuAspSerHisLeuSerPhePheAlaSerLysProSerProThrAlaMet 858
Db 2604 AAATCCTCCTGGACAGCCATCTCAGCTTCTTTGCTTCCAAAGCCAGCCACAGCCATG 2663
Qy 859 IleLeuAsnLeuTrpGluAlaArgHisPheProAsnGlyAsnLeuSerGlnLeuAlaAla 878
Db 2664 ATCCTCAACCTGTGGGAGGCGCGCACTTCCCCAAGCGCAACCTCAGCCAGCTGGCTGCA 2723
Qy 879 AlaValAlaGlyLeuGlyGlnProAspAlaGlyLeuPheThrValSerGluAlaGluCys 898
Db 2724 GCAGTGGCTGGACTGGGCCAGCAGCTGGGCTCTTTCACAGTGTGGAGGCTGAGTGC 2783
RESULT 6
ADH71627
ID ADH71627 standard; DNA; 2881 BP.
XX
AC ADH71627;
XX
DT 25-MAR-2004 (first entry)
XX
DE Human gene of the invention NOV21j SEQ ID NO:523.
XX
KW ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
KW anorectic; antidiabetic; antimicrobial; antilipemic; gene therapy;
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW obesity; diabetes; infectious disease; metabolic syndrome X;
KW dyslipidaemia.
XX
OS Homo sapiens.
XX
PN WO2003102155-A2.
XX
PD 11-DEC-2003.
XX
PF 03-JUN-2003; 2003WO-US017430.
XX
PR 03-JUN-2002; 2002US-0385120P.
PR 04-JUN-2002; 2002US-0385784P.
PR 05-JUN-2002; 2002US-0386041P.
PR 06-JUN-2002; 2002US-0386047P.
PR 06-JUN-2002; 2002US-0386376P.
PR 06-JUN-2002; 2002US-0386453P.
PR 06-JUN-2002; 2002US-0386864P.
PR 07-JUN-2002; 2002US-0387016P.
PR 07-JUN-2002; 2002US-0386796P.
PR 07-JUN-2002; 2002US-0386816P.
PR 07-JUN-2002; 2002US-0386931P.
PR 07-JUN-2002; 2002US-0386942P.
PR 07-JUN-2002; 2002US-0386971P.
PR 07-JUN-2002; 2002US-0387262P.
PR 08-JUN-2002; 2002US-0296960P.
PR 10-JUN-2002; 2002US-0387400P.
PR 11-JUN-2002; 2002US-0387535P.
PR 11-JUN-2002; 2002US-0387610P.
PR 11-JUN-2002; 2002US-0387625P.
PR 11-JUN-2002; 2002US-0387634P.
PR 11-JUN-2002; 2002US-0387668P.
PR 11-JUN-2002; 2002US-0387696P.
PR 11-JUN-2002; 2002US-0387702P.
PR 11-JUN-2002; 2002US-0387836P.
PR 11-JUN-2002; 2002US-0387859P.
PR 12-JUN-2002; 2002US-0387933P.
PR 12-JUN-2002; 2002US-0387934P.
PR 12-JUN-2002; 2002US-0387960P.
PR 12-JUN-2002; 2002US-0388022P.
PR 12-JUN-2002; 2002US-0388096P.

OS	Homo sapiens.	PR	30-SEP-2002; 2002US-0414840P.	PI	Alsbrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
XX		PR	30-SEP-2002; 2002US-0414954P.	PI	Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
PN	WO2003102155-A2.	PR	09-OCT-2002; 2002US-0417186P.	PI	Ettenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
XX		PR	09-OCT-2002; 2002US-0417406P.	PI	Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, MacDougall JR;
PD	11-DEC-2003.	PR	23-OCT-2002; 2002US-0420639P.	PI	MacLachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;
XX		PR	28-OCT-2002; 2002US-0421156P.	PI	Padigaru M, Patturajan M, Pena CE, Peyman JA, Raha D, Rastelli L;
PF	03-JUN-2003; 2003WO-US017430.	PR	31-OCT-2002; 2002US-0422690P.	PI	Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shinkets RA;
XX		PR	01-NOV-2002; 2002US-0423130P.	PI	Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
XX		PR	05-NOV-2002; 2002US-00423798.		
PR		PR	05-NOV-2002; 2002US-0423798P.		
PR		PR	12-NOV-2002; 2002US-0425453P.		
XX		XX			(CURA-) CURAGEN CORP.
XX		XX			Alsbrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
PI		PI			Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
PI		PI			Ettenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
PI		PI			Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, MacDougall JR;
PI		PI			MacLachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;
PI		PI			Padigaru M, Patturajan M, Pena CE, Peyman JA, Raha D, Rastelli L;
PR		PR			Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shinkets RA;
PR		PI			Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
PR		PI			Zhong H;
XX		XX			WPI; 2004-081935/08.
DR		DR			P-PSDB; ADH71636.
XX		XX			
PT		PT			New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT		PT			treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
XX		XX			obesity, and in chromosome mapping, tissue typing or pharmacogenomics.
PS		PS			Example 21; SEQ ID NO 531; 1880pp; English.
XX		XX			The invention relates to a novel isolated polypeptide (NOVX). A
CC		CC			polypeptide of the invention has cytostatic, immunomodulator,
CC		CC			neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
CC		CC			antilipemic activity, and may have a use in gene therapy, and as a
CC		CC			vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
CC		CC			any of the 303 fully defined nucleotide sequences given in the
CC		CC			specification. The polypeptide is useful in the manufacture of a
CC		CC			medicament for treating a syndrome associated with a human disease. The
CC		CC			polypeptide, polynucleotide and antibody are useful in diagnosing,
CC		CC			treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
CC		CC			Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
CC		CC			diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
CC		CC			further used as hybridisation probes, in chromosome mapping, tissue
CC		CC			typing, preventive medicine, and pharmacogenomics. The present sequence
XX		XX			encodes a NOVX polypeptide of the invention.
SQ	Sequence 2881 BP; 527 A; 985 C; 867 G; 502 T; 0 U; 0 Other;	SQ			
Alignment Scores:					
Pred. No.:	2.74e-298	Length:	2881		
Score:	4697.50	Matches:	887		
Percent Similarity:	98.89%	Conservative:	3		
Best Local Similarity:	98.56%	Mismatches:	7		
Query Match:	98.05%	Indels:	3		
DB:	12	Gaps:	3		
US-10-624-932C-2 (1-898) x ADH71635 (1-2881)					
QY	1	MetAlaValArgProGlyLeuTrpProAlaLeuLeuGlyIleValLeuAlaTrpLeu	20		
Db	87	ATGGCGCTCCGGCCCGGCTGTGGCCAGCGCTCTCTGGGATAGTCTCGCGCTTGGCTC	146		
QY	21	ArgGlySerGlyAlaGlnSerAlaThrValAlaAsnProValProGlyValAlaAsnPro	40		
Db	147	CGCGGCTCGGGTGGCCAGAGATGCCACCGTGGCCACCCAGTGTCTGTGCAACCCG	206		
QY	41	AspLeuLeuProHisPheLeuValGluProGluAspValTyrIleValIysAsnLysPro	60		
Db	207	GACCTGCTTCCCACTTCTCTGTGGAGCCGAGGATGTGTACATCGTCAAGAACAGCCA	266		

61 ValLeuLeuValCysLysAlaValProAlaThrGlnIlePhePheLysCysAsnGlyGlu 80
 267 GTGCTGCTTGTTGTCAGAGCCGTGCCCGCCACGACAGATCTTCTCAAGTGCACCGGGAG 326
 81 TrpValArgGlnValAspHisValIleGluArgSerThrAspGlySerSerGlyLeuPro 100
 327 TGGGTGGCCAGGTGGACACACGTATCGAGCGCAGCACAGACGGGAGCAGTGGTGGAGCG 386
 101 ThrMetGluValArgIleAsnValSerArgGlnGlnValGluLysValPheGlyLeuGlu 120
 387 ACCATGAGGTCCCATTAATGTCTCAAGGAGCAGGTTCGGAAGGTGTTTCGGGCTGGAG 446
 121 GluTyrTrpCysGlnCysValAlaTrpSerSerGlyThrThrLysSerGlnLysAla 140
 447 GAATACTGGTGCCAGTGGTGCCATGAGCTCTCCGGGCACCAAGAGTCAGAGGCC 506
 141 TyrIleArgIleAlaArgLeuArgLysAsnPheGluGlnGluProLeuAlaLysGluVal 160
 507 TACATCGCATAGCCAGATTGGCGAAGAACTTCGAGCAGGAGCGCTGGCCAAAGAGGTG 566
 161 SerLeuGluGlnGlyIleValLeuProCysArgProGluGlyIleProProAlaGlu 180
 567 TCCCTGGAGCAGGCGATCGTCTGCCCTGCCGTCCACCGAGGGCATCCCTCCAGCCGAG 626
 181 ValGluTrpLeuArgAsnGluAspLeuValAspProSerLeuAspProAsnValTyrIle 200
 627 GTGGAGTGGCTCCGGAACGAGGACCTGGTGGACCCGTCCTGGACCCCAATGTATACATC 686
 201 ThrArgGluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThr 220
 687 ACGGGGAGCACACCTGGTGGTGGCAGCAGCGCCGCTTGTCTGACAGCGCCAACTACACC 746
 221 CysValAlaLysAsnIleValAlaArgArgSerAlaSerAlaValIleValTyr 240
 747 TGCCTGGCCAAAGAACATCTGGGACGTCGCCGACGCCCTCCGCTGCTGTCATGCTATC 806
 241 ValAsnGlyGlyTrpSerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArg 260
 807 GTGAACGGTGGTGGTGCAGCTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGCGC 866
 261 GlyTrpGlnLysArgSerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPhe 280
 867 GGCTGGCAGAAACGGAGCCGAGCTGCACCAACCCGCGCGCTCTTCAACGGGGCGCTTTC 926
 281 CysGluGlyGlnAsnVal---GlnLysThrAlaCysAlaThrLeuCysProValAspGly 299
 927 TGTGAGGGGCAAGATGCCATGACCCGACCGCTCTCTCTGCTGTCTGTGGACGGC 986
 300 SerTrpSerProTrpSerLysTrpSerAlaCysGlyLeuAspCysThrHisTrpArgSer 319
 987 AGCTGGAGCCCGTGGACAGTGGTCCGCTGTGGCTGGACTGCACCCACTGGCGGAGC 1046
 320 ArgGluCysSerAspProAlaProArgAsnGlyGlyGluCysGlnGlyThrAspLeu 339
 1047 CGTGAGTGTCTTGACCCAGCACCCCGCAACGGAGGGAGGAGTGCACGGGCACTGACCTG 1106
 340 AspThrArgAsnCysThrSerAspLeuCysValHisSerAlaSerGlyProGluAspVal 359
 1107 GACACCCGCAACTGTATACAGTACCTCTGTGTACACAGTGTCTTGTGCCCTGGAGGAGCTG 1166
 360 AlaLeuTyrValGlyLeuIleAlaValAlaValCysLeuValLeuLeuLeuValLeu 379
 1167 GCCCTCTATGTGGGCTCATCGCGCTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTC 1226
 380 IleLeuValTyrCysArgLysLysGluGlyLeuAspSerAspValAlaAspSerSerIle 399
 1227 ATCTCTGTTTATTCGCGAAGAGGAGGGCTGGACTCAGATGTGGTGTGACTCGTCCATT 1286
 400 LeuThrSerGlyPheGlnProValSerIleLysProSerLysAlaAspAsnProHisLeu 419
 1287 CTCACCTCAGGCTTCCAGCCGCTGAGCATCAAGCCCAAGCAAGCAGCAACCCCACTCTG 1346
 420 LeuThrIleGlnProAspLeuSerThrThrThrThrThrThrThrThrThrThrThrThr 439

1347 CTCAACCTCCAGCGGACCTCAGC---ACCACACACCTACACGAGGAGTCTCTGTCCC 1403
 440 ArgGlnAspGlyProSerProLysPheGlnLeuThrAsnGlyHisLeuLeuSerProLeu 459
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 460 GlyGlyGlyValArgHisLeuHisSerSerProThrSerGluAlaGluPheVal 479
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 1584 TATGGGACCTTCAACTTCTCGGGGCGCGCTGATGATCCCTAATACAGGTATCAGGCTC 1643
 520 LeuIleProProAspAlaIleProArgGlyValIleTyrGluIleTyrLeuThrLeuHis 539
 1644 CTATCCCGCCAGATGCCATACCCCGAGGAAGATCTATGAGATCTACCTACAGCTGCAC 1703
 540 LysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeuLeuSerProIleVal 559
 1704 AAGCCGGAAGACGTGAGGTGGCCCTAGCTGGCTGTCCAGACCTGTGAGTCCCATCGTT 1763
 560 SerCysGlyProProGlyValLeuLeuThrArgProValIleLeuAlaMetAspHisCys 579
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 580 GlyGluProSerProAspSerTrpSerLeuArgLeuLysLysGlnSerCysGluGlySer 599
 1824 GGGAGCGCCAGCCCTGACAGCTGGAGCTGGCTCCTCAAAAGCAGTCTGCGAGGGGAGC 1883
 600 TrpGlu---AspValLeuHisLeuGlyGluAlaProSerHisLeuTyrTyrCysGln 618
 1884 TGGAGCAGGATGTGTGCACCTGGCGGAGGAGCGCCCTCCACCTCTACTACTGCGCAG 1943
 619 LeuGluAlaSerAlaCysTyrValPheThrGluGlnLeuGlyArgPheAlaLeuValGly 638
 1944 CTGGAGCGCAGTGCCTGTACATCTTTCACCGCAGCAGCTGGCGCGCTTGTGCTGGTGGGA 2003
 639 GluAlaSerValAlaAlaLysArgLeuLysLeuLeuLeuLeuPheAlaProValAla 658
 2004 GAGCCCTCAGCGTGGCTGCCCGCAAGCGCTCAAGCTGCTTCTGTTTGGCGCGGTGGCC 2063
 659 CysThrSerLeuGluTyrAsnIleArgValTyrCysLeuHisAspThrHisAspAlaLeu 678
 2064 TGCACCTCCCTCGAGTACAACATCCGGGTCTACTGCTGCATGCACCCACGATGCACCTC 2123
 679 LysGluValValGlnLeuGluLysGlnLeuGlyGlyGlnLeuIleGlnGluProArgVal 698
 2124 AAGGAGTGTGTGAGTGGAGAGCAGCTGGGGGAGCAGCTGATCCAGGAGCCACGCGTC 2183
 699 LeuHisPheLysAspSerTyrHisAsnLeuArgLeuSerIleHisAspValProSerSer 718
 2184 CTGCATCTCAAGGACAGTACCAACACCTGCGCTATCCATCCAGATGTGCCAGGTCC 2243
 719 LeuTrpLysSerLysLeuLeuValSerTyrGlnGluIleProPheTyrHisIleTrpAsn 738
 2244 CTGTGGAGAGTAAAGTCTCTGTGAGTACCAGGAGATCCCTTTTATCATCATCTGGAAT 2303
 739 GlyThrGlnArgTyrLeuHisCysThrPheThrLeuGluArgValSerProSerThrSer 758
 2304 GGCACGCGCGGTACTGTGCACTGCACCTTCACCCCTGAGGCGGTGTGAGCCCGCAGCTAGT 2363
 759 AspLeuAlaCysLysLeuTrpValTrpGlnValGluGlyAspGlyGlnSerPheSerIle 778
 2364 GACCTGGCTGCAAGCTGTGGGTGTGGCAGGTGGAGGGGAGCGGAGAGCTTCAGCATC 2423
 779 AsnPheAsnIleThrLysAspThrArgPheAlaGluLeuAlaLeuGluSerGluAla 798

Db 2424 AACTTCAACATCACCAAGGACACAGGTTTGTCTGAGCTGCTGGCTCTGGAGAGTGAAGCG 2483
QY 799 GlyValProAlaLeuValGlyProSerAlaPheLysIleProPheLeuIleArgGlnLys 818
Db 2484 GGGGTCCACGCTGTGGGCCCGAGTCCCTTCAAGATCCCTTCTCATTCGGCAGAAG 2543
QY 819 IleIleSerSerLeuAspProProCysArgGlyAlaAspTrpArgThrLeuAlaGln 838
Db 2544 ATAAATTCAGCTGGACCCACCTGTAGCGGGGTGCCACTGGCGGACTCTGGCCCCAG 2603
QY 839 LysLeuHisLeuAspSerHisLeuSerPhePheAlaSerLysProSerProThrAlaMet 858
Db 2604 AAATCCACCTGCACGCCATCTCAGCTTCTTTGGCTCCAAAGCCAGCCACAGCCATG 2663
QY 859 IleLeuAsnLeuTrpGluAlaArgHisPheProAsnGlyAsnLeuSerGlnLeuAlaAla 878
Db 2664 ATCTCAACCTGTGGAGGCGCGCACTTCCCAAGCGCAACCTCAGCCAGCTGGCTGCA 2723
QY 879 AlaValAlaGlyLeuGlyGlnProAspAlaGlyLeuPheThrValSerGluAlaGluCys 898
Db 2724 GCAGTGGCTGACTGGGCCAGCAGACGCTGGCCCTTTCACAGTGTGGAGGCTGAGTGC 2783
RESULT 8
ADH71641
ID ADH71641 standard; DNA; 2881 BP.
AC ADH71641;
XX
XX
DT 25-MAR-2004 (first entry)
XX
XX Human gene of the invention NOV21q SEQ ID NO:537.
DE
DE ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
KW anorectic; antidiabetic; antimicrobial; antilipaemic; gene therapy;
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW obesity; diabetes; infectious disease; metabolic syndrome X;
KW dyslipidaemia.
XX
XX Homo sapiens.
XX
XX WC2003102155-A2.
XX
XX 11-DEC-2003.
XX
XX 03-JUN-2003; 2003WO-US017430.
XX
XX 03-JUN-2002; 2002US-0385120P.
PR 04-JUN-2002; 2002US-0385784P.
PR 05-JUN-2002; 2002US-0386041P.
PR 05-JUN-2002; 2002US-0386047P.
PR 06-JUN-2002; 2002US-0386376P.
PR 06-JUN-2002; 2002US-0386453P.
PR 06-JUN-2002; 2002US-0386864P.
PR 06-JUN-2002; 2002US-0387016P.
PR 07-JUN-2002; 2002US-0386796P.
PR 07-JUN-2002; 2002US-0386816P.
PR 07-JUN-2002; 2002US-0386931P.
PR 07-JUN-2002; 2002US-0386942P.
PR 07-JUN-2002; 2002US-0386971P.
PR 07-JUN-2002; 2002US-0387262P.
PR 08-JUN-2002; 2002US-0296960P.
PR 10-JUN-2002; 2002US-0387400P.
PR 10-JUN-2002; 2002US-0387535P.
PR 11-JUN-2002; 2002US-0387610P.
PR 11-JUN-2002; 2002US-0387625P.
PR 11-JUN-2002; 2002US-0387634P.
PR 11-JUN-2002; 2002US-0387668P.
PR 11-JUN-2002; 2002US-0387696P.
PR 11-JUN-2002; 2002US-0387702P.
PR 11-JUN-2002; 2002US-0387836P.
PR 11-JUN-2002; 2002US-0387859P.
PR 12-JUN-2002; 2002US-0387933P.
PR 12-JUN-2002; 2002US-0387934P.

PR 12-JUN-2002; 2002US-0387960P.
PR 12-JUN-2002; 2002US-0388022P.
PR 12-JUN-2002; 2002US-0388096P.
PR 13-JUN-2002; 2002US-0389123P.
PR 14-JUN-2002; 2002US-0389118P.
PR 14-JUN-2002; 2002US-0389120P.
PR 14-JUN-2002; 2002US-0389144P.
PR 14-JUN-2002; 2002US-0389146P.
PR 17-JUN-2002; 2002US-0389729P.
PR 17-JUN-2002; 2002US-0389742P.
PR 18-JUN-2002; 2002US-0389884P.
PR 19-JUN-2002; 2002US-0390066P.
PR 19-JUN-2002; 2002US-0390209P.
PR 21-JUN-2002; 2002US-0390763P.
PR 17-JUL-2002; 2002US-0396706P.
PR 06-AUG-2002; 2002US-0401628P.
PR 09-AUG-2002; 2002US-0402156P.
PR 09-AUG-2002; 2002US-0402256P.
PR 09-AUG-2002; 2002US-0402389P.
PR 12-AUG-2002; 2002US-0402786P.
PR 12-AUG-2002; 2002US-0402816P.
PR 12-AUG-2002; 2002US-0402821P.
PR 12-AUG-2002; 2002US-0402832P.
PR 13-AUG-2002; 2002US-0403448P.
PR 13-AUG-2002; 2002US-0403459P.
PR 13-AUG-2002; 2002US-0403531P.
PR 13-AUG-2002; 2002US-0403532P.
PR 13-AUG-2002; 2002US-0403563P.
PR 13-AUG-2002; 2002US-0403617P.
PR 15-AUG-2002; 2002US-0403617P.
PR 26-AUG-2002; 2002US-0406182P.
PR 26-AUG-2002; 2002US-0406352P.
PR 27-AUG-2002; 2002US-0406240P.
PR 12-SEP-2002; 2002US-0410084P.
PR 20-SEP-2002; 2002US-0412528P.
PR 23-SEP-2002; 2002US-0412731P.
PR 30-SEP-2002; 2002US-0414801P.
PR 30-SEP-2002; 2002US-0414839P.
PR 30-SEP-2002; 2002US-0414840P.
PR 30-SEP-2002; 2002US-0414954P.
PR 09-OCT-2002; 2002US-0417186P.
PR 09-OCT-2002; 2002US-0417406P.
PR 23-OCT-2002; 2002US-0420639P.
PR 28-OCT-2002; 2002US-0421156P.
PR 31-OCT-2002; 2002US-0422690P.
PR 01-NOV-2002; 2002US-0423130P.
PR 05-NOV-2002; 2002US-00423798.
PR 05-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.
XX
XX (CURA-) CURAGEN CORP.
XX
XX
PI Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
PI Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
PI Ettenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
PI Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
PI MacLachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;
PI Padigar M, Patturajan M, Pena CE, Peyman JA, Raha D, Rastelli L;
PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA;
PI Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
Zhong H;
XX
XX WPI; 2004-081935/08.
DR P-PSDB; ADH71642.
XX
XX New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.
XX
XX Example 21; SEQ ID NO 537; 1880pp; English.
PS
XX The invention relates to a novel isolated polypeptide (NOVX). A
CC polypeptide of the invention has cytostatic, immunomodulator,
CC

CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
 CC antilipemic activity, and may have a use in gene therapy, and as a
 CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
 CC any of the 303 fully defined nucleotide sequences given in the
 CC specification. The polypeptide is useful in the manufacture of a
 CC medicament for treating a syndrome associated with a human disease. The
 CC polypeptide, polynucleotide and antibody are useful in diagnosing,
 CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
 CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
 CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
 CC further used as hybridisation probes, in chromosome mapping, tissue
 CC typing, preventive medicine, and pharmacogenomics. The present sequence
 CC encodes a NOVX polypeptide of the invention.

XX
 SQ Sequence 2881 BP; 526 A; 986 C; 867 G; 502 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 3,71e-298 Length: 2881
 Score: 4695.50 Matches: 887
 Percent Similarity: 98.89% Conservative: 3
 Best Local Similarity: 98.56% Mismatches: 7
 Query Match: 98.01% Indels: 3
 DB: 12 Gaps: 3

US-10-624-932C-2 (1-898) x ADH71641 (1-2881)

Qy 1 MetAlaValArgProGlyLeuTrpProAlaLeuLeuGlyIleValLeuAlaAaTrpLeu 20
 Db 87 ATGGCCGCTCCGGCCCGCGCTGTGGCCAGCGCTCTCTGGGCATAGTCTTCGCCGCTTGGCTC 146
 Qy 21 ArgGlySerGlyAlaGlnSerAlaThrValAlaAaProValProGlyAlaAaPro 40
 Db 147 CGCGGCTCGGGTCCAGCAGAGTGCCACCGTGGCCCAACCCAGTGCCTGGTGCCACCCG 206
 Qy 41 AspLeuLeuProHisPheLeuValGluProGluAspValTyrIleValAsnLeuPro 60
 Db 207 GACCTGTCTTCCCACTTCTCTGGTGGAGCCCGAGGATGTATCATCTGTCAGAAACAAGCCA 266
 Qy 61 ValLeuLeuValCysLysAlaValProAlaThrGlnIlePhePheLysCysAsnGlyGlu 80
 Db 267 GTGCTGTCTGTGCAAGCGCGTCCCGCCACGAGATCTTCTTCAAGTGTCAACGGGGAG 326
 Qy 81 TrpValArgGlnValAspHisValIleGluArgSerThrAspGlySerSerGlyLeuPro 100
 Db 327 TGGGTGGCCAGGTGGACCGTGTATCGAGCGCAGCAGACAGCGGAGCAGTGTGTGAGCCG 386
 Qy 101 ThrMetGluValArgIleAenValSerArgGlnValGluLysValPheGlyLeuGlu 120
 Db 387 ACCATGGAGGTCCGATTAATGTCTCAAGGCAGCAGGTCTGAGAAAGTGTTCGGGCTGGAG 446
 Qy 121 GluTyrTrpCysGlnCysValAlaTrpSerSerGlyThrThrLysSerGlnLysAla 140
 Db 447 GAATACTGTGTGCCAGTCCGTGGCATGAGTCTCTCGGGCCACCACCAAGAGTCAAGAGGCC 506
 Qy 141 TyrIleArgIleAlaArgLeuArgLysAenPheGlnGluProLeuAlaLysGluVal 160
 Db 507 TACATCCGATAGCCAGATGGCGAAGAACTTCAGCAGCAGAGCCGCTGGCCAGAGGAGTG 566
 Qy 161 SerLeuGluGlnGlyIleValLeuProCysArgProProGluGlyIleProProAlaGlu 180
 Db 567 TCCCTGGAGCAGGGCAGTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 626
 Qy 181 ValGluTrpLeuArgAenGluAspLeuValAspProSerLeuAspProAenValTyrIle 200
 Db 627 GTGAGTGTGCTCCGGACAGAGGAGCTGTGGTGGACCCGCTTGGACCCCAATGTATATCATC 686
 Qy 201 ThrArgGluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAaSerThr 220
 Db 687 ACGCGGAGCAGACGCTGTGTGGCAGACGCGCCGCTTGTGTGACAGCGCCCACTACACC 746
 Qy 221 CysValAlaLysAenIleValAlaArgArgSerAlaSerAlaAlaValIleValTyr 240
 Db 747 TGGTGGCCCAAGAACATCTGGGACGTCGCGCAGCGCTCCGCTGTGTCTATCTGTCTAC 806

Qy 241 ValAenGlyGlyTyrTrpSerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyVal 260
 Db 807 GTGACCGGTGGTGGTGTGAGCGTGGACCGAGTGGTCTCTGACGGCCAGCTGTGGGGCC 866
 Qy 261 GlyTrpGlnLysArgSerArgSerCysThrAenProAlaProLeuAenGlyGlyAlaPhe 280
 Db 867 GGCTGGCAGAAACGGAGCCGAGCTGACCAACCGCGGCTCTCAACGGGGGCGCTTTC 926
 Qy 281 CysGluGlyGlnAenVal---GlnLysThrAlaCysAlaThrLeuCysProValAspGly 299
 Db 927 TGTGAGGGGAGAAATGTCCATGCCCGCACCTCTCTCTCTGTGTGTCTCTGTGTGGAGCGC 986
 Qy 300 SerTrpSerProTrpSerLysTrpSerAlaCysGlyLeuAspCysThrHisTrpArgSer 319
 Db 987 AGCTGGAGCCCGTGGAGCAAGTGGTGGCTGTGGGCTGGAGCTGACCCACTGCGGGAGC 1046
 Qy 320 ArgGluCysSerAspProAlaProArgAenGlyGlyGluGluCysGlnGlyThrAspLeu 339
 Db 1047 CGTGAGTGTCTTGACCCAGCACCCCGCAACGGAGGGGAGGAGTGCACAGGGCACTGACCTG 1106
 Qy 340 AspThrArgAenCysThrSerAspLeuCysValHisSerAlaSerGlyProGluAspVal 359
 Db 1107 GACACCCGCAACTGTATCCAGTGACCTCTGTGTACACAGTGTCTTGGCCCTTGGAGGAGTG 1166
 Qy 360 AlaLeuTyrValGlyLeuIleAlaValAlaValCysLeuValLeuLeuLeuValLeu 379
 Db 1167 GCCTCTATGTGGGCTCATCGCGTGGCCGTCTGCTGTGTCTGCTGTGTGTCTGCTC 1226
 Qy 380 IleLeuValTyrCysArgLysGlyGluGlyLeuAspSerAspValAlaAaSerSerIle 399
 Db 1227 ATCTCGTATTTATTCGCGAAGAGAGGGGCTGGACTCAGATGTGGTGTGACTGCTGCATT 1286
 Qy 400 LeuThrSerGlyPheGlnProValSerIleIysPheSerLysAlaAaAenProHisLeu 419
 Db 1287 CTACCTCAGGCTTCCAGCCCGCTCAGCATCAAGCCCAAGCAAGCAGCAACCCCACTGTG 1346
 Qy 420 LeuThrIleGlnProAspLeuSerThrThrThrThrTyrTyrGlnGlySerLeuCysPro 439
 Db 1347 CTACCATTCAGCGGGACCTCAGC---ACCACCAACCACTTACCGAGGCGAGTCTCTGTCCC 1403
 Qy 440 ArgGlnAspGlyProSerProLysPheGlnLeuThrAenGlyHisLeuLeuSerProLeu 459
 Db 1404 CGCAGGATGGGCCCGCCAGCCCAAGTTCCAGCTCACCATGGGCACTGTCTCAGCCCCCTG 1463
 Qy 460 GlyGlyGlyArgHisThrLeuHisHisSerSerProThrSerGluAlaGluGluPheVal 479
 Db 1464 GGTGGCGGCGCCACACACTGCACCACTCTCCCACTCTGAGGCGCGAGGATTCGTC 1523
 Qy 480 SerArgLeuSerThrGlnAenTyrPheArgSerLeuProArgGlyThrSerAenMetThr 499
 Db 1524 TCCGCTCTCCACCCCGAGAACTTCTCCGCTCTCCGCTCCCGCCGAGGACACAGCAATGACC 1583
 Qy 500 TyrGlyThrPheAenPheLeuGlyArgLeuMetIleProAenThrGlyIleSerLeu 519
 Db 1584 TATGGACCTTCACTTCTCCGGGCGCGCTGATGATCCCTAATACAGGTATCAGCCTC 1643
 Qy 520 LeuIleProProAspAlaIleProArgGlyLysIleTyrGluIleTyrLeuThrLeuHis 539
 Db 1644 CTATCCCCCAGATGCCATACCCCGAGGGAAGATCTATGAGATCTACCTCAGCTGCAC 1703
 Qy 540 LysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeuLeuSerProIleVal 559
 Db 1704 AACCCGGAAGACGTGAGTGTGCCCTAGCTGGTGTGAGACCTGTGTGAGTCCCATCGTT 1763
 Qy 560 SerCysGlyProProGlyValLeuLeuThrArgProValIleLeuAlaMetAspHisCys 579
 Db 1764 AGCTGTGGACCCCTGGCGTCTGTCTCACCAGCCAGTCTATCTGGCTATGGACCACTGT 1823
 Qy 580 GlyGluProSerProAspSerTrpSerLeuArgLeuLysGlnSerCysGluGlySer 599
 Db 1824 GGGAGGCCAGCCCTGACAGCTGGAGCTGCGCTCTCAAAAGAGCAGTGTGCGAGGCGAGC 1883

PR 11-JUN-2002; 2002US-0387859P.
 PR 12-JUN-2002; 2002US-0387933P.
 PR 12-JUN-2002; 2002US-0387934P.
 PR 12-JUN-2002; 2002US-0387960P.
 PR 12-JUN-2002; 2002US-0388032P.
 PR 12-JUN-2002; 2002US-0388096P.
 PR 13-JUN-2002; 2002US-0389123P.
 PR 14-JUN-2002; 2002US-0389118P.
 PR 14-JUN-2002; 2002US-0389120P.
 PR 14-JUN-2002; 2002US-0389144P.
 PR 14-JUN-2002; 2002US-0389146P.
 PR 17-JUN-2002; 2002US-0389729P.
 PR 17-JUN-2002; 2002US-0389742P.
 PR 18-JUN-2002; 2002US-0389884P.
 PR 19-JUN-2002; 2002US-0390006P.
 PR 19-JUN-2002; 2002US-0390209P.
 PR 21-JUN-2002; 2002US-0390763P.
 PR 17-JUL-2002; 2002US-0396706P.
 PR 06-AUG-2002; 2002US-0401628P.
 PR 09-AUG-2002; 2002US-0402156P.
 PR 09-AUG-2002; 2002US-0402256P.
 PR 09-AUG-2002; 2002US-0402389P.
 PR 12-AUG-2002; 2002US-0402786P.
 PR 12-AUG-2002; 2002US-0402816P.
 PR 12-AUG-2002; 2002US-0402821P.
 PR 13-AUG-2002; 2002US-0402832P.
 PR 13-AUG-2002; 2002US-0403448P.
 PR 13-AUG-2002; 2002US-0403459P.
 PR 13-AUG-2002; 2002US-0403531P.
 PR 13-AUG-2002; 2002US-0403532P.
 PR 13-AUG-2002; 2002US-0403563P.
 PR 13-AUG-2002; 2002US-0406317P.
 PR 15-AUG-2002; 2002US-0403617P.
 PR 26-AUG-2002; 2002US-0406182P.
 PR 26-AUG-2002; 2002US-0406355P.
 PR 27-AUG-2002; 2002US-0406240P.
 PR 12-SEP-2002; 2002US-0410084P.
 PR 20-SEP-2002; 2002US-0412528P.
 PR 23-SEP-2002; 2002US-0412731P.
 PR 30-SEP-2002; 2002US-0414801P.
 PR 30-SEP-2002; 2002US-0414839P.
 PR 30-SEP-2002; 2002US-0414840P.
 PR 30-SEP-2002; 2002US-0414954P.
 PR 09-OCT-2002; 2002US-0417186P.
 PR 09-OCT-2002; 2002US-0417406P.
 PR 23-OCT-2002; 2002US-0420639P.
 PR 28-OCT-2002; 2002US-0421156P.
 PR 31-OCT-2002; 2002US-0422690P.
 PR 01-NOV-2002; 2002US-0423130P.
 PR 05-NOV-2002; 2002US-0423798P.
 PR 05-NOV-2002; 2002US-0423798P.
 PR 12-NOV-2002; 2002US-0425453P.

(CURA-) CURAGEN CORP.

XX Alsebrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
 XX Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
 PI Etenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
 PI Gusev V, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
 PI MacLachlan T, Malyankar UM, Mezik AJ, Millet I, Mishra VS;
 PI Padigara M, Patturajan M, Pena CE, Peyman JA, Raha D, Rastelli L;
 PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shinkets RA;
 PI Sneathon G, Spytek KA, Stone DJ, Vernet CM, Voss EZ, Zhong M;
 PI Zhong H;

XX WPI; 2004-081935/08.
 DR P-PSDB; ADH71638.

XX New NOVX polypeptides and nucleic acid molecules useful for preventing or
 PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
 PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.

XX Example 21; SEQ ID NO 533; 1880pp; English.

XX The invention relates to a novel isolated polypeptide (NOVX). A
 CC polypeptide of the invention has cytostatic, immunomodulatory, and
 CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
 CC antilipemic activity, and may have a use in gene therapy, and as a
 CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
 CC any of the 303 fully defined nucleotide sequences given in the
 CC specification. The polypeptide is useful in the manufacture of a
 CC medicament for treating a syndrome associated with a human disease. The
 CC polypeptide, polynucleotide and antibody are useful in diagnosing,
 CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
 CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
 CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
 CC further used as hybridisation probes, in chromosome mapping, tissue
 CC typing, preventive medicine, and pharmacogenomics. The present sequence
 CC encodes a NOVX polypeptide of the invention.

XX SQ Sequence 2881 BP; 527 A; 985 C; 867 G; 502 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 4,32e-298 Length: 2881
 Score: 4694.50 Matches: 887
 Percent Similarity: 98.78% Conservative: 2
 Best Local Similarity: 98.56% Mismatches: 8
 Query Match: 97.99% Indels: 3
 DB: 12 Gaps: 3

US-10-624-932C-2 (1-898) x ADH71637 (1-2881)

QY 1 MetAlaValArgProGlyLeuTrpProAlaLeuLeuGlyLeValLeuAlaTrpLeu 20
 DB 87 ATGGCGTCCGGCCCGGCTGTGGCCAGCGCTCTGGGCATAGTCTCGCGCTTGGCTC 146
 QY 21 ArgGlySerGlyAlaGlnSerAlaThrValAlaAsnProValProGlyValaAsnPro 40
 DB 147 CGCGGCTCGGGTCCCGCAGCAGTGCACCGTGGCCAAACCAAGTGTGTGGCAACCCG 206
 QY 41 AspLeuLeuProHisPheLeuValGluProGluAspValTyrlleVallyAsnLysPro 60
 DB 207 GACCTGCTTCCCCACTTCTCTGGTGGAGCCCGAGAGTGTACATCTGTCAAGTCAACAGCCA 266
 QY 61 ValLeuLeuValCysLysAlaValProAlaThrGlnIlePhePheLysCysAsnGlyGlu 80
 DB 267 GTGCTGCTTGTGCAAGCCGCTGCGCCAGCCAGATCTTCTCAAGTCAACGGGAG 326
 QY 81 TrpValArgGlnValAspHisValIleGluArgSerThrAspGlySerSerGlyLeuPro 100
 DB 327 TGGGTGCGCCAGGTGGACCAACGTCGATCGAGCGCAGCAGCAGCGGAGCAGTGTGAGCCG 386
 QY 101 ThrMetGluValArgIleAsnValSerArgGlnGlnValGluLysValPheGlyLeuGlu 120
 DB 387 ACCATGAGGTCCGCATTATGTCTCAAGCAGCAGGTCCGAAGGTGTTCGGGCTGGAG 446
 QY 121 GluTyTrpCysGlnCysValAlaTrpSerSerSerGlyThrThrLysSerGlnLysAla 140
 DB 447 GAATACTGTGTCCAGTGGCTGGCATGGAGTCTCTCGGGCACCACCAAGAGTCAAGAGGCC 506
 QY 141 TyrlleArgIleAlaArgLeuArgLysAsnPheGluGlnGluProLeuAlaLysGluVal 160
 DB 507 TACATCCGATAGCCAGATGGCCAAAGAACTTCGAGCAGGAGCGCTGGCCAAAGAGGTG 566
 QY 161 SerLeuGluGlnGlyIleValLeuProCysArgProGluGlyIleProProAlaGlu 180
 DB 567 TCCCTGGAGCAGGGCATCTGTCTGCCCTGCCCTCCACCGGAGGGCATCCCTCCAGCCGAG 626
 QY 181 ValGluTrpLeuArgAsnGluAspLeuValAspProSerLeuAspProAsnValTyrlle 200
 DB 627 GTGGAGTGTCTCGGAACCGAGGACCTGTGTGGACCCGCTCTGGACCCCAATGTATACATC 686
 QY 201 ThrArgGluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyThr 220
 DB 687 ACACGGGAGCAGACCGCTGTGTGGTGGCAGACGGCCCGCTTGTCTGACACGGCCCAACTACACC 746

221 CysValAlaLysAsnIleValAlaArgArgSerAlaSerAlaValIleValTyr 240
747 TGGTGGCCAAAGAACATCGTGGGCACGTCGGCGCAGCGCTCCCGCTGTCATCTGCTAC 806
241 ValAsnGlyGlyTrpSerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArg 260
807 GTGAACGGTGGTGGTCCGAGCTGACCGAGTGGTCCGCTGTCAGAGCCAGCTGTGGGCGC 866
261 GlyTrpGlnLysArgSerArgSerCysThrAsnProAlaProLeuAsnGlyAlaPhe 280
867 GGCTGGCAGAAACGAGCGCGAGCTGCACCAACCGCGCGCTCTCAACGGGGCGCTTTC 926
281 CysGluGlyGlnAsnVal---GlnLysThrAlaCysAlaThrLeuCysProValAspGly 299
927 TGTGAGGGGAGAATGTGCATGACCGCGCTCTCTCTCTGCTGTCTGTGGACGGC 986
300 SerTrpSerProTrpSerLysTrpSerAlaCysGlyLeuAspCysThrHisTrpArgSer 319
987 AGCTGGAGCCCGTGGAGCAAGTGGTGGGCTGTGGGCTGGACTGCAACCACTGGCGGAGC 1046
320 ArgGluCysSerAspProAlaProArgAsnGlyGluGluCysGlnGlyThrAspLeu 339
1047 CGTGAAGTGTCTCACCAGCAGCAGCCCGCAACGAGGGGAGGAGTGCAGGGCACTGACCTG 1106
340 AspThrArgAsnCysThrSerAspLeuCysValHisSerAlaSerGlyProGluAspVal 359
1107 GACCCCGCAACTGTACAGTACCTCTGTGTACAGTGTCTTGGCCCTGAGGACGTG 1166
360 AlaLeuTyrValGlyLeuIleAlaValAlaValCysLeuValLeuLeuLeuValLeu 379
1167 GCCCTCTATGTGGCCTCATCGCGCGTGGCGCTGCTGCTGCTGCTGCTGCTGCTC 1226
380 IleLeuValTyrCysArgLysLysGluGlyLeuAspSerAspValAlaAspSerSerIle 399
1227 ATCCTCGTTTATTTCGCGGAAGAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATT 1286
400 LeuThrSerGlyPheGlnProValSerIleLysProSerLysAlaAspAsnProHisLeu 419
1287 CTCACCTCAGGCTTCCAGCCCGTCAGCATCAAGCCAGCAAGACACACCCCAATCTG 1346
420 LeuThrIleGlnProAspLeuSerThrThrThrThrThrTyrGlnGlySerLeuCysPro 439
1347 CTCACCATCCAGCCGACCTCAGC---ACCACCAACCACTACCGAGGAGTCTCTGCCC 1403
440 ArgGlnAspGlyProSerProLysPheGlnLeuThrAsnGlyHisLeuSerProLeu 459
1404 CGGAGGATGGGCCAGCCCAAGTTCCAGCTCACCATTGGGCACCTGTCTCAGCCCCCTG 1463
460 GlyGlyGlyArgHisThrLeuHisHisSerSerProThrThrThrThrThrThrThr 479
1464 GGTGGCGGCGGCACACATGCAACACAGCTCTCCCACTCTGAGGCCGAGGAGTTTCGTC 1523
480 SerArgLeuSerThrGlnAsnTyrPheArgSerLeuProArgGlyThrSerAsnMetThr 499
1524 TCCCGCTCTCCACCCAGAACTACTTCCGCTCTCCCGCTCCCGGAGCCACGACATGACC 1583
500 TyrGlyThrPheAsnPheLeuGlyArgLeuMetIleProAsnThrGlyIleSerLeu 519
1584 TATGGACCTTCAACTCTCTCGGGGGCGCGCTGATGATCCCTAATACAGGTATCAGCCCTC 1643
520 LeuIleProProAspAlaIleProArgGlyLysIleTyrGluIleTyrLeuThrLeuHis 539
1644 CTCATCCCCCAGATGCCATACCCCGAGGAAGATCTATGAGATCTACCTCAGCGCTGCAC 1703
540 LysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeuLeuSerProIleVal 559
1704 AAGCCGAAGACGTGAGGTGGCCCTAGCTGGCTGTGTCAGACCCCTGCTGAGTCCCATCGTT 1763
560 SerCysGlyProProGlyValLeuLeuThrArgProValIleLeuAlaMetAspHisCys 579
1764 AGCTGGGACCCCTCGCGCTGCTGCTACCCCGCCAGTATCTGCTGATGGACCACTGT 1823
580 GlyGluProSerProAspSerTrpSerLeuArgLeuLysLysGlnSerCysGluGlySer 599

1824 GGGGAGCCAGCCCTGACAGCTGGAGCCTCAAAAGAGAGTCTGTCGAGGGGAGC 1883
600 TrpGlu---AspValLeuHisLeuGlyGluAlaProSerHisLeuTyrTyrCysGln 618
1884 TGGGAGCAGGATGTGTGCACCTTGGGCGAGGAGCGCCCTCCACCTCTACTACTGCCAG 1943
619 LeuGluAlaSerAlaCysTyrValPheThrGluGlnLeuGlyArgPheAlaLeuValGly 638
1944 CTGGAGCCAGTGCCTGTCTACGTCTTCCAGCAGCAGCTGGCGCGCTTGTCCCTGTGGGA 2003
639 GluAlaLeuSerValAlaAlaLysArgLeuLysLeuLeuLeuPheAlaProValAla 658
2004 GAGGCCCTCAGCGTGGCTGCCAACAGCGCTCAAGCTCTTGTGTGGCGCGGTGGCC 2063
659 CysThrSerLeuGluTyrAsnIleArgValTyrCysLeuHisAspThrHisAspAlaLeu 678
2064 TGCACCTCCTCGAGTACAACTCCGGGTCTACTGCTGCATGCACACCCAGATGCACCTC 2123
679 LysGluValValGlnLeuGluLysGlnLeuGlyGlyGlnLeuIleGlnGluProArgVal 698
2124 AAGGAGGTGGTGCAGCTGGAGAAGCAGCTGGGGGAGCAGCTCATCCAGGAGCCACGGTC 2183
699 LeuHisPheLysAspSerTyrHisLeuLeuArgLeuSerIleHisAspValProSerSer 718
2184 CTGACCTTCAAGACAGATTACCAACCTTGGCGCTATCCATCCAGATGTGCCAGCTCC 2243
719 LeuTrpLysSerLysLeuLeuValSerTyrGlnGluIleProPheTyrHisIleTrpAsn 738
2244 CTGTGGAAGAGTAAGCTCTTGTGAGTACAGGAGATCCCCCTTTATCACATCTGGAAT 2303
739 GlyThrGlnArgTyrLeuHisCysThrPheThrLeuGluArgValIleSerProSerThrSer 758
2304 GGCACGACGCGTACTTGCACCTTCCACCTTGGAGCGTGTACAGCCCCAGCACACTAGT 2363
759 AspLeuAlaCysLysLeuTrpValTrpGlnValGluGlyAspGlyGlnSerPheSerIle 778
2364 GACCTGGCCTCGACGCTGGGTGTGGAGGTGGAGGGGAGCGGGGAGAGCTTCAGCAATC 2423
779 AsnPheAsnIleThrLysAspThrArgPheAlaGluLeuLeuAlaLeuGluSerGluAla 798
2424 AACTTCAACATCACCAAGGACACAAGGTTTGTGTAGCTGTGCTCTGGAGAGTGAAGCG 2483
799 GlyValProAlaLeuValGlyProSerAlaPheLysIleProPheLeuIleArgGlnLys 818
2484 GGGGTCCTCCAGCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCCTTCTCATTTGGGCAGAAG 2543
819 IleIleSerSerLeuAspProProCysArgArgGlyAlaAspTrpArgThrLeuAlaGln 838
2544 ATAAATTCAGGCTGGACCCACCTGTAGCGGGGTGCCGACTGGCGGAGCTCTGGGCCAG 2603
839 LysLeuHisLeuAspSerHisLeuSerPhePheAlaSerLysProSerProThrAlaMet 858
2604 AAATCCACCTGGACAGCCATCTCAGCTTCTTTTGGCTCCAAAGCCCCAGCCCCACAGCATG 2663
859 IleLeuAsnLeuTrpGluAlaArgHisPheProAsnGlyAsnLeuSerGlnIleAlaAla 878
2664 ATCTCTCAACCTGTGGAGCGCGGCACTTCCCAACCGCAACCTCAGCCAGCTGGGTGCA 2723
879 AlaValAlaGlyLeuGlyGlnProAspAlaGlyLeuPheThrValSerGluAlaGluCys 898
2724 GCAGTGGCTGGACTGGGCCAGCCAGACGCTGGCCTCTTTCACAGTGTCCGAGGCTGAGTGC 2783
RESULT 11
ADH71631
ID ADH71631 standard; DNA; 2881 BP.
XX
AC ADH71631;
XX
DT 25-MAR-2004 (first entry)
XX
DE Human gene of the invention NOV211 SEQ ID NO:527.
XX

KW ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
KW anorectic; antidiabetic; antimicrobial; antilipaeamic; gene therapy;
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW obesity; diabetes; infectious disease; metabolic syndrome X;
KW dyslipidaemia.
XX

OS Homo sapiens.

XX WO2003102155-A2.

XX 11-DEC-2003.

XX 03-JUN-2003; 2003WO-US017430.

XX 03-JUN-2002; 2002US-0385120P.

XX 04-JUN-2002; 2002US-0385784P.

XX 05-JUN-2002; 2002US-0386041P.

XX 06-JUN-2002; 2002US-0386047P.

XX 06-JUN-2002; 2002US-0386453P.

XX 06-JUN-2002; 2002US-0386864P.

XX 07-JUN-2002; 2002US-0387016P.

XX 07-JUN-2002; 2002US-0386796P.

XX 07-JUN-2002; 2002US-0386816P.

XX 07-JUN-2002; 2002US-0386931P.

XX 07-JUN-2002; 2002US-0386942P.

XX 07-JUN-2002; 2002US-0386971P.

XX 07-JUN-2002; 2002US-0387262P.

XX 08-JUN-2002; 2002US-0236960P.

XX 10-JUN-2002; 2002US-0387400P.

XX 10-JUN-2002; 2002US-0387535P.

XX 11-JUN-2002; 2002US-0387610P.

XX 11-JUN-2002; 2002US-0387625P.

XX 11-JUN-2002; 2002US-0387634P.

XX 11-JUN-2002; 2002US-0387688P.

XX 11-JUN-2002; 2002US-0387696P.

XX 11-JUN-2002; 2002US-0387702P.

XX 11-JUN-2002; 2002US-0387836P.

XX 11-JUN-2002; 2002US-0387859P.

XX 12-JUN-2002; 2002US-0387933P.

XX 12-JUN-2002; 2002US-0387934P.

XX 12-JUN-2002; 2002US-0387960P.

XX 12-JUN-2002; 2002US-0388022P.

XX 12-JUN-2002; 2002US-0388036P.

XX 13-JUN-2002; 2002US-0389123P.

XX 13-JUN-2002; 2002US-0389118P.

XX 14-JUN-2002; 2002US-0389120P.

XX 14-JUN-2002; 2002US-0389144P.

XX 14-JUN-2002; 2002US-0389146P.

XX 17-JUN-2002; 2002US-0389146P.

XX 17-JUN-2002; 2002US-0389729P.

PR 27-AUG-2002; 2002US-0406240P.
PR 12-SEP-2002; 2002US-0410084P.
PR 20-SEP-2002; 2002US-0412528P.
PR 23-SEP-2002; 2002US-0412731P.
PR 30-SEP-2002; 2002US-0414801P.
PR 30-SEP-2002; 2002US-0414839P.
PR 30-SEP-2002; 2002US-0414840P.
PR 30-SEP-2002; 2002US-0414954P.
PR 09-OCT-2002; 2002US-0417186P.
PR 09-OCT-2002; 2002US-0417406P.
PR 23-OCT-2002; 2002US-0420639P.
PR 28-OCT-2002; 2002US-0421156P.
PR 31-OCT-2002; 2002US-0422690P.
PR 01-NOV-2002; 2002US-0423130P.
PR 05-NOV-2002; 2002US-00423798.
PR 05-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.
XX
PA (CURA-) CURAGEN CORP.

XX Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
PI Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
PI Etenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
PI Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, MacDougall JR;
PI MacLachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;
PI Padigaru M, Patturajan M, Pena CEA, Peyman JA, Raha D, Rastelli L;
PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA;
PI Smithson G, Spytek KA, Stone DJ, Vernet CM, Voss EZ, Zhong M;
PI Zhong H;

XX WPI; 2004-081935/08.

DR P-PSDB; ADH71632.

XX New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.

XX Example 21; SEQ ID NO 527; 1880pp; English.

XX The invention relates to a novel isolated polypeptide (NOVX). A
CC polypeptide of the invention has cytostatic, immunomodulator, and
CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
CC antilipaeamic activity, and may have a use in gene therapy, and as a
CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
CC any of the 303 fully defined nucleotide sequences given in the
CC specification. The polypeptide is useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease. The
CC polypeptide, polynucleotide and antibody are useful in diagnosing,
CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
CC further used as hybridisation probes, in chromosome mapping, tissue
CC typing, preventive medicine, and pharmacogenomics. The present sequence
CC encodes a NOVX polypeptide of the invention.

XX SQ Sequence 2881 BP; 526 A; 984 C; 868 G; 503 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	4.32e-298	Length:	2881
Score:	4694.50	Matches:	887
Percent Similarity:	98.78%	Conservative:	2
Best Local Similarity:	98.56%	Mismatches:	8
Query Match:	97.99%	Indels:	3
DB:	12	Gaps:	3

US-10-624-932C-2 (1-898) x ADH71631 (1-2881)

Qy 1 MetAlaValArgProGlyLeuTrpProAlaLeuLeuGlyIleValLeuAlaTrpLeu 20
Db 87 ATGGCCGTCGGCCCGCCCTGTGGCCAGCGCTCTGGGCATAGTCTCGCGGCTTGGCTC 146
Qy 21 ArgGlySerGlyAlaGlnGlnSerAlaThrValAlaAsnProValProGlyAlaAsnPro 40

Db 147 CGCGGCTCGGTCGCCAGCAGAGTGCCACCCTGGCCCAACCCAGTGCTGGTGTGCCAACCCG 206
Qy 41 AspLeuLeuProHisPheLeuValGluProGluAspValTyrIleValIysAsnLysPro 60
Db 207 GACCTGCTTCCCTCCACTCTCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGAAACAAGCCA 266
Qy 61 ValLeuLeuValCysLysAlaValProAlaThrGlnIlePhePheLysCysAsnGlyGlu 80
Db 267 GTGCTGCTGTGTGCAAGGCGGTGCCCGCCACGACATCTTCTCAAGTGCACAACGGGGAG 326
Qy 81 TrpValArgGlnValAspHisValIleGluArgSerThrAspGlySerSerGlyLeuPro 100
Db 327 TGGGTGGCCAGGTGGACCACTGTATCGAGCGCAGCAGACGGAGCAGTGGTGGAGCCG 386
Qy 101 ThrMetGluValArgIleAsnValSerArgGlnGlnValGluLysValPheGlyLeuGlu 120
Db 387 ACCATGGAGGTCCGCATTAATGTCTCAAGGCAGCAGTCCAGAGGCGTGTGGGCTGGAG 446
Qy 121 GluTyrTrpCysGlnCysValAlaTTrpSerSerSerGlyThrThrLysSerGlnLysAla 140
Db 447 GAATACTGGTGGCAGTGGCGTGGCATGGAGCTCTCGGGCACCAACCAAGAGTCAAGAGGCC 506
Qy 141 TyrIleArgIleAlaArgLeuArgLysAsnPheGluGlnGluProLeuAlaLysGluVal 160
Db 507 TACATCCGCATAGCCAGATTGCCAGAACTTCAGCAGAGGAGCGCTGGCCAAAGAGGTG 566
Qy 161 SerLeuGluGlnGlyIleValLeuProCysArgProProGluGlyIleProProAlaGlu 180
Db 567 TCCCTGGAGCAGGCGCATCGTGTGCGCTGCGCTGCCAGCCAGGCGCATCCCTCCAGCCGAG 626
Qy 181 ValGluTrpLeuArgGlnAspLeuValAspProSerLeuAspProAsnValTyrIle 200
Db 627 GTGGAGTGGCTCCGGAAACAGGAGACCTGGTGGACCCCTCGGACCCCAATGTATACATC 686
Qy 201 ThrArgGluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThr 220
Db 687 ACCGGGAGCAGACCTGGTGGTGGCAGAGCCCGCTTGCTGACACGGCCCACTACACC 746
Qy 221 CysValAlaLysAsnIleValAlaArgArgSerAlaSerAlaAlaValIleValTyr 240
Db 747 TGGTGGCCCAAGAAACATCGTGGCACGCTCGCGCAGCGCCCTCCGCTGCTGTATCGTCTAC 806
Qy 241 ValAsnGlyGlyTrpSerThrTrpGluTrpSerValCysSerAlaSerCysGlyArg 260
Db 807 GTAAACGGTGGGTGGTGGAGCTGGACCGAGTGTGCTGTGACGCCACAGCTGTGGGCGC 866
Qy 261 GlyTrpGlnLysArgSerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPhe 280
Db 867 GGCTGCGCAGAAACGGAGCCGGAGCTGCACCAACCCCGCGCCCTCTCAACGGGGGCGCTTTC 926
Qy 281 CysGluGlyGlnAsnVal---GlnLysThrAlaCysAlaThrLeuCysProValAspGly 299
Db 927 TGTGAGGGGCGAATATCCATGACCGCACCGCTCTCCTCTCTGCTGTCTGTGGACGGC 986
Qy 300 SerTrpSerProTrpSerLysTrpSerAlaCysGlyLeuAspCysThrHisTrpArgSer 319
Db 987 AGCTGAGGCCGTGGAGCAAGTGGTGGGCTGTGGGCTGGAGCTGCACCCACCTGGCGGAGC 1046
Qy 320 ArgGluCysSerAspProAlaProArgAsnGlyGlyGluGluCysGlnGlyThrAspLeu 339
Db 1047 CGTGTGCTGTGACCCAGCACCCCGCAACGGAGGGGAGAGTGGCCAGGGCACTGACCTG 1106
Qy 340 AspThrArgAsnCysThrSerAspLeuCysValHisSerAlaSerGlyProGluAspVal 359
Db 1107 GACACCGCGCAACTGTACAGTACCTCTGTGTACACAGTGTCTTGGCCCTCGAGACGCTG 1166
Qy 360 AlaLeuTyrValGlyLeuIleAlaValAlaValCysLeuValLeuLeuLeuValLeu 379
Db 1167 GCCCTCTATGTGGGCTCATTCGCCGTGGCGGCTGTGCTGGTCTGTGCTGTGCTTC 1226
Qy 380 IleLeuValTyrCysArgLysLysGluGlyLeuAspSerAspValAlaAspSerSerIle 399
Db 1227 ATCCTCGTTTATTGCCGAAGAAGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATT 1286

Qy 400 LeuThrSerGlyPheGlnProValSerIleLysProSerLysAlaAspAsnProHisLeu 419
Db 1287 CTCACCTCAGGCTTCCAGCCCGTCAGCATCAAGCCCGCAGCAAGCAGCAACCCCATCTG 1346
Qy 420 LeuThrIleGlnProAspLeuSerThrThrThrThrThrThrThrThrThrThrThrThr 439
Db 1347 CTCACCATCCAGCCGACCTCAGC---ACCACCCACCATCTACAGGGCAGTCTCTGTGCC 1403
Qy 440 ArgGlnAspGlyProSerProLysPheGlnLeuThrAsnGlyHisIleLeuLeuSerProLeu 459
Db 1404 CGCAGAGTGGGCCCGCCAGCTTCCAGTTCAGCTACCAATGGGCACCTGTCTCAGCCCTCG 1463
Qy 460 GlyGlyGlyArgHisThrLeuHisHisSerSerProThrSerGluAlaGluGluPheVal 479
Db 1464 GGTGGCGGCGCCACACACTGCACACACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTC 1523
Qy 480 SerArgLeuSerThrGlnAsnTyrPheArgSerLeuProArgGlyThrSerAsnMetThr 499
Db 1524 TCCCGCTCTCCACCCAGAACTACTTCCGCTCCCTGCCCCGAGGCCACCAAGCAACATGACC 1583
Qy 500 TyrGlyThrPheAsnPheLeuGlyArgLeuMetIleProAsnThrGlyIleSerLeu 519
Db 1584 TATGGACCTTCAACTTCTCGGGGCGCGCTGATGATCCCTAATACAGGTATCAGCCCTC 1643
Qy 520 LeuIleProProAspAlaIleProArgGlyLysIleTyrGluIleTyrLeuThrLeuHis 539
Db 1644 CTCATCCCCCAGATGTCTATACCCGAGGGAAGATCTATGAGATCTATCCTCAGCTGCAC 1703
Qy 540 LysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeuLeuSerProIleVal 559
Db 1704 AAGCCGGAAGAGTGTGAGGTGGCCCTAGCTGCTGTGACACCTGTGCTAGTCTCCATCGTT 1763
Qy 560 SerCysGlyProProGlyValLeuLeuThrArgProValIleLeuAlaMetAspHisCys 579
Db 1764 AGCTGTGGACCCCTGGCTGCTGTCCACCCCGCCAGTCTCTCTGGCTATGGACCACTGT 1823
Qy 580 GlyGluProSerProAspSerTrpSerLeuArgLeuLysLysGlnSerCysGluGlySer 599
Db 1824 GGGGAGCCCGACCTGACAGCTGGAGCTGCGCCTCAAAAGACAGTGTGTGCGAGGGCAGC 1883
Qy 600 TrpGlu---AspValIleHisLeuGlyGluAlaProSerHisLeuTyrTrpCysGln 618
Db 1884 TGGAGAGAGATGTGTGACCTGGCGGAGGAGGCGCCCTCCACCTCTACTACTGCCAG 1943
Qy 619 LeuGluAlaSerAlaCysTyrValPheThrGluGlnLeuGlyArgPheAlaLeuValGly 638
Db 1944 CTGGAGCCAGTGTCTGTCTCTTCCAGCAGAGCTGGGCGCTTTTCCCTGGTGGGA 2003
Qy 639 GluAlaLeuSerValAlaAlaLysArgLeuLysLeuLeuLeuPheAlaProValAla 658
Db 2004 GAGGCCCTCAGCGTGGCTGCCCGCAAGCGCTCAAGCTGCTCTGTGTTGCGCGGTGGCC 2063
Qy 659 CysThrSerLeuGluTyrAsnIleArgValTyrCysLeuHisAspThrHisAspAlaLeu 678
Db 2064 TGCACCTCCTCGAGTACAACTCCGGTCTACTGCTGCATGCATGACACCCACCATGCACTC 2123
Qy 679 LysGluValValGlnLeuGluLysGlnLeuGlyGlyGlnLeuIleGlnLeuProArgVal 698
Db 2124 AAGGAGGTGTGCAGCTGGAGAAGCAGCTGGGGGAGCAGCTGATCCAGGAGCCACGGGTC 2183
Qy 699 LeuHisPheLysAspSerTyrHisAsnLeuArgLeuSerIleHisAspValProSerSer 718
Db 2184 CTGCATCTCAAGAGAGATTACCAACCTGCGCCCTATCCATCCACGATGTGCCAGCTCC 2243
Qy 719 LeuTrpLysSerLysLeuLeuValSerTyrGlnGluIleProPheTyrHisIleTrpAsn 738
Db 2244 CTGTGGAAGAGTAACTCTCTGTGAGCTACCAAGAGATCCCCCTTTTATCACAATCTGGAAT 2303
Qy 739 GlyThrGlnArgTyrLeuHisCysThrPheThrLeuGluArgValSerProSerThrSer 758
Db 2304 GGCACGCGCGGTACTGTGCATCGCACTTCACCTGGAGCGGTGTGAGCCCGCAGCACTAGT 2363

PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.
XX Example 21; SEQ ID NO 529; 1880pp; English.
XX The invention relates to a novel isolated polypeptide (NOVX). A
CC polypeptide of the invention has cytostatic, immunomodulator,
CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
CC antilipaemic activity, and may have a use in gene therapy, and as a
CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
CC any of the 303 fully defined nucleotide sequences given in the
CC specification. The polypeptide is useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease. The
CC polypeptide, polynucleotide and antibody are useful in diagnosing, the
CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
CC further used as hybridisation probes, in chromosome mapping, tissue
CC typing, preventive medicine, and pharmacogenomics. The present sequence
CC encodes a NOVX polypeptide of the invention.
XX
SQ Sequence 2880 BP; 527 A; 984 C; 867 G; 502 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 5.02e-298 Length: 2880
Score: 4693.50 Matches: 887
Percent Similarity: 98.78% Conservative: 2
Best Local Similarity: 98.56% Mismatches: 8
Query Match: 97.96% Indels: 3
DB: 12 Gaps: 3

US-10-624-932C-2 (1-898) x ADH71633 (1-2880)

QY 1 MetAlaValArgProGlyLeuTyrProAlaLeuLeuGlyLeValLeuAlaTyrLeu 20
DB 86 ATGGCGCTCCGGCCCGGCTGTGGCAGCGCTCTGGGATATGCTCTGGCGCTGGCTC 145

QY 21 ArgGlySerGlyAlaGlnSerAlaThrValAlaAsnProValProGlyAlaAsnPro 40
DB 146 CGCGGCTCGGGTCCCGCAGAGATGCCCGTGGCCAAACCGATGCTGTGTCACACCG 205

QY 41 AspLeuLeuProHisPheLeuValGluProGluAspValTyrIleValLysAsnLysPro 60
DB 206 GACCTGCTTCCCCACTTCTCGTGGAGCCGAGGATGTGTACATCGTCAAGAACAGCCA 265

QY 61 ValLeuLeuValCysLysAlaValProAlaThrGlnIlePhePheLysCysAsnGlyGlu 80
DB 266 GTGCTGCTTGTGTGCAAGGCGGTGCCCGCCACAGATCTTCTCAAGTGCACACGGGGAG 325

QY 81 TrpValArgGlnValAspHisValIleGluArgSerThrAspGlySerSerGlyLeuPro 100
DB 326 TGGGTGGCCAGGTGGACCAAGTGTGAGCGGACGACAGCGGAGCAGTGTGTGAGCCG 395

QY 101 ThrMetGluValArgIleAsnValSerArgGlnGlnValGluLysValPheGlyLeuGlu 120
DB 386 ACCATGGAGGTCCGCATTATGTCTCAAGCAGCAGGTTCGAGAGGTTCGGGCTGGAG 445

QY 121 GluTyrTrpCysGlnCysValAlaTyrPheSerSerSerGlyThrThrLysSerGlnLysAla 140
DB 446 GAATACTGTGTGCGAGTGGTGGATGGAGTCTCGGGCCACCAAGAGTTCAGAAAGGCC 505

QY 141 TyrIleArgIleAlaArgLeuArgLysAsnPheGluGlnGluProLeuAlaLysGluVal 160
DB 506 TACATCCGCATAGCCAGATTGCCAAGAACTTCGAGCAGGAGCCGCTGGCCAAAGGAGTG 565

QY 161 SerLeuGluGlnGlyIleValLeuProCysArgProProGluGlyIleProProAlaGlu 180
DB 566 TCCCTGGAGCAGGGCATCGTGTGCTGCCCTGCCGTCACCGGAGGGCATCCCTCCAGCCGAG 625

QY 181 ValGluTyrLeuArgAsnGluAspLeuValAspProSerLeuAspProAsnValTyrIle 200
DB 626 GTGGAGTGGCTCCGGACACGAGGACCTGGTGGACCCGCTCCGACCCCAATGTATATCATC 695

QY 201 ThrArgGluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThr 220

DB 686 ACCTGGGAGCAGAGCTGTGGTGGCAGAGCCCGCTTGTCTGACAGCGCAACTACACC 745
QY 221 CysValAlaLysAsnIleValAlaArgArgSerAlaSerAlaAlaValIleValTyr 240
DB 746 TGGCTGGCCCAAGAACATCGTGGCAGCTGCGCGCAGCGCTCTCCGCTGTGTCTCATCGTCTAC 805
QY 241 ValAsnGlyGlyTyrPheSerThrTrpThrGluTyrPheSerValCysSerAlaSerCysGlyArg 260
DB 806 GTGAACCGTGGGTGGTGGACCGAGTGGTCTGTGACAGCCAGCTGTGGCGGC 865
QY 261 GlyTrpGlnLysArgSerArgSerCysThrAsnProAlaProLeuAsnGlnGlyAlaPhe 280
DB 866 GGTGGCAGAAACGAGCGCGAGCTGCACCAACCGCGCGCTCTCAACGGGGCGCTTTC 925
QY 281 CysGluGlyGlnAsnVal---GlnLysThrAlaCysAlaThrLeuCysProValAspGly 299
DB 926 TGTGAGGGGCAGAAATGTCATGACCGCAGCGTCTCTCTGCTGTGTCTGTGGAGCGC 985
QY 300 SerTrpSerProTrpSerLysTrpSerAlaCysGlyLeuAspCysThrHisTrpArgSer 319
DB 986 AGCTGGAGCCCGTGGAGCAAGTGGTGGCTGTGGCTGTGACTGCACCCACCTGCGGAGC 1045
QY 320 ArgGluCysSerAspProAlaProArgAsnGlyGlyGluGluCysGlnGlyThrAspLeu 339
DB 1046 CGTGAGTGTCTGACCCAGACACCCCAACGGAGGGGAGAGTGGCAGGGCACTGACCTG 1105
QY 340 AspThrArgAsnCysThrSerAspLeuCysValHisSerAlaSerGlyProGluAspVal 359
DB 1106 GACACCCGCAACTGTATACAGTACCTCTGTGTACACAGTGTCTTGTGGCTGTAGGACGTG 1165
QY 360 AlaLeuTyrValGlyLeuIleAlaValAlaValCysLeuValLeuLeuLeuValLeu 379
DB 1166 GGCCTCTATGTGGCGCTCATCGCGTGGCGCTGTGCTGTGCTGTGCTGTGCTGTGCTC 1225
QY 380 IleLeuValTyrCysArgLysLysGluGlyLeuAspSerAspValAlaAspSerSerIle 399
DB 1226 ATCTCTGTTTATTCGCCGGAAGAGGGGCTGGACTCAGATGTGGCTGACTGCTCATT 1285
QY 400 LeuThrSerGlyPheGlnProValSerIleLysProSerLysAlaAspAsnProHisLeu 419
DB 1286 CTCACCTCAGGCTTTCAGCCCGTGCAGCTCAAGCCAGCAAGCAGACAAACCCCATCTG 1345
QY 420 LeuThrIleGlnProAspLeuSerThrThrThrThrThrThrThrThrThrThrThrThr 439
DB 1346 CTCACCATCCAGCCGACCTCAGC---ACCACCACTTACCAGGGCAGTCTCTGTGCC 1402
QY 440 ArgGlnAspGlyProSerProLysPheGlnLeuThrAsnGlyHisLeuLeuSerProLeu 459
DB 1403 CGGCAGAGTGGGCCCGCCAGCTTCCAGCTCACCAGTGGGACCTGTCTCAGCCCCCTG 1462
QY 460 GlyGlyGlyArgHisThrLeuHisHisSerSerProThrSerGluAlaGluGluPheVal 479
DB 1463 GGTGGCGGCGCCACACACTGCACACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTC 1522
QY 480 SerArgLeuSerThrGlnAsnTyrPheArgSerLeuProArgGlyThrSerAsnMetThr 499
DB 1523 TCCCGCTCTCCACCCAGAACTACTTCCGCTCCCTCCCGGAGCCAGCAGCAACATGACC 1582
QY 500 TyrGlyThrPheAsnPheLeuGlyArgLeuMetIleProAsnThrGlyIleSerLeu 519
DB 1583 TATGGACCTTCACTTCTCGGGGCCCGGTGTAGTATCCCTAATACAGGTATCAGCCTC 1642
QY 520 LeuIleProProAspAlaIleProArgGlyLysIleTyrGluIleTyrLeuThrLeuHis 539
DB 1643 CTCATCCCCCAGATGCCATACCCCGAGGGAAGATCTATGAGATCTACCTCAGCTGCAC 1702
QY 540 LysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeuLeuSerProIleVal 559
DB 1703 AAGCCGGAAGAGTGAAGTGGCTGTAGTGGCTGTGACACCTCTGTAGTCCATCGTT 1762
QY 560 SerCysGlyProProGlyValLeuLeuThrArgProValIleLeuAlaMetAspHisCys 579

PR 15-AUG-2002; 2002US-0403617P.
 PR 26-AUG-2002; 2002US-0406182P.
 PR 26-AUG-2002; 2002US-0406355P.
 PR 27-AUG-2002; 2002US-0406240P.
 PR 12-SEP-2002; 2002US-0410084P.
 PR 20-SEP-2002; 2002US-0412528P.
 PR 23-SEP-2002; 2002US-0412731P.
 PR 30-SEP-2002; 2002US-0414801P.
 PR 30-SEP-2002; 2002US-0414839P.
 PR 30-SEP-2002; 2002US-0414840P.
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 PR 09-OCT-2002; 2002US-0417186P.
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 PR 31-OCT-2002; 2002US-0422690P.
 PR 01-NOV-2002; 2002US-0423130P.
 PR 05-NOV-2002; 2002US-0423798.
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 PR 12-NOV-2002; 2002US-0425453P.
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 PA (CURA-) CURAGEN CORP.
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 PI Alsebrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
 PI Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
 PI Etenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
 PI Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
 PI MacLachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;
 PI Padigaru M, Patturajan M, Pena CBA, Peyman JA, Raha D, Rastelli L;
 PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shinkets RA;
 PI Smithson G, Spytek KA, Stone DJ, Vernet CM, Voss EZ, Zhong M;
 PI Zhong H;
 XX
 DR WPI; 2004-081935/08.
 DR P-PSDB; ADH71630.
 XX
 PT New NOVX polypeptides and nucleic acid molecules useful for preventing or
 PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
 PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.
 XX
 PS Example 21; SEQ ID NO 525; 1880pp; English.
 XX
 CC The invention relates to a novel isolated polypeptide (NOVX). A
 CC polypeptide of the invention has cytostatic, immunomodulator, A
 CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
 CC antilipemic activity, and may have a use in gene therapy, and as a
 CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
 CC any of the 303 fully defined nucleotide sequences given in the
 CC specification. The polypeptide is useful in the manufacture of a
 CC medicament for treating a syndrome associated with a human disease. The
 CC polypeptide, polynucleotide and antibody are useful in diagnosing,
 CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
 CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
 CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
 CC further used as hybridisation probes, in chromosome mapping, tissue
 CC typing, preventive medicine, and pharmacogenomics. The present sequence
 CC encodes a NOVX polypeptide of the invention.
 XX
 SQ Sequence 2881 BP; 526 A; 986 C; 868 G; 501 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 6-79e-298 Length: 2881
 Score: 4691.50 Matches: 887
 Percent Similarity: 98.78% Conservative: 2
 Best Local Similarity: 98.56% Mismatches: 8
 Query Match: 97.92% Indels: 3
 DB: 12 Gaps: 3

US-10-624-932c-2 (1-898) x ADH71629 (1-2881)

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Qy 21 ArgGlySerGlyAlaGlnGlnSerAlaThrValAlaAsnProValProGlyAlaAsnPro 40
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 Qy 41 AspLeuLeuProHisPheLeuValGluProGluAspValTyrtleValLysAsnLysPro 60
 Db GACCTGCTTCCCCACTTCTGTGGAGCCCGAGGATGTGTACATCTCTCAAGTCAACAGGCCA 266
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 Db GTGCTGCTGTGTGCAAGGCCGTGCCGCCACCGCAGATCTTCTCAAGTCAACAGGCCGAG 326
 Qy 81 TrpValArgGlnValAspHisValIleGluArgSerThrAspGlySerSerGlyLeuPro 100
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 Qy 121 GluTyTrpCysGlnCysValAlaTrpSerSerSerGlyThrThrLysSerGlnLysAla 140
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 Db TACATCCGATAGCCAGATTTGGCAAGAACTTCGAGCAGGAGCGCTGGCCCAAGAGAGTG 566
 Qy 161 SerLeuGluGlnGlyIleValLeuProCysArgProProGluGlyIleProProAlaGlu 180
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 Qy 181 ValGluTrpLeuArgAsnGluAspLeuValAspProProSerLeuAspProAsnValTyrtle 200
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 Qy 201 ThrArgGluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyThr 220
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 Qy 241 ValAsnGlyGlyTrpSerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArg 260
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Qy	400	LeuThrSerGlyPheGlnProValSerIleIysProSerLysAlaAaspAaspProHisLeu	419
Db	1287	CTACCTTCAGGCTTCAGCCCGTTCAGCATCAAGCCCGAAGCAGACAACCCCCATCTG	1346
Qy	420	LeuThrIleGlnProAaspLeuSerThrThrThrThrThrThrThrThrThrThrThrThr	439
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Qy	440	ArgGlnAaspGlyProSerProLysPheGlnLeuThrAenGlyHisLeuLeuSerProLeu	459
Db	1404	CGGCAGGATGGGCCAGCCCAAGTTCCAGCTCACCAATGGGCACCTGTCTCAGCCCCCTG	1463
Qy	460	GlyGlyGlyArgHisThrLeuHisHisSerSerProThrSerGluAlaGluGluPheVal	479
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Qy	480	SerArgLeuSerThrGlnAenTyrPheArgSerLeuProArgGlyThrSerAaspMetThr	499
Db	1524	TCCGCTCTCCACCCAGACTACTTCGCTCCCTGCCCCGAGGCACCAACATGACC	1583
Qy	500	TyrGlyThrPheAenPheLeuGlyGlyArgLeuMetIleProAenThrGlyIleSerLeu	519
Db	1584	TATGGGACCTTCACTTCTCGGGGCGGCTGATGATCCCTAATACAGGTATCAGGCCTC	1643
Qy	520	LeuIleProAaspAlaIleProArgGlyIleTyrGluIleTyrLeuThrLeuHis	539
Db	1644	CTCATCCCCCAGATGCCATACCCCGAGGAGAACTATGAGATCTACCTTCACGCTGCAC	1703
Qy	540	LysProGluAaspValArgLeuProLeuAlaGlyCysGlnThrLeuLeuSerProIleVal	559
Db	1704	AAGCCGGAAGCGTAGGTTGCCCTAGCTGGCTGTCTCAGACCTGTCTGAGTCCCATCTT	1763
Qy	560	SerCysGlyProProGlyValLeuLeuThrArgProValIleLeuAlaMetAaspHisCys	579
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Qy	580	GlyGluProSerProAaspSerTrpSerLeuArgLeuLysGlnSerCysGluGlySer	599
Db	1824	GGGAGGCCAGCCCTGCACGTGAGCCTGGCCCTCAAAAAGCAGTCTGTCGAGGGCAGC	1883
Qy	600	TrpGlu--AaspValLeuHisLeuGlyGluAlaProSerHisLeuTyrTyrCysGln	618
Db	1884	TGGGACAGCATGTGCTGCACCTGGGCGCAGAGGGCCCTCCACCTCTACTACTGCCAG	1943
Qy	619	LeuGluAlaSerAlaCysTyrValPheThrGluGlnLeuGlyArgPheAlaLeuValGly	638
Db	1944	CTGGAGGCCAGTGCCTGACTAGCTTTCACCGAGCAGCTGGGCGCTTTGCTGTGGTGGGA	2003
Qy	639	GluAlaLeuSerValAlaAlaLysArgLeuLysLeuLeuLeuPheAlaProValAla	658
Db	2004	GAGGCCCTCAGCTGGCTGGCGCCAGCGCTCAAGCTGCTTCTGTTTGGCGCGGTGGCC	2063
Qy	659	CysThrSerLeuGluTyrAenIleArgValTyrCysLeuHisAaspThrHisAaspAlaLeu	678
Db	2064	TGCACCTCCCTCGAGTHCAACATCCGGGTCTACTGCTGTCATGACCCACGATGACATC	2123
Qy	679	LysGluValValGlnLeuGluLysGlnLeuGlyGlyGlnLeuIleGlnGluProArgVal	698
Db	2124	AAGGAGGTGTCAGCTGGAGAGCAGCTGGGGGACAGCTGATCCAGGAGCCACGGGTC	2183
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Db	2244	CTGTGGAAGAGTAGCTCTGTGTCAGCTACAGGAGATCCCCCTTTATCATCATCTGGAAT	2303
Qy	739	GlyThrGlnArgTyrLeuHisCysThrPheThrLeuGluArgValSerProSerThrSer	758

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Qy	759	AsnLeuAlaCyValysLeuTrrpValTrrpGlnValGlucIlyAspGlyGlnSerPheSerIle	778
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Qy	779	AsnPheAsnIleThrLysAspThrArgPheAlaGlululeuAlaLeuGluSerGluAla	798
Db	2424	AACITTCACATCACCAAGGACACAAAGGTTTTGCTGAGCTGTGGCTCTGGAGAGTGAAGCG	2483
Qy	799	GlyValProAlaLeuValGlyProSerAlaPheIlyIleProPheLeuIleArgGlnLys	818
Db	2484	GGGGTCCAGCCCTGGTGGGCCCGAGTGCCTTCAAGATCCCTCTCTCATTCGCGAGAAG	2543
Qy	819	IleIleSerSerLeuAspProProCysArgArgGlyAlaAspTrrpArgThrLeuAlaGln	838
Db	2544	ATAATTTCCAGCTGGHACCCACCTGTAGCGGGGTGCCAGCTGGCGAGCTCTGGGCCAG	2603
Qy	839	LysLeuHisLeuAspSerHisLeuSerPhePheAlaSerLysProSerProThrAlaMet	858
Db	2604	AAACTCCACCTGGACAGCCATCTCAGCTTCTTTGGCTTCCAAGCCAGCCCCACAGCCATG	2663
Qy	859	IleLeuAsnLeuTrrpGluAlaArgHisPheProAsnGlyAsnLeuSerGlnLeuAlaAla	878
Db	2664	ATCCTCAACCTGTGGAGGGCGCGCACTTCCCAACGGCAACCTCAGCCAGCTGGCTGCA	2723
Qy	879	AlaValAlaGlyLeuGlyGlnProAspAlaGlyLeuPheThrValSerGluAlaGluCys	898
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AC			
XX			
DT	25-MAR-2004 (first entry)		
XX			
DE	Human gene of the invention NOV21r SEQ ID NO:539.		
XX			
KW	ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;		
KW	anorectic; anti-diabetic; antimicrobial; antilipemic; gene therapy;		
KW	vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;		
KW	obesity; diabetes; infectious disease; metabolic syndrome X;		
KW	dyslipidaemia.		
OS	Homo sapiens.		
XX			
FN	WO2003102155-A2.		
XX			
PD	11-DEC-2003.		
XX			
PF	03-JUN-2003; 2003WO-US017430.		
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PR 23-SEP-2002; 2002US-0412731P.
PR 30-SEP-2002; 2002US-0414801P.
PR 30-SEP-2002; 2002US-0414839P.
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PR 30-SEP-2002; 2002US-0414954P.
PR 09-OCT-2002; 2002US-0417186P.
PR 09-OCT-2002; 2002US-0417406P.
PR 23-OCT-2002; 2002US-0420639P.
PR 28-OCT-2002; 2002US-0421156P.
PR 31-OCT-2002; 2002US-0422690P.
PR 01-NOV-2002; 2002US-0423130P.
PR 05-NOV-2002; 2002US-00423798.
PR 05-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.
XX
XX (CURA-) CURAGEN CORP.
XX
XX
XX
XX Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
XX Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
XX Ettenberg S, Gangoli EH, Gerlach VL, Gorman L, Gunther E, Guo X;
XX Gusev VT, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
XX Maclachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;
XX Padigar M, Patturajan M, Pena CEA, Peyman JA, Raha D, Rastelli L;
XX Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shinkets RA;
XX Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
XX Zhong H;
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XX WPI; 2004-081935/08.
XX P-PSDB; ADH71644.
XX
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XX New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.
XX
XX Example 21; SEQ ID NO 539; 1880pp; English.
XX
CC The invention relates to a novel isolated polypeptide (NOVX). A
CC polypeptide of the invention has cytostatic, immunomodulator,
CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
CC antilipase activity, and may have a use in gene therapy, and as a
CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
CC any of the 303 fully defined nucleotide sequences given in the
CC specification. The polypeptide is useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease. The
CC polypeptide, polynucleotide and antibody are useful in diagnosing,
CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
CC further used as hybridisation probes, in chromosome mapping, tissue
CC typing, preventive medicine, and pharmacogenomics. The present sequence
CC encodes a NOVX polypeptide of the invention.
XX
SQ Sequence 2881 BP; 527 A; 985 C; 867 G; 502 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6.79e-298 Length: 2881
Score: 4691.50 Matches: 887
Percent Similarity: 98.78% Conservative: 2
Best Local Similarity: 98.56% Mismatches: 8
Query Match: 97.92% Indels: 3
DB: 12 Gaps: 3

US-10-624-932C-2 (1-898) x ADH71643 (1-2881)

QY 1 MetAlaValArgProGlyLeuTrpProAlaLeuLeuGlyValLeuAlaAlaTrpLeu 20
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Db 87 ATGGCCGTCGGCCCGGCTGTGGCCAGCGCTCTGGGCATAGTCTCGCCGCTTGGCTC 146
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QY 21 ArgGlySerGlyAlaGlnGlnSerAlaThrValAlaAsnProValProGlyAlaAsnPro 40
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QY 41 AspLeuLeuProHisPheLeuValGluProGluAspValTyrIleValIysAsnLysPro 60
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QY 400 LeuThrSerGlyPheGlnProValSerIleLysProSerLysAlaAspAsnProHisLeu 419
Db 1287 CTCACCTCAGGCTTCCAGCCGCTCAGCATCAAGCCCGAGCAAGCAACCCCATCTG 1346
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Db 1347 CTCACCATCCAGCCGACCTCAGC---ACCACCAACCACTTACCAGGGCAGTCTCTGTCCC 1403
QY 440 ArgGlnAspGlyProSerProLysPheGlnLeuThrAsnGlyHisLeuLeuSerProLeu 459
Db 1404 CGGACAGATGGGCCCAAGCCCAAGTTCCAGCTCACCATATGGGCACCTGCTCAGCCCCCTG 1463
QY 460 GlyGlyGlyArgHisThrLeuHisHisSerSerProThrSerGluAlaGluGluPheVal 479
Db 1464 GGTGGCGGCGCCACACACTGCACCAAGCTCTCCACCTCTCAGGCCGAGGATTCGTC 1523
QY 480 SerArgLeuSerThrGlnAsnTyrPheArgSerLeuProArgGlyThrSerAsnMetThr 499
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Db 1644 CTCAATCCCCCAGATGCCATACCCCGAGGGAAGATCTATGAGATCTACCTCAGCTGCAC 1703
QY 540 LysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeuLeuSerProIleVal 559
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RESULT 15

ADH71647

ID ADH71647 standard; DNA; 2881 BP.

XX

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Db 1884 TGGAGCAGCAGATGTGTGCACCTGGCGCAGGAGGCCCTCCACCTCTACTACTGCAG 1943
QY 619 LeuGluAlaSerAlaCysTyrValPheThrGluGlnLeuGlyArgPheAlaLeuValGly 638
Db 1944 CTGGAGGCCAGTGCCTGCTACGCTTTCACCGAGCAGCTGGGCGCTTGTGCTTGGTGGGA 2003
QY 639 GluAlaLeuSerValAlaAlaAlaLysArgLeuLysLeuLeuLeuPheAlaProValAla 658
Db 2004 GAGGCCCTCAGCGTGGCTGCGGCCAAGCGCCTCAAGCTGCTTCTGTTGGCGGTGGCC 2063
QY 659 CysThrSerLeuGluTyrAsnIleArgValTyrCysLeuHisAspThrHisAspAlaLeu 678
Db 2064 TGCACCTCCTCGAGTACAACATCCGGGTCTACTGCTGTCATGACACCCACGATGCACTC 2123
QY 679 LysGluValValGlnLeuGluLysGlnLeuGlyGlyGlnLeuIleGlnGluProArgVal 698
Db 2124 AAGGAGTGGTGCAGCTGGAGAGCAGCTGGGGGGACAGCTGATCAGGAGCCACCGGTC 2183
QY 699 LeuHisPheLysAspSerTyrHisAsnLeuArgLeuSerIleHisAspValProSerSer 718
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QY 839 LysLeuHisLeuAspSerHisLeuSerPhePheAlaSerLysProSerProThrAlaMet 858
Db 2604 AAATCCACTGGACAGCATCTCAGCTTCTTTGGCTCCAAAGCCCAAGCCCCACAGCCATG 2663
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AC ADH71647;
XX
XX
XX 25-MAR-2004 (first entry)
DE Human gene of the invention NOV21t SEQ ID NO:543.
DE
KW ds; gene, human; cytostatic; immunomodulator; neuroprotective; nootropic;
KW anorectic; antidiabetic; antimicrobial; antilipemic; gene therapy;
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW obesity; diabetes; infectious disease; metabolic syndrome X;
KW dyslipidaemia.
XX
XX Homo sapiens.
XX
XX WO2003102155-A2.
XX
XX 11-DEC-2003.
XX
XX 03-JUN-2003; 2003WO-US017430.
XX
XX 03-JUN-2002; 2002US-0385120P.
XX 04-JUN-2002; 2002US-0385784P.
XX 05-JUN-2002; 2002US-0386041P.
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XX 06-JUN-2002; 2002US-0386453P.
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XX 12-JUN-2002; 2002US-0388022P.
XX 12-JUN-2002; 2002US-0388096P.
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XX 14-JUN-2002; 2002US-0389118P.
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PR 13-AUG-2002; 2002US-0406317P.
PR 15-AUG-2002; 2002US-0403617P.
PR 26-AUG-2002; 2002US-0406182P.
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PR 27-AUG-2002; 2002US-0406240P.
PR 12-SEP-2002; 2002US-0410084P.
PR 20-SEP-2002; 2002US-0412528P.
PR 23-SEP-2002; 2002US-0412731P.
PR 30-SEP-2002; 2002US-0414801P.
PR 30-SEP-2002; 2002US-0414839P.
PR 30-SEP-2002; 2002US-0414840P.
PR 30-SEP-2002; 2002US-0414954P.
PR 09-OCT-2002; 2002US-0417186P.
PR 09-OCT-2002; 2002US-0417406P.
PR 23-OCT-2002; 2002US-0420639P.
PR 28-OCT-2002; 2002US-0421156P.
PR 31-OCT-2002; 2002US-0422690P.
PR 01-NOV-2002; 2002US-0423130P.
PR 05-NOV-2002; 2002US-00423798.
PR 05-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
XX Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
XX Ettenberg S, Gangolli EA, Gerlach VU, Gorman L, Gunther E, Guo X;
XX Gusev VV, Herrmann JU, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
XX MacLachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;
XX Padigaru M, Patturajan M, Pena CEA, Peyman JA, Raha D, Rastelli L;
XX Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shinkets RA;
XX Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
XX Zhong H;
XX
XX WPI: 2004-081935/08.
XX P-PSDB; ADH71648.
XX
XX New NOVX polypeptides and nucleic acid molecules useful for preventing or
XX treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
XX obesity, and in chromosome mapping, tissue typing or pharmacogenomics.
XX
XX Example 21; SEQ ID NO 543; 1880pp; English.
XX
XX The invention relates to a novel isolated polypeptide (NOVX). A
XX polypeptide of the invention has cytostatic, immunomodulator,
XX neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
XX antilipemic activity, and may have a use in gene therapy, and as a
XX vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
XX any of the 303 fully defined nucleotide sequences given in the
XX specification. The polypeptide is useful in the manufacture of a
XX medicament for treating a syndrome associated with a human disease. The
XX polypeptide, polynucleotide and antibody are useful in diagnosing,
XX treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
XX diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
XX further used as hybridisation probes, in chromosome mapping, tissue
XX typing, preventive medicine, and pharmacogenomics. The present sequence
XX encodes a NOVX polypeptide of the invention.
XX
XX Sequence 2881 BP; 525 A; 985 C; 869 G; 502 T; 0 U; 0 Other;
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Best Local Similarity:	98.56%	Mismatches:	8
Query Match:	97.92%	Indels:	3
DB:	12	Gaps:	3

US-10-624-932C-2 (1-898) x ADH71647 (1-2881)

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Db 147 CGCGGCTCGGGTGCAGCAGAGTGCACCGTGGCCCAACCCAGTGCCTGGTGGCCAAACCG 206
Qy 41 AspLeuLeuProHisPheLeuValGluProGluAspValTyrIleValLysAenLysPro 60
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Db 267 GTGCTGTGTGTGCAAGGCGCTGCCCGCCACGCAGATCTTTCAAAGTGCACGGGGAG 326
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Db 327 TGGGTGCGCCAGGTGGACCACTGTATCGATCGAGCGCAGCACAGACGGGAGCGTGTGAGCCG 386
Qy 101 ThrMetGluValArgIleAenValSerArgGlnGlnValGluLysValPheGlyLeuGlu 120
Db 387 ACCATGAGGTTCGCATTAATGCTCAAGGCAGCAGGTTCGAGAAAGTGTTCGGGCTGGAG 446
Qy 121 GluTyrTrpCysGlnCysValAlaTrpSerSerGlyThrThrLysSerGlnLysAla 140
Db 447 GAATACTGGTGCAGTCCGTGGCATGGAGCTCTCTCGGGCACCAACAGAGTCAGAGGCC 506
Qy 141 TyrIleArgIleAlaArgLeuArgLysAenPheGluGlnGluProLeuAlaLysGluVal 160
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Qy 161 SerLeuGluGlnGlyIleValLeuProCysArgProProGluGlyIleProProAlaGlu 180
Db 567 TCCCTGGAGCAGGCGATCTGTGCTGCCCTGCCGTCACCGAGGCGATCCCTCCAGCCGAG 626
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Qy 241 ValAenGlyGlyTrpSerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArg 260
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Db 1644 CTCTATCCCCCAGATGCCATACCCCGAGGGAAGATCTATGAGATCTACCTCAGCTGCAC 1703
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Db 1704 AAGCCGGAAGACGTGAGTGTGGCTTAGCTGGCTGTGAGACCTGTGAGTCCCATCGTT 1763
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Db 1764 AGTGTGGACCCCTCGCGTCTGTGCTCACCCGGCCAGTCTATCTGGCTATGGACCACTGT 1823
Qy 580 GlyGluProSerProAspSerTrpSerLeuArgLeuLysLysGlnSerCysGluGlySer 599
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Db 1884 TGGGAGCAGATGTGTGCACCTGGGCGAGGAGGCGCCCTCCACCTCTACTACTGTCAG 1943
Qy 619 LeuGluAlaSerAlaCysTyrValPheThrGluGlnLeuGlyArgPheAlaLeuValGly 638
Db 1944 CTGGAGGCGAGTGCCTGTGCTACGCTTTCACCGAGCAGCTGGGGCGCTTGTGCCCTGGTGGGA 2003
Qy 639 GluAlaLeuSerValAlaAlaLysArgLeuLysLeuLeuPheAlaProValAla 658
Db 2004 GAGGCCCTCAGGTGGCTGGCCCAAGCGCTCAGCTGCTTCTGTGTTGGCCCGGTGGCC 2063
Qy 659 CysThrSerLeuGluTyrAenIleArgValTyrCysLeuHisAenThrHisAenAlaLeu 678
Db 2064 TGCACCTCTCGAGTACAACATCCGGTCTACTGCTGTGCATGCACCCACGATGCACCTC 2123
Qy 679 LysGluValValGlnLeuGluLysGlnLeuGlyGlnLeuIleGlnLeuProArgVal 698
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Job time : 1765 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

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3029.642 Million cell updates/sec

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Searched: 1202784 seqs, 818138359 residues

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Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Match Length DB ID	Description
1	4638	96.8 3014 2	US-08-808-982-1
2	4638	96.8 3014 3	US-09-306-902A-1
3	2710	56.6 1787 2	US-08-808-982-2
4	2710	56.6 1787 3	US-08-808-982-2
5	2544.5	53.1 2831 2	US-09-306-902A-2
6	2544.5	53.1 2831 3	US-08-808-982-3
7	2337.5	48.8 3008 4	US-09-306-902A-3
8	1895	39.6 2661 4	US-09-949-016-4794
9	1886.5	39.4 2694 4	US-09-969-532-15
10	1878	39.2 2703 4	US-09-969-532-13
11	1869.5	39.0 2736 4	US-09-969-532-9
12	1869.5	39.0 3411 4	US-09-969-532-33

13	1259.5	26.3	1968	4	US-09-969-532-31	Sequence 31, Appl
14	1251	26.1	2001	4	US-09-969-532-29	Sequence 29, Appl
15	1242.5	25.9	2010	4	US-09-969-532-27	Sequence 27, Appl
16	1234	25.8	2043	4	US-09-969-532-25	Sequence 25, Appl
17	1124	23.5	1659	4	US-09-969-532-7	Sequence 7, Appl
18	1115.5	23.3	1692	4	US-09-969-532-5	Sequence 5, Appl
19	1107	23.1	1701	4	US-09-969-532-3	Sequence 3, Appl
20	1098.5	22.9	1734	4	US-09-969-532-1	Sequence 1, Appl
c 21 611 12.8 771 1						
22	578	12.1	349	4	US-08-253-155A-17	Sequence 17, Appl
c 23 525.5 11.0 19326 4						
24	488.5	10.2	966	4	US-09-471-276-345	Sequence 345, App
25	480	10.0	999	4	US-09-949-016-16776	Sequence 16776, A
26	471.5	9.8	1008	4	US-09-969-532-23	Sequence 23, Appl
27	463	9.7	1041	4	US-09-969-532-21	Sequence 21, Appl
28	307	6.4	5784	4	US-09-969-532-19	Sequence 19, Appl
29	290	6.1	114139	4	US-09-969-532-17	Sequence 17, Appl
30	288.5	6.0	4074	4	US-09-949-016-462	Sequence 462, App
31	280	5.8	2820	4	US-09-949-016-16536	Sequence 16536, A
32	280	5.8	3105	4	US-09-854-845-1	Sequence 17, Appl
33	280	5.8	3237	4	US-09-854-845-15	Sequence 15, Appl
34	280	5.8	3237	4	US-09-854-845-5	Sequence 5, Appl
35	279	5.8	3411	4	US-09-854-845-7	Sequence 7, Appl
36	279	5.8	3150	4	US-09-854-845-11	Sequence 11, Appl
37	279	5.8	3282	4	US-09-854-845-13	Sequence 13, Appl
38	279	5.8	3456	4	US-09-854-845-1	Sequence 1, Appl
39	275	5.7	5749	4	US-09-854-845-9	Sequence 9, Appl
40	272.5	5.7	5722	4	US-09-854-845-3	Sequence 3, Appl
41	272.5	5.7	7231	4	US-09-262-537-48	Sequence 48, Appl
42	253	5.3	305	2	US-09-657-472-1	Sequence 1, Appl
43	253	5.3	305	3	US-09-919-172-64	Sequence 64, Appl
44	252.5	5.3	1326	3	US-08-808-982-4	Sequence 4, Appl
c 45 249 5.2 2006 4						
US-08-985-526-4						
US-09-270-767-15258						

ALIGNMENTS

RESULT 1
US-08-808-982-1
; Sequence 1, Application US/08808982
; Patent No. 5939271
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; APPLICANT: Leonardo, E. David
; APPLICANT: Hink, Lindsey
; APPLICANT: Masu, Masayuki
; APPLICANT: Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/808,982
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 3014 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-808-982-1

Alignment Scores:

Pred. No.: 0 Length: 3014
Score: 4638.00 Matches: 862
Percent Similarity: 97.88% Conservativeness: 17
Best Local Similarity: 95.99% Mismatches: 19
Query Match: 96.81% Indels: 0
DB: 2 Gaps: 0

US-10-624-932C-2 (1-898) x US-08-808-982-1 (1-3014)

Qy	1	MetAlaValArgProGlyLeuTyrProAlaLeuLeuGlyLeuValLeuAlaTyrLeu	20
Db	1	ATGGCCGTCCGGCCCGGCGCTGTGGCCAGTGTCTCTGGGCATAGTCTCGCCGCTGGCTT	60
Qy	21	ArgGlySerGlyAlaGlnSerAlaThrValAlaAsnProValProGlyAlaAlaAsnPro	40
Db	61	CGTGGTTCCGGTCCCGCAGCAGAGTGCCACGGTGGCCCAATCCAGTGCCTGGTGCACACCC	120
Qy	41	AspLeuLeuProHisPheLeuValGluProGluAspValTyrIleValIysAsnLysPro	60
Db	121	GACCTGTGCTCCCTCTCTGGTAGAGCTGTGGCCAGTGTACATTGTCAAGTGCATATGGGAA	180
Qy	61	ValLeuLeuValCysIysAlaValProAlaThrGlnIlePhePheLysCysAsnGlyGlu	80
Db	181	GTGTGTGTGTGTGCAAGGTGTGCTGTGCCACCCAGATCTTCTCAAGTGCATATGGGAA	240
Qy	81	TyrValArgGlnValAspHisValIleGluArgSerThrAspGlySerSerGlyLeuPro	100
Db	241	TGGGTCCGCGAGTTCGATACGTAATTTGAACGACGACGCCACGACGAGCGATGGCCA	300
Qy	101	ThrMetGluValArgIleAsnValSerArgGlnGlnValGluLysValPheGlyLeuGlu	120
Db	301	ACCATGAGGTCCGTATCAACGTATCGAGGACGAGTAGAGAAAGTGTGTGGCTGGAG	360
Qy	121	GluTyrTrpCysGlnCysValAlaTyrSerSerGlyThrThrLysSerGlnLysAla	140
Db	361	GAATACTGGTGCCAGTGTGGCATGAGTCTCTCGGTACCAACCAAAAGTCAGAAAGGCC	420
Qy	141	TyrIleArgIleAlaArgLeuArgLysAsnPheGluGlnGluProLeuAlaLysGluVal	160
Db	421	TACATCCGGATTGCTATTTGGCAAGAACTTTGAGCAGGAGCCACTGGCCRAAGGAGTG	480
Qy	161	SerLeuIleGlnGlyIleValLeuProCysArgProProGluGlyIleProProAlaGlu	180
Db	481	TCAGTGGAGCAGGCAATGTACTACTTGTTCGCCCCCAGAGGAATCCCCCGAGCTGAG	540
Qy	181	ValGluTrpLeuArgAsnGluAspLeuValAspProSerLeuAspProAsnValTyrIle	200
Db	541	GTGGAGTGGCTTCCGAATAGGACCTCGTGGACCCCTCTCCATCCCAATGTGTATC	600
Qy	201	ThrArgGluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThr	220
Db	601	ACGGGGAGCACACCTAGTGTGCGGTGAGTCCAGCCCGCTGGCCGACACGCGCAACTACAC	660
Qy	221	CysValAlaLysAsnIleValAlaArgArgArgSerAlaSerAlaValIleValTyr	240
Db	661	TGTGTGGCCAAAGCACTCGTAGCCGCTGGCCGAGCACCTCTCTGAGCGGTCAATGTTAT	720
Qy	241	ValAsnGlyIlyTrpSerThrThrThrGluTrpSerValCysSerAlaSerCysGlyArg	260
Db	721	GTGAACGTGGGTGGTGCAGTGCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	780
Qy	261	GlyTrpGlnLysArgSerArgSerCysThrAsnProAlaProLeuAsnGlyIlyAlaPhe	280
Db	781	GGCTGGCAGAAACGGAGCCGGAGCTGCACCAACCCCGGACCTCTCAACGGGGCGCTTC	840

Qy	281	CysGluGlyGlnAsnValGlnLysThrAlaCysAlaThrLeuLeuCysProValAspGlySer	300
Db	841	TGTGAGGGGCAGAAATGCCAGAAAAACAGCTTCGCCCACTCTGTGCCAGTGGATGGGAGC	900
Qy	301	TrpSerProTrpSerLysTrpSerAlaCysGlyLeuAspCysThrHisTrpArgSerArg	320
Db	901	TGGAGTTCGTGGAGTAAGTGGTGCAGCTGTGGCTTGTGACACCCACCTGGCGGAGCCGC	960
Qy	321	GluCysSerAspProAlaProArgAsnGlyGlyGluGluCysGlnGlyThrAspLeuAsp	340
Db	961	GAGTGTCTGTAGCCAGCACCCCGCAATGGAGTGGAGTGTGGGGTGTGACCTGGAC	1020
Qy	341	ThrArgAsnCysThrSerAspLeuCysValHisSerAlaSerGlyProGluAspValAla	360
Db	1021	ACCGCAACTGTACAGTACCTCTGCTGTCACACCGCTTCTTGGCCCCGAGGACGTGGCT	1080
Qy	361	LeuTyrValGlyLeuIleAlaValAlaValCysLeuValLeuLeuLeuValLeuIle	380
Db	1081	CTCTACATCGGCTTGTGCTGTGGCTGTGGCTTCTTCTTGTGTGTGTGGCCCTTGGG	1140
Qy	381	LeuValTyrCysArgLysLysGlyLeuAspSerAspValAlaAspSerSerIleLeu	400
Db	1141	CTCATTTACTGTGCAAGAAAGAGGCTGGACTCGGATGTGGCGCACTCGTCCATCTC	1200
Qy	401	ThrSerGlyPheGlnProValSerIleLysProSerLysAlaAspAsnProHisLeuLeu	420
Db	1201	ACCTCGGGCTTCAGCCTGTGACATCAAGCCAGCAACAGCAGCAACCCCACTGCTC	1260
Qy	421	ThrIleGlnProAspLeuSerThrThrThrThrThrThrThrThrThrThrThrThr	440
Db	1261	ACATCCAGCCAGACCTCAGCACCACTACCACTACCACTACCACTACCACTACCACTAC	1320
Qy	441	GlnAspGlyProSerProLysPheGlnLeuThrAsnGlyHisLeuLeuSerProLeuGly	460
Db	1321	CAGGATGGACCCAGCCCAAGTTCAGCTCTCTAATGGTCACTGCTCAGCCCACTGGGG	1380
Qy	461	GlyGlyArgHisThrLeuHisHisSerSerProThrSerGluAlaGluLysPheValSer	480
Db	1381	AGTGGCGCCACATACGTTGCACACAGCTCACCACTCTGAGGCTGAGGACTTCGTCTCC	1440
Qy	481	ArgLeuSerThrGlnAsnTyrPheArgSerLeuProArgGlyThrSerAsnMetThrTyr	500
Db	1441	CGCTCTCCACCCCAAACTACTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	1500
Qy	501	GlyThrPheAsnPheLeuGlyArgLeuMetIleProAsnThrGlyIleSerLeuLeu	520
Db	1501	GGGACCTTCAACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	1560
Qy	521	IleProProAspAlaIleProArgGlyLysIleTyrGluIleTyrLeuThrLeuHisLys	540
Db	1561	ATACCCCGGATGCCATCCCGAGAAAGATCTACGAGATCTACCTACACTGCACAAG	1620
Qy	541	ProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeuLeuSerProIleValSer	560
Db	1621	CCAGAGAGCTGAGGTTGGCCCTAGCTGCTGTGAGCCCTGCTGAGTCCAGTCTGTAGC	1680
Qy	561	CysGlyProProGlyValLeuLeuThrArgProValIleLeuAlaMetAspHisCysGly	580
Db	1681	TGTGGGCCCCAGGAGTCTGCTCACCCGGCCAGTCACTCTTGCATGGACCACTGCTGGA	1740
Qy	581	GluProSerProAspSerTrpSerLeuArgLeuLysLysGlnSerCysGluGlySerTrp	600
Db	1741	GAGCCAGCCCTGACAGCTGGAGTGTGCGCTCAAAAAGAGTCTTCGCGGAGGAGTTGG	1800
Qy	601	GluAspValLeuHisLeuGlyGluAlaAlaProSerHisLeuTyrTyrCysGlnLeuGlu	620
Db	1801	GAGGATGTCTGCACCTTGTGGTGGAGTCACTTCTCCACCTCTACTACTGCGAGTGGAG	1860
Qy	621	AlaSerAlaCysTyrValPheThrGluGlnLeuGlyArgPheAlaLeuValGlyGluAla	640
Db	1861	GGCGGGGCGCTGTATGTCTTTCAGGAGCAGCTGGGCGCTTTTGGCTGTGGAGAGGCC	1920

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Qy 641 LeuSerValAlaAlaLysArgLeuLysLeuLeuPheAlaProValAlaCysThr 660
Db 1921 CTACGCTGGCTGCCACCAAGCGCTCAGGCTCTCTGTTGCTCCGTCGCTGACG 1980
Qy 661 SerLeuGluTyrAsnIleArgValTyrCysLeuHisAspThrHisAspAlaLeuLysGlu 680
Db 1981 TCCCTTGAGTACAACATCCGAGTGTACTGCTCACCACACCCACGAGCTCTCAAGGAG 2040
Qy 681 ValValGlnLeuGluLysGlnLeuGlyGlnLeuLysGlnLeuPheArgValLeuHis 700
Db 2041 GTGGTGCAGCTGGAGAGCAGTACGTGGAAGCTGATCAGAGAGCTTCGGTCTCTGCAC 2100
Qy 701 PheLysAspSerTyrHisAsnLeuArgLeuSerIleHisAspValProSerSerLeuTyr 720
Db 2101 TTCAAGACAGATTACCAACAACCTACGTCTCTCCATCCAGAGCTGCCAGCTCCCTCTGG 2160
Qy 721 LysSerLysLeuLeuValSerTyrGlnGluIleProPheTyrHisIleTyrAsnGlyThr 740
Db 2161 AAGAGCAAGCTACTTGTACAGTACCAAGAGATCCCTTTTACCAATCTCTGGAACGGCACC 2220
Qy 741 GlnArgTyrLeuHisCysThrPheThrLeuGluArgValSerProSerThrSerAspLeu 760
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Qy 761 AlaCysLysLeuTyrValTyrGlnValGluGlyAspGlyGlnSerPheSerIleAsnPhe 780
Db 2281 GCCTGCAAGCTGGGTGTGGCAGTGGAGAGATGGGAGAGCTTCAACATCAACTTC 2340
Qy 781 AsnIleThrLysAspThrArgPheAlaGluLeuLeuAlaLeuGluSerGluAlaGlyVal 800
Db 2341 AACATCACTAAGGACACAAAGCTTGTGTAATTTGTGGCTCTGGAGAGTGAAGGGGGGCTC 2400
Qy 801 ProAlaLeuValGlyProSerAlaPheLysIleProPheLeuIleArgGlnLysIleIle 820
Db 2401 CCAGCCTGTGTGGCCCGCAGTGCCTTCAGATCCCTTCCTCATTCGCGCAAGATCATC 2460
Qy 821 SerSerLeuAspProProCysArgArgGlyAlaAspTyrArgThrLeuAlaGlnLysLeu 840
Db 2461 GCCAGTCTGACCCACACCTGCAGCGGGGGCGGAGCTGGAGAACTCTAGCCCAAGAACTT 2520
Qy 841 HisLeuAspSerHisLeuSerPhePheAlaSerLysProSerProThrAlaMetIleLeu 860
Db 2521 CACTGACAGCACTATCTAGCTCTTTGCTTCAAGCCCAAGCCCTACAGCCATGATCCTC 2580
Qy 861 AsnLeuTyrGluAlaArgHisPheProAsnGlyAsnLeuSerGlnLeuAlaAlaVal 880
Db 2581 AACCTATGGAGGACGAGCACTTCCCAAGCGCAACCTCGCCAGCTGGCAGCAGCTGTG 2640
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Db 2641 GCCGGACTGGGCCAACAGATGCTGGCTCTTCAAGGCTGGAGGGCCGAGTGT 2694
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RESULT 2

US-09-306-902A-1

; Sequence 1, Application US/09306902A

; Patent No. 6277585

; GENERAL INFORMATION:

; APPLICANT: Tessier-Lavigne, Marc

; Leonardo, E. David

; Hink, Lindsey

; Masu, Masayuki

; Kazuko, Keino-Masu

; TITLE OF INVENTION: Netrin Receptors

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

; STREET: 268 BUSH STREET, SUITE 3200

; CITY: SAN FRANCISCO

; STATE: CALIFORNIA

; COUNTRY: USA

; ZIP: 94104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

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;
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US/09/306,902A

FILING DATE: 07-May-1999

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: OSMAN, RICHARD A

REGISTRATION NUMBER: 36,627

REFERENCE/DOCKET NUMBER: UC96-217

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 343-4341

TELEFAX: (415) 343-4342

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 3014 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-306-902A-1

Alignment Scores:

Pred. No.:	0	Length:	3014
Score:	4638.00	Matches:	862
Percent Similarity:	97.88%	Conservative:	17
Best Local Similarity:	95.99%	Mismatches:	19
Query Match:	96.81%	Indels:	0
DB:	3	Gaps:	0

US-10-624-932C-2 (1-898) x US-09-306-902A-1 (1-3014)

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Qy 21 ArgGlySerGlyValGlnGlnSerAlaThrValAlaAsnProValProGlyAlaAsnPro 40
Db 61 CGTGGTTCGGGTGCCAGCAGAGTGCCTGGTGGCAATCCAGTGGCGCTGCGCAACCCC 120
Qy 41 AspLeuLeuProHisPheLeuValGluProGluAspValTyrIleValLysAsnLysPro 60
Db 121 GACCTCTGCCCCACTCTCTGGTAGAGCTGTAGAGCTGTACATTGTCAAGAACAGCCG 180
Qy 61 ValLeuLeuValCysLysAlaValProAlaThrGlnIlePhePheLysCysAsnGlyGlu 80
Db 181 GTGTTCTTGGTGTGCAAGCTGTGCTGCCACCCAGATCTTCTTCAAGTGCATGGGAA 240
Qy 81 TrpValArgGlnValAspHisValIleGluArgSerThrAspGlySerSerGlyLeuPro 100
Db 241 TGGTTCGCGCAGGTGCGATCAGCTAATTTGAACGCGACGACGAGCAGCGGATTTGCCA 300
Qy 101 ThrMetGluValArgIleAsnValSerArgGlnGlnValGlnLysValPheGlyLeuGlu 120
Db 301 ACCATGGAGGTCCGTATCAACGTATCGAGCAGCAGCAGTAGAGAAAGTGTGTTGGCTGGAG 360
Qy 121 GluTyrTyrCysGlnCysValAlaTyrPheSerSerGlyThrThrLysSerGlnLysAla 140
Db 361 GAATACCTGGTGGCAGTGTGTGGCATGGAGCTCTCTCGGGTACCAACCAAAAGTCAGAGGCC 420
Qy 141 TyrIleArgIleAlaArgLeuArgLysAsnPheGluGlnGlnProLeuAlaLysGluVal 160
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Qy 161 SerLeuGluGlnGlyIleValLeuProCysArgProProGluGlyIleProProAlaGlu 180
Db 481 TCACTGGAGCAGGCAATTTACTACTTGTCCGCCCCCAGAGAGGATCCCCCAGCTGAG 540
Qy 181 ValGluTyrLeuArgAsnGluAspLeuValAspProSerLeuAspProLeuValTyrIle 200
Db 541 GTGGAGTGGCTTCGAAATGAGGACCTCGTGGAGCCCCCTCCCTCGATCCCAATGTGTACATC 600
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QY 201 ThrArgGluHisSerLeuValValArgGlnAlaAArgLeuAlaAspThrAlaIenTyrThr 220
Db 601 AC CGGGAGCACAGCCTAGTCGTGCGTCAAGCCCGCTGCGCCACACGCCCACTACACC 660
QY 221 CysValAlaLysAsnIleValAlaAArgArgSerAlaSerAlaAlaValIleValTyr 240
Db 661 TGTGTGGCCAGAACATCGTAGCCCGTGGCCGAAGCACCTCTGCAGCGGTCAATGTGTTAT 720
QY 241 ValAsnGlyGlyTrpSerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArg 260
Db 721 GTGAACGGTGGGTGGTGGAGTGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 780
QY 261 GlyTrpGlnLysArgSerArgSerCysThrAsnProAlaProLeuAsnGlyAlaAlaPhe 280
Db 781 GGCTGGCAGAAACCGAGCGGAGCTGCACCAACCGGCACCTCTCAACGGGGCGCTTC 840
QY 281 CysGluGlyGlnAsnValGlnLysThrAlaCysAlaThrLeuCysProValAspGlySer 300
Db 841 TGTAGGGGCGAGNATGTCCAGAAAAAGCCTTGGCCCACTGTGGCCCACTGTGGATGGAGC 900
QY 301 TrpSerProTrpSerLysTrpSerAlaCysGlyLeuAspCysThrHisTrpArgSerArg 320
Db 901 TGGAGTTCTGTGGAGTAAAGTGTGAGCTGTGGCTTGTGACTGCACCCACTGGCGGAGCCGC 960
QY 321 GluCysSerAspProAlaProArgAsnGlyGlyGluGlyCysGlnGlyThrAspLeuAsp 340
Db 961 GAGTGTCTGTGACCCAGCACCGCCCAATGAGAGTGGAGAGTGTGGGGTGTGACTGGAC 1020
QY 341 ThrArgAsnCysThrSerAspLeuCysValHisSerAlaSerGlyProGluAspValAla 360
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QY 361 LeuTyrValGlyLeuIleAlaValAlaValCysLeuValLeuLeuLeuValLeuIle 380
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QY 381 LeuValTyrCysArgLysLysGluGlyLeuAspSerAspValAlaAspSerSerIleLeu 400
Db 1141 CTCATTACTGTGCGCAAGAGGAAGGGCTGGACTCCGATGTGGCCGACTCGTCCATCCTC 1200
QY 401 ThrSerGlyPheGlnProValSerIleLysProSerLysAlaAspAsnProHisLeuLeu 420
Db 1201 ACCTCGGGCTTCAGCTGTGAGCATCAAGCCAGCAAGCAGACAAACCCACCTGCTC 1260
QY 421 ThrIleGlnProAspLeuSerThrThrThrThrThrThrThrThrThrThrThrThrThr 440
Db 1261 ACCATCCAGCCAGACCTCAGCACCACTACCACTACCACTACCACTACCACTACCACTAC 1320
QY 441 GlnAspGlyProSerProLysPheGlnLeuThrAsnGlyHisLeuLeuSerProLeuGly 460
Db 1321 CAGGATGGACCCAGCCCAAGTTCAGCTCTCTAATGGTCACTGTGCTCAGCCCACTGGGG 1380
QY 461 GlyGlyArgHisThrLeuHisSerSerProThrSerGluAlaGluPheValSer 480
Db 1381 AGTGGCGGCATACGTTGACCAACACCTCACCCACCTCTGAGGCTGAGGACTTGTCTCC 1440
QY 481 ArgLeuSerThrGlnAsnTyrPheArgSerLeuProArgGlyThrSerAsnMetThrTyr 500
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Db 1501 GGGACCTTCAACTTCTCGGGGGCCGGCTGTAGTATCCCTAATACGGGATCAGCTCCTC 1560
QY 521 IleProAspAlaIleProArgGlyLysIleTyrGluIleTyrLeuThrLeuHisLys 540
Db 1561 ATACCCCGGATGCCATCCCGGAGGAAGATCTACAGATCTACCTCACACTGCACAG 1620
QY 541 ProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeuLeuSerProIleValSer 560
Db 1621 CCAGAAAGCGTGAAGTTGGCCCTAGCTGGCTGTGCAGACCTGTGTAGTCCAGTCCGTAGC 1680
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QY 561 CysGlyProProGlyValLeuLeuThrArgProValIleLeuAlaMetAspHisCysGly 580
Db 1681 TGTGGGCCCCAGAGAGTCTCTGCTCACCCGCCAGTCACTCTTGCATAGCACCTGTGA 1740
QY 581 GluProSerProAspSerTrpSerLeuArgLeuLysLysLysSerCysGluGlySerTrp 600
Db 1741 GAGCCCGAGCCCTGCAGCTGGAGTCTGCGCCTCAAAAGCAGTCTCTGCGAGGCGAGTTGG 1800
QY 601 GluAspValLeuHisLeuGlyGluAlaProSerHisLeuTyrTyrCysGlnLeuGlu 620
Db 1801 GAGGATGTCTGCACCTTGTGAGGAGTCACTCTCCACCTCTACTACTGCCAGCTGGAG 1860
QY 621 AlaSerAlaCysTyrValPheThrGlnGlnLeuGlyArgPheAlaLeuValGlyGluAla 640
Db 1861 GCCGGGGCTGTATGTCTTTCAGGAGCAGCTGGGCGCTTGTGCCCTGTGTGAGAGGGCC 1920
QY 641 LeuSerValAlaAlaAlaLysArgLeuLysLeuLeuLeuPheAlaProValAlaCysThr 660
Db 1921 CTCAGGCTGGCTGCCACCAAGCGCTCAGGCTCTCTTGTGCTCCCGTGGCTGTAGC 1980
QY 661 SerLeuGluTyrAsnIleArgValTyrCysLeuHisAspThrHisAspAlaLeuLysGlu 680
Db 1981 TCCCTTGTAGTACAACATCCAGTGTACTGCTTACAGCACACCCAGCAGCTCTCAAGGAG 2040
QY 681 ValValGlnLeuLysGlnLeuGlyGlnLeuIleGlnGluProArgValLeuHis 700
Db 2041 GTGGTGCAGCTGGAGAGCAGCTAGTGTGACAGCTGATCCAGGAGCTCGCTCTGCAC 2100
QY 701 PheLysAspSerTyrHisAsnLeuArgLeuSerIleHisAspValProSerSerLeuTrp 720
Db 2101 TTCAAAGACAGTTACCAACAACCTAGCTCTCTCCATCCACAGAGTCCCGAGCTCCCTGTGG 2160
QY 721 LysSerLysLeuLeuValSerTyrGlnGluIleProPheTyrHisIleTrpAsnGlyThr 740
Db 2161 AAGAGCAAGCTACTTGTGAGTACCAAGAGATCCCTTTTACACATCTGGAACGCGCAC 2220
QY 741 GlnArgTyrLeuHisCysThrPheThrLeuGluArgValSerProSerThrSerAspLeu 760
Db 2221 CAGCAGTATCTGCATCTGCACCTTCCCTTGGAGCGCATCAACGCCAGCACCGACCTG 2280
QY 761 AlaCysLysLeuTrpValTrpGlnValGluGlyAspGlyGlnSerPheSerIleAsnPhe 780
Db 2281 GCCTGCAAGGTGTGGGTGTGGCAGGTGGAGGGAGATGGGCAGAGCTTCAACATCACTTC 2340
QY 781 AsnIleThrLysAspThrArgPheAlaGluLeuLeuAlaLeuGluSerGluAlaGlyVal 800
Db 2341 AACATCACTAAGGACACAAAGGTTTGTGAATTTGTTGGCTCTGGAGAGTGAAGGGGGTCTC 2400
QY 801 ProAlaLeuValGlyProSerAlaPheLysIleProPheLeuIleArgGlnLysIleIle 820
Db 2401 CCAGCCCTTGTGGGCCCCAGTGCCTTCAAGATCCCTTCTCATTCGGCAAAAGATCATC 2460
QY 821 SerSerLeuAspProProCysArgArgGlyAlaAspTrpArgThrLeuAlaGlnLysLeu 840
Db 2461 GCCAGTCTGGACCCACCTGACCGCGGGCGCGAGTGGAGAACTCTAGCCAGAACTT 2520
QY 841 HisLeuAspSerHisLeuSerPheAlaSerLysProSerProThrAlaMetIleLeu 860
Db 2521 CACCTGGACAGCACTCTTAGCTTCTTTGCTTCAAGCCCGAGCCCTACAGCCATGATCCTC 2580
QY 861 AsnLeuTrpGluAlaArgHisPheProAsnGlyAsnLeuSerGlnLeuAlaAlaVal 880
Db 2581 AACCTATGGAGGACGAGCACTTCCCAACGCAACCTCGGCCAGCTGCGCAGCAGCTGTG 2640
QY 881 AlaGlyLeuGlyGlnProAspAlaGlyLeuPheThrValSerGluAlaGluCys 898
Db 2641 GCCGAGCTGGGCCAACAGATGCTGCGCTCTTTCAGGTGTGCGAGGCGCGAGTGT 2694
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RESULT 3

US-08-808-982-2

; Sequence 2, Application US/0808982

; Patent No. 5939271

; GENERAL INFORMATION:

APPLICANT: Tessier-Lavigne, Marc
 APPLICANT: Leonardo, E. David
 APPLICANT: Hink, Lindsay
 APPLICANT: Masu, Masayuki
 APPLICANT: Kazuko, Keino-Masu
 TITLE OF INVENTION: Netrin Receptors
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
 STREET: 268 BUSH STREET, SUITE 3200
 CITY: SAN FRANCISCO
 STATE: CALIFORNIA
 COUNTRY: USA
 ZIP: 94104
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/808,982
 FILING DATE:
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: OSMAN, RICHARD A
 REGISTRATION NUMBER: 36,627
 REFERENCE/DOCKET NUMBER: UC96-217
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 343-4341
 TELEFAX: (415) 343-4342
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1787 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: CDNA
 US-08-808-982-2


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Qy 722 rLysLeuLeuValSerTyrGlnGluIleProPheTyrHisIleTrpAsnGlyThrGlnAr 742
Db 1137 TAAGCTCTCTGTCAGCTACAGGAGATCCCTTTTATCACAATCGAATGCGACGCG 1196
Qy 742 gTyrLeuHisCysThrPheThrLeuGluArgValSerProSerThrSerAspLeuAlaCy 762
Db 1197 GTACTTGACCTGCACCTTACCTCGAGCGGTGTGAGCCCGACGACCTAGTGACCTGGCGCTG 1256
Qy 762 sLysLeuTrpValTrpGlnValGluGlyAspGlyGlnSerPheSerIleLeuAsnIle 782
Db 1257 CAACTGTGGGTGTGGCGAGGTGGAGGGCGCGACGAGCTTTCAGCATCAACTTCAACAT 1316
Qy 782 eThrLysAspThrArgPheAlaGluLeuLeuAlaLeuGluSerGluAlaGlyValProAl 802
Db 1317 CACCAAGGACACAAGGTTTGTGAGCTGTGGCTCTGGAGAGTGAAGGGGGTCCCGAGC 1376
Qy 802 aLeuValGlyProSerAlaPheLysIleProPheLeuIleArgGlnLysIleSerSe 822
Db 1377 CCTGGTGGGCCCGGAGTCCCTTCAAGATCCCTTCTCATTTGGCGAGAAGATAAATTTCCAG 1436
Qy 822 rLeuAspProProCysArgArgGlyAlaAspTrpArgThrLeuAlaGlnLysLeuHisLe 842
Db 1437 CCTGAGACCCACCTGTAGCGGGGTGGCGACTGGCGGACTCTGGCCCCAGAACTCCACCT 1496
Qy 842 uAspSerHisLeuSerPhePheAlaSerLysProSerProThrAlaMetIleLeuAsnLe 862
Db 1497 GGACAGCCATCTCAGCTTCTTTGGCTCCAGGCCCGAGCCCGACAGCCATGATCTCAACCT 1556
Qy 862 uTrpGluAlaArgHisPheProAsnGlyAsnLeuSerGlnLeuAlaAlaValAlaGl 882
Db 1557 GTGGAGCGCGGCACTTCCCAACGGCAACCTCAGCGAGCTGGCTCGAGCAGTGGGTGG 1616
Qy 882 yLeuGlyGlnProAspAlaGlyLeu-PheThrVal-SerGluAlaGluCys 898
Db 1617 GACTGGCCAGCAGGCGGTGCTTCTTTCACAGTGTTCGGAGGTGAGTGC 1667
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RESULT 5

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US-08-982-3
; Sequence 3, Application US/0808982
; Patent No. 5939271
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; APPLICANT: Leonardo, E. David
; APPLICANT: Hink, Lindsey
; APPLICANT: Masu, Masayuki
; APPLICANT: Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/808,982
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
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; LENGTH: 2831 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-08-808-982-3
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Alignment Scores:

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Pred. No.: 1,46e-226 Length: 2831
Score: 2544.50 Matches: 503
Percent Similarity: 68.18% Conservative: 142
Best Local Similarity: 53.17% Mismatches: 222
Query Match: 53.11% Indels: 80
DB: 2 Gaps: 16

US-10-624-932C-2 (1-898) x US-08-808-982-3 (1-2831)
Qy 9 ProAlaLeuLeuGlyIleValLeuAlaAlaTrpLeuArgGlySerGlyAlaGlnGlnSer 28
Db 61 CCAGCTTTAGCAGGCATT-----GACTCTGTGTCAG----- 93
Qy 29 AlaThrValAlaAsnProValProGlyAlaAsnProAspLeuLeuProHisPheLeuVal 48
Db 94 ---GGACTCCCACTCTCTCCCATCAGCACCCCGGAGCAGCTGCCTCACTTCTCTGCTG 150
Qy 49 GluProGluAspValTyrIleValLysAsnLysProValLeuLeuValCysLysAlaVal 68
Db 151 GAACAGAGGATCGCTACATCGTAAGAACACAGCCAGTGAATGCACTGCCGAGCCCTTC 210
Qy 69 ProAlaThrGlnIlePhePheLysCysAsnGlyGluTrpValArgGlnValAspHisVal 88
Db 211 CCTGCCACACAGATCTACTTCAAGTGTAAATGGCGAGTGGGTAGCCAGAAAGGCCACGTC 270
Qy 89 IleGluArgSerThrAspGlySerSerGlyLeuProThrMetGluValArgIleAsnVal 108
Db 271 ACAGAGAGAGCCTGGATGAGGCCACAGAGCTTGCATAACAGAGAGGTGCAGATAGAGGTG 330
Qy 109 SerArgGlnGlnValGluLysValPheGlyLeuGluGluTyrTrpCysGlnCysValAla 128
Db 331 TCAGCGGAGCAGGTGGAGGAACCTTTTGGCTCAGGAGTACTGGTGTAGTGGTGGCC 390
Qy 129 TrpSerSerSerGlyThrThrLysSerGlnLysAlaTyrIleArgIleAlaArgLeuArg 148
Db 391 TGGAGCTCTTCGGGAAACCAAGAGTCCGCGAGCTTACATCCGCTTACTTCTGCTTGGCG 450
Qy 149 LysAsnPheGluGlnGluProLeuAlaLysGluValSerLeuGluGlnGlyIleValLeu 168
Db 451 AAGAACTTTGACCAGGAGCCTCTGGCGAAGAGGTACCCCTTGGATCATGAGGTCTTCTGT 510
Qy 169 ProCysArgProProGluGlyIleProProAlaGluValGluTrpLeuArgAsnGluAsp 188
Db 511 CAGTGGCGCCACAGAGGAGTGGCTGTGGCTGAGGTGAATGGCTCAGAAATGAAGAT 570
Qy 189 LeuValAspProSerLeuAspProAsnValTyrIleThrArgGluHisSerLeuValVal 208
Db 571 GTCATGATCCCGCTCAGGACACTAATCTCTGCTCACCATTGACACACACCTCATCATC 630
Qy 209 ArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysValAlaLysAsnIleValAla 228
Db 631 CGCCAGGCGCGCTCTCAGACACAGCCCACTACACCTGTGTGGCAAGAAATATTGTGGCC 690
Qy 229 ArgArgSerAlaSerAlaAlaValIleValTyrValAsnGlyGlyTyrSerThrTrp 248
Db 691 AAGCGCGGAGACAGCGCCACAGTCATCGTCTATGTGAACGAGAGGTGGTCAGCTGG 750
Qy 249 ThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArgSerArgSer 268
Db 751 GCAGATGCTCACCCTGCTCTAACCCCTGCGGCGAGGTGGCAGAAACCTACTAGGACC 810
Qy 269 CysThrAsnProAlaProLeuAsnGlyIleValPheCysGluGlyGlnAsnValGlnLys 288
Db 811 TGCACCAACCCAGCCCCCACTCAATGAGGTGCTTCTTGCAGGGGACAGGGCTTGCAGAG 870
```


TITLE OF INVENTION: Netrin Receptors
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
 STREET: 268 BUSH STREET, SUITE 3200
 CITY: SAN FRANCISCO
 STATE: CALIFORNIA
 COUNTRY: USA
 ZIP: 94104
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/306,902A
 FILING DATE: 07-May-1999
 CLASSIFICATION: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: OSMAN, RICHARD A.
 REGISTRATION NUMBER: 36,627
 REFERENCE/DOCKET NUMBER: UC96-217
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 343-4341
 TELEFAX: (415) 343-4342
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2831 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 SEQUENCE DESCRIPTION: SEQ ID NO: 3:
 US-09-306-902A-3

Alignment Scores:
 Pred. No.: 1,466-226 Length: 2831
 Score: 2544.50 Matches: 503
 Percent Similarity: 68.18% Conservative: 142
 Best Local Similarity: 53.17% Mismatches: 222
 Query Match: 53.11% Indels: 80
 DB: 3 Gaps: 16

US-10-624-932C-2 (1-898) x US-09-306-902A-3 (1-2831)

QY 9 ProAlaLeuLeuGluGlyIleValLeuAlaAlaTrpLeuArgGlySerGlyAlaGlnInSer 28
 DB 61 CCGAGCTTAGCAGGCATT-----GACTCTGGTGGCCAG----- 93
 QY 29 AlaThrValAlaAlaProValProGlyAlaAsnProAspLeuLeuProHisPheLeuVal 48
 DB 94 ---GGACTCCGAGCTCTCCATCAGCACCCGCGGAGCAGTGCCTCACTTCCTGCTG 150
 QY 49 GluProGluAspValTrpIleValLysAsnLysProValLeuLeuValCysLysAlaVal 68
 DB 151 GAACACAGAGGATGCTACATCGTAAAGAACACAGCCAGTGAATTCGACTCCGAGCCTC 210
 QY 69 ProAlaThrGlnIlePhePheLysCysAsnGlyGluTrpValArgGlnValAspHisVal 88
 DB 211 CCTGCCACACAGATCTACTTCAAGTGAATGGCGAGTGGGTAGCCAGAAAGCCACGTC 270
 QY 89 IleGluArgSerThrAspGlySerSerGlyLeuProThrMetGluValArgIleAsnVal 108
 DB 271 ACCGAGAGAGCTGGATGAGGCCACAGGCTTGGATACGAGAGGTGAGATAGAGGTG 330
 QY 109 SerArgGlnGlnValGluLysValPheGlyLeuGluGluTrpCysGlnCysValAla 128
 DB 331 TCGGCGCAGCAGGTGGAGGAACCTTTTGGGCTCGAGGACTACTGGTGTCTAGTGGTGGCC 390
 QY 129 TrpSerSerGlyThrThrLysSerGlnLysAlaTrpIleArgIleAlaArgLeuArg 148
 DB 391 TGGAGCTCTTCGGGAACACCAAGAGTCCGCGAGCTTACATCCGCAATTGGCTTACTTGGCG 450

QY 149 LysAsnPheGluGlnGluProLeuAlaLysGluValSerLeuGluGlnGlyIleValLeu 168
 DB 451 AAGAACTTTGACACGAGGAGCTCTGGCGAGGAGTACCTTGGATCATGAGGTCTTCTG 510
 QY 169 ProCysArgProProGluGlyIleProProAlaGluValGluTrpLeuArgAsnGluAsp 188
 DB 511 CAGTGGCGGCCACACAGAGGAGTGCCTGTGGCTGAGGTGAATGGCTCAAGATGAAGAT 570
 QY 189 LeuValAspProSerLeuAspProAsnValTrpIleThrArgGluHisSerLeuValVal 208
 DB 571 GTCATGATCCCGCTCAGGACACTTCTCTCCTCACCATTGACCAACACCTCATCATC 630
 QY 209 ArgGlnAlaArgLeuAlaAspThrAlaAsnTrpCysValAlaLysAsnIleValAla 228
 DB 631 CGCCAGCGCGCTCTCAGACACAGCACTACACCTGTGTGCAAGAATATTGTGGCC 690
 QY 229 ArgArgSerAlaSerAlaValIleValTrpValAsnGlyGlyTrpSerThrTrp 248
 DB 691 AAGCGCGGAGCAGCAGCGCCACAGTCATCGCTATGTGAACGAGGTTGGTCCAGCTGG 750
 QY 249 ThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArgSerArgSer 268
 DB 751 GCAGAATGGTCACTCTTAACCGCTGGCGCGAGTTGGCAGAAACGTACTTAGACC 810
 QY 269 CysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsnValGlnLys 288
 DB 811 TGCACCAACCCAGCCCACTCAATGGAGTGCCTCTTCGCGAGGAGCAGGCTTGCACAG 870
 QY 289 ThrAlaCysAlaThrLeuCysProValAspGlySerTrpSerProTrpSerLysTrpSer 308
 DB 871 ACGGCTTGCACCAACCGTGTGCCAGTGGATGGAGCGTGGACTGAGTGGAGCAAGTGGTCC 930
 QY 309 AlaCysGlyLeuAspCysThrHisTrpArgSerArgGluCysSerAspProAlaProArg 328
 DB 931 GCCTGACGACAGAGTGGCGCACTGGCGAGCGCGAGTGCATGGCAGCCGCCGCCAG 990
 QY 329 AsnGlyGlyGluGluCysGlnGlyThrAspLeuAspThrArgAsnCysThrSerAspLeu 348
 DB 991 AACGGAGCGCTGACTGCGACGCGGAGCGCTACTTGCATCCCAAGAACTGCACCGATGGGCTG 1050
 QY 349 CysVal-----HisSerAlaSerGlyProGlu----- 357
 DB 1051 TGGCTGCTGAATCAGAGAACTCTAAACAGACCTTAAAGAGCGCCCTCGGAGCGCTCGGGA 1110
 QY 358 AspValAlaLeuTrpValGlyLeu-----IleAlaValAlaValCysLeuValLeuLeu 376
 DB 1111 GAGCTGGCGCTGATCGGGGCTCTGGTGGCGGCTCTTTGGTTCGGCAGTTCTCATG 1170
 QY 377 LeuValLeuIleLeuValTrpCysArgLysLysGluGlyLeuAspSerAspValAlaAsp 396
 DB 1171 GCTGTAGGAGTGTGTTACCGGAGAACTGCGCGGACTTCGACACGAGCATCCTGAC 1230
 QY 397 SerSer---IleLeuThrSerGlyPheGlnProValSerIleLysProSerLysAlaAsp 415
 DB 1231 TCCTCTGCTGCTCACTGCTGTTTCCACCGCTCAACTTCAAGACTGCAAGGCCCCAGC 1290
 QY 416 AsnProHisLeuLeu-----ThrIleGlnProAspLeuSerThrThrThrThrTyr 433
 DB 1291 AACCCACAGCTCTCTGCACCCATCCGCCCTCCGAGCTTAACGCCGAGTGTGGCATCTAC 1350
 QY 434 GlnGlySerLeuCysProArgGlnAspGlyProSerProLysPheGlnLeuThrAsnGly 453
 DB 1351 CGCGGAGCTGTGATGCCCTGCGAGGACTCT--GCCGACAAAGATCCCTATGACTTAATCA 1407
 QY 454 HisLeuLeuSerProLeu----- 459
 DB 1408 CCCTTCTGGATCCCTTGGCCAGCCTCAAGATCAAGGTCTATGACTCCAGCACCATCGC 1467
 QY 460 ---GlyGlyGly----- 462
 DB 1468 TCTGGGGCTGGCTGGCTGATGAGCGGACCTGCTGGTGTCTTACACCCCGGTACATAC 1527
 QY 463 -----ArgHisThrLeuHisSerSerProThrSerProThrSerGluAla 475

Db	1528	CGAGCGATTCTCCCGGACACCCCACTTCCTGCACCTGGCGACG-----	1572
QY	476	GluGluPheValSerArgLeuSerThrGlnAsnTyrPheArgSerLeuProArgGlyThr	495
Db	1573	-----GCCAGCCTTGGTTCACG--CACTCTCTGGGCTCCTCGAGACCCC	1617
QY	496	SerAsnMetThrTyrGlyThrPheAsnPheLeuGlyGlyArgLeuMetLeuProAsnThr	515
Db	1618	AGCAGCAGTGTCACTGGCCACTTTGGTGTGCTGGGTGGGAGGCTGACCATTCCTCCGGCACA	1677
QY	516	GlyLeuSerLeuLeuLeuProProAspAlaIleProArgGlyLysIleTyrGluIleTyr	535
Db	1678	GGGGTCAGCTGTGTGTCAAAATGAGGCAATTCCTCCCAAGTTCCTATGACTTGTAT	1737
QY	536	LeuThrLeuHisLysProGluAspValArgLeuProLeuAla--GlyCysGlnThrLeu	554
Db	1738	CTACGTATCAACAAGACTGAAACACC--CTCCCACTTTCGGAAGTTCCTCCAGACAGTA	1794
QY	555	LeuSerProIleValSerCysGlyProProGlyValLeuLeuThrArgProValIleLeu	574
Db	1795	TTGAGCCCTCCGTGACCTCGCGGCCACCGGGCTCTCTGTGCGCCCTGTGTGCTC	1854
QY	575	AlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArgLeuLysGln	594
Db	1855	ACTGTGCCCCCACTGTGCTGAAGTCATTGCGGGAGACTGGATCTTCAGCTCAAGACCCAG	1914
QY	595	SerCysGluGlySerTrpGluAspValLeuHisLeuGlyGluGluAlaProSerHisLeu	614
Db	1915	GCCCATCAGGGCCACTGGGAGGAGTGGTCACTTTGGATGAGAGACTCTGAACACCCCC	1974
QY	615	TyrTyrCysGlnLeuGluAlaSerAlaCysTyrValPheThrGluGlnLeuGlyArgPhe	634
Db	1975	TGCTACTGCCAGCTAGAGGCTAAATCTGCCACATCTGTGTGACCAGCTGGGTACTAC	2034
QY	635	AlaLeuValGlyGluAlaLeuSerValAlaAlaAlaLysArgLeuLysLeuLeuPhe	654
Db	2035	GTGTTCAAGGGCGAGTCTTACTCCCGCTCGCGAGTCAAGCGGCTCAGCTAGCATCTTC	2094
QY	655	AlaProValAlaCysThrSerLeuGluTyrAsnIleArgValTyrCysLeuHisAspThr	674
Db	2095	GCCCCAGCCCTCTGCACCTCCCTGGAGTATAGTCTCAGGGTCTACTGTCTGGAGGACACT	2154
QY	675	HisAspAlaLeuLysGluValValGlnLeuGluLysGlnLeuGlyGlnLeuIleGln	694
Db	2155	CCTGCAGCACTGAAGGAGTCTTAGAGCTGGAGGACTCTGGGTGGCTACTTTGGTGGAG	2214
QY	695	GluProArgValLeuHisPheLysAspSerTyrHisAsnLeuArgLeuSerIleHisAsp	714
Db	2215	GAGCCCAAGACTTTGTCTTTAAGGACAGTTACCAACCTACGCTC-TCCCTCCATGAC	2273
QY	715	ValProSerSerLeuTrpLysSerLysLeuLeuValSerTyrGlnGluIleProPheTyr	734
Db	2274	ATCCCCATGCCACTGGAGGACCAACTACTTGCCCAAGTACAGAGATTCCTCTCTAC	2333
QY	735	HisIleTrpAsnGlyThrGlnArgTyrLeuHisCysThrPheThrLeuGluArgValSer	754
Db	2334	CATGTGTGAACGCCAGCCAGAAAGCCCTGCATCTGCATCTTACCCTCGAGACATAGC	2393
QY	755	ProSerThrSerAspLeuAlaCysLysLeuTrpValTrpGlnValGluGlyAspGlyGln	774
Db	2394	CTAGCTTCCACTGAGTTCACTGTAGGTCTGGCTGGCGAGGTAGAGGGGAGGCCAG	2453
QY	775	SerPheSerIleAsnPheAsnIleThrLysAspThrArgPheAlaGluLeuLeuAlaLeu	794
Db	2454	ATTTTCCAGCTGCACACCAACGCTGGCT--GAGACGCTCTGCTGCCCTGGATGCATC	2510
QY	795	GluSerGluAlaGlyValProAlaLeu-----ValGlyProSerAlaPheLysIlePro	812
Db	2511	TGCTCTGCCCTGGCAATGTGTCACCACACAGCTGGGACCTTATGCTTCAAGATACCA	2570
QY	813	PheLeuIleArgGlnLysIleIleSerSerLeuAspProProCysArgArgGlyAlaAsp	832
Db	2571	CTGTCCATCCGCCAGAGAGATCTGCAACAGCCCTGGAGCGCCCACTCAACGCGGCAATGAC	2630
QY	833	TrpArgThrLeuAlaGlnLysLeuHisLeuAspSerHisLeuSerPhePheAlaSerLys	852
Db	2631	TGGCGGCTGTGGCACAGAGCTCTCCATGGACCGGTACTCTGAACCTACTTCGCACCAAA	2690
QY	853	ProSerProThrAlaMetIleLeuAsnLeuTrpGluAlaArgHisPheProAsnGlyAsn	872
Db	2691	GCTAGTTCCTCCACAGGCGTGTATCTTAGACCTCTGGGAAGCTTCGCAGCAGGATGATGGGAC	2750
QY	873	LeuSerGlnLeuAlaAlaValAlaGlyLeuGlyGlnProAspAlaGlyLeuPheThr	892
Db	2751	CTCAACAGCTGCGCAGTCCCTTGAGGAGATGGGCAAGTGAGATGCTGTGATGCCATG	2810
QY	893	ValSerGluAlaGluCys 898	
Db	2811	ACCACCTGATGGCGATTGC 2828	
RESULT 7			
US-09-949-016-4794			
; Sequence 4794, Application US/09949016			
; Patent No. 6812339			
; GENERAL INFORMATION:			
; APPLICANT: VENTER, J. Craig et al.			
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED			
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF			
; FILE REFERENCE: CL001307			
; CURRENT APPLICATION NUMBER: US/09/949,016			
; CURRENT FILING DATE: 2000-04-14			
; PRIOR APPLICATION NUMBER: 60/241,755			
; PRIOR FILING DATE: 2000-10-20			
; PRIOR APPLICATION NUMBER: 60/237,768			
; PRIOR FILING DATE: 2000-10-03			
; PRIOR APPLICATION NUMBER: 60/231,498			
; PRIOR FILING DATE: 2000-09-08			
; NUMBER OF SEQ ID NOS: 207012			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 4794			
; LENGTH: 3008			
; TYPE: DNA			
; ORGANISM: Human			
US-09-949-016-4794			
Alignment Scores:			
Pred. No.:	3,26e-207	Length:	3008
Score:	2337.50	Matches:	432
Percent Similarity:	73.77%	Conservative:	136
Best Local Similarity:	56.10%	Mismatches:	179
Query Match:	48.79%	Indels:	23
DB:	4	Gaps:	7
US-10-624-932C-2 (1-898) x US-09-949-016-4794 (1-3008)			
QY	147	LeuArgLysAsnPheGluGlnProLeuAlaLysGluValSerLeuGluGlnGlyIle	166
Db	9	CTACGGAAGACATTTGAGCAGGAACCCCTAGGAAGAAAGTGTCTTTGGAAACAGGAGTC	68
QY	167	ValLeuProCysArgProProGluGlyIleProProAlaGluValGluTrpLeuArgAsn	186
Db	69	TTACTCCAGTGTGCACCACTGAAGGATCCCAAGTGGCTGAGTGAATGGTTGAAAAAT	128
QY	187	GluAspLeuValAspProSerLeuAspProAsnValTyrIleThrArgGluHisSerLeu	206
Db	129	GAAGACATATGATCCCGTTGAAGATCGGAATTTTATATTAATACTATTGATCAACACCTC	188
QY	207	ValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysValAlaLysAsnIle	226
Db	189	ATCATTAAGCAGGCCCGACTCTCTGATCTGCAAAATACACCTGTGTGCCAAAAACATT	248
QY	227	ValAlaArgArgSerAlaSerAlaValIleValTyrValAsnGlyGlyTrpSer	246
Db	249	GTTCGCAAGAGGAAAAAGTCAACTGCCACTGTCTATGTCTATGTCAACGCGTGGCTGCC	308

Db	1377	AAAATACTGCTCAAGAACCAAGCAGCAGCAGGACAGTGGAGAGATGTGTGGTGGTCGGG	1436
Qy	608	GlulGluAlaProSerHisLeuTyrTyCyagInLeuGluAlaSerAlaCySyrValPhe	627
Db	1437	GAGNAACCTTACCACCCCTCTACTATCAGCTGGATGCAGAGCGCTGCCACATCCTC	1496
Qy	628	ThrGluInLeuGlyArgPheAlaLeuValGlyGluAlaLeuSerValAlaAlaLys	647
Db	1497	ACAGAGAACCTCAGCACCTCAGCCCTGGTAGGACATTCACACCAACCAAGCGGCTGCGAAG	1556
Qy	648	ArgLeuLysLeuLeuLeuPheAlaProValAlaCyThrSerLeuGluTyrAsnIleArg	667
Db	1557	CGCTCAAGCTGACCATCTTTGGGCGCCCTGTGCTCTCTCGCTGGAGTACAGCATCCGA	1616
Qy	668	ValTyrCysLeuHisAspThrHisAspAlaLeuLysGluValValGlnLeuGluLysGln	687
Db	1617	GTCTACTGCTGATGATACACCCAGGATGCCCTGAGGAAATTTTACATCTTGAGAGACAG	1676
Qy	688	LeuGlyGlyGlnLeuIleGlnGluProArgValLeuHisPheLysAspSerTyrHisAsn	707
Db	1677	ATGGAGGACAGCTCCTAGAGAACCTTAAGGCTCTTCAATTTAAAGCAGCACCACCAAC	1736
Qy	708	LeuArgLeuSerIleHisAspValProSerSerLeuTrrpLysSerLysLeuValSer	727
Db	1737	CTCGCGCTGTCAATTCACGATATCGGCCCATTCCTCTGGAAGAGCAAAATGTGTGGCTAAA	1796
Qy	728	TyrGlnGluIleProPheTyrHisIleTrrpAsnGlyThrGlnArgTyrLeuHisCysThr	747
Db	1797	TATCAGAAATTCATTTTACCATGTTTGAGTGGATCTCAAGAAACCTGCACTGCACC	1856
Qy	748	PheThrLeuGluArgValSerProSerThrSerAspLeuAlaCysLysLeuTrrpValTrrp	767
Db	1857	TTCACTCTGGAAAGATTAGCCTGAACACAGTGGAGCTGGTTTGCAAACTCTGTGTGCGG	1916
Qy	768	GlnValGluGlyAspGlyGlnSerPheSerIleAsnGlnPheAsnIleThrLysAspThrArg	787
Db	1917	CAGGTGGAAGAGAGAGGCGAGATCTTCCAGCTCAACTGCACCGTGTGAGAGAACTGCACT	1976
Qy	788	PheAlaGluLeuAlaLeuGluSerGluAlaGlyValProAlaLeuValGlyProSer	807
Db	1977	GGCATCGATTGGCGTGTGGATCTCTGGACACCATCACCGTGCAGGGGGCCAGT	2036
Qy	808	AlaPheLysIleProPheLeuIleArgGlnLysIleSerSerLeuAspProProCys	827
Db	2037	GCITTCAGCATCCTCTCCCTATCCGCGAGAGCTCTGTAGCAGCTGTGATGCCCCCAG	2096
Qy	828	ArgArgGlyAlaAspTrrpArgThrLeuAlaGlnLysLeuHisLeuAspSerHisLeuSer	847
Db	2097	ACGAGAGGCCATGACTGGAGGATCTGGGCCCATAGCTGAACCTGGACAGGTACTTGAAT	2156
Qy	848	PhePheAlaSerLysProSerProThrAlaMetIleLeuAsnLeuTrrpGluAlaArgHis	867
Db	2157	TACTTTTGCCACCAAAATCCAGCCCACTGGCGTAAATCTCGGATCTTTGGGAAGCAGAGAAC	2216
Qy	868	PheProAsnGlyAsnLeuSerGlnLeuAlaAlaValAlaGlyLeuGlyGlnProAsp	887
Db	2217	TTCCAGATGGAAACCTTGAGCATGCTGGCAGCTGCTTGGAGAAATGGGAGACATGAA	2276
Qy	888	AlaGlyLeuPheThrValSerGluAlaGlu	897
Db	2277	ACGGTGTGTCTTAGCAGCAGAGAGGGCAG	2306

RESULT 8

US-09-969-532-15

; Sequence 15, Application US/09969532

; Patent No. 6777232

; GENERAL INFORMATION:

; APPLICANT: Walke, D. Wade

; APPLICANT: Scoville, John

; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides

; FILE REFERENCE: LEX-0244-USA

; CURRENT APPLICATION NUMBER: US/09/969,532

US-09-969-532-15

Patent No. 6777232

; APPLICANT: Walke, D. Wade

; TITLE OF INVENTION: No. 6777

; CURRENT APPLICATION NUMBER: US/09/969,532


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; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 2661
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-969-532-15

Alignment Scores:
Pred. No.: 4 84e-166 Length: 2661
Score: 1895.00 Matches: 383
Percent Similarity: 58.13% Conservative: 157
Best Local Similarity: 41.23% Mismatches: 277
Query Match: 39.55% Indels: 112
DB: 4 Gaps: 14

US-10-624-932C-2 (1-898) x US-09-969-532-15 (1-2661)
QY 8 TrpProAlaLeuLeuGlyLeuValLeuAlaAlaTrpLeuArgGlySer----- 23
Db TGGCTCCCGTGGCTGGGG-----CTGTGCTTCTGGCGGCGAGCGCGCTGCCCGA 102
QY 24 GlyAlaGlnGlnSerAlaThrValAlaAlaAsnProValProGlyAlaAlaAsnProAlaLeu 43
Db 103 GGAACGTGACAAATGGCGAAGCCCTCCCGAATCCATCCATCAGCT---CCTGGGACACTG 159
QY 44 ProHisPheLeuValGluProGluAspValTyrIleValLysAsnLysProValLeuLeu 63
Db 160 CCTCATTTTCATAGGAGCGCAGATGATGTTATATTATCATAGAGCAACCTATTGCACATC 219
QY 64 ValCysLysAlaValProAlaThrGlnIlePhePheLysCysAsnGlyGluTrpValArg 83
Db 220 AGGTGCAAAAGCGAGCGCAGCATGTCAGATATTCTTCAAAATGCAACGCGAGTGGGTCCAT 279
QY 84 GlnValAspHisValIleGluArgSerThrAspGlySerSerGlyLeuProThrMetGlu 103
Db 280 CAGAACGAGCAGCTCTCTGAAGAGACTCTGGAGGAGCTCAGGTTTGAAGTCCCGCAA 339
QY 104 ValArgIleAsnValSerArgGlnGlnValGluLysValPheGlyLeuGluGluTyrTrp 123
Db 340 GTGTTTCATCAATCTTACTAGGCAACAGGTGGAGACTTCCATGGGCCCGGAGACTATTGG 399
QY 124 CysGlnCysValAlaTrpSerSerGlyThrThrLysSerGlnLysAlaTyrIleArg 143
Db 400 TGCACAGTGTGTGGCGTGGAGCCACCTGGGTACCTCCAAAGAGCAGGAAGCCCTCTGTGCGC 459
QY 144 IleAlaArgLeuArgLysAsnPheGluGlnGluProLeuAlaLysGluValSerLeuGlu 163
Db 460 ATAGCTATTTCGGAAGAACTTTGAAACAGACCCCAAGAAAGGAAGTTCCCATTTGAA 519
QY 164 GlnGlyIleValLeuProCysArgProProGluGlyIleProProAlaGluValGluTrp 183
Db 520 GGCATGATTGTACTGCACCTGCCGCCACCCAGAGGGAGTCCCTGCTGCCGAGGTGGATGG 579
QY 184 LeuArgAsnGluAspLeuValAspProSerLeuAspProAsnValTyrIleThrArgGlu 203
Db 580 CTGAAATAATGAGAGGCCATTGACTCTGAACAAGACGAGAAACATTGCACCCAGGGCTGAC 639
QY 204 HisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysValAla 223
Db 640 CATTAACCTGATCATAGCGAGGACCGCTCTCCGACTCAGAAATATACACCTGCATGGCA 699
QY 224 LysAsnIleValAlaArgArgSerAlaSerAlaAlaValIleValTyrValAsnGly 243
Db 700 GCCAACATCGTGGCTAAGAGGAGAGCCTGTCGCCCACTGTTGTGCTTACGTGGATGG 759
QY 244 GlyTrpSerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGln 263
Db 760 AGCTGGGAAGTGTGGAGCGAATGTCCTGTCGAGTCCA----- 798
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QY 264 LysArgSerArgSerCysThrAsnProAlaProLeuAsnGlyClyAlaPheCysGluGly 283
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QY 284 GlnAsnValGlnLysThrAlaCysAlaThrLeuCysProValAspGlySerTrpSerPro 303
Db 798 ----- 798
QY 304 TrpSerLysTrpSerAlaCysGlyLeuAspCysThrHisTrpArgSerArgGluCysSer 323
Db 799 -----GAGTGTGAACATTTCGGGATCCGGAGTGACCA 831
QY 324 AspProAlaProArgAsnGlyGlyGluGluCysGlnGlyThrAspLeuAspThrArgAsn 343
Db 832 GCACCAACCCCGAGAAATGGGGCAAAATCTGTGAAGGTCTAAGCCAGGAATCTGAAAAAC 891
QY 344 CysThrSerAspLeuCysValHisSerAlaSerGlyProGluAspValAlaLeuTyrVal 363
Db 892 TGCACAGATGGTCTTTGCATCTTAGGCATTGAGAATGCCAGCGACATTGCTTTGTACTCG 951
QY 364 GlyLeuIleAlaValAlaValCysLeuValLeuLeuLeuValLeuLeuValLeuValTyr 383
Db 952 GGCCTTG---GGTGTCTCCGTCGTCGGCGTTCAGTCTCTGTCATTGCTGTCACCTTTAC 1008
QY 384 CysArgLysLysGluGlyLeuAspSerAspValAlaAspSerSerIleLeuThrSerGly 403
Db 1009 AGACGGAGCCAGAGTACTATGGCGTGGAGCTCATTTGACTCTTCTGCATTGACAGGTGGC 1068
QY 404 PheGlnProValSerIleLysProSerLysAlaAspAsnProHisLeuLeu-----Thr 421
Db 1069 TTCAGACCTTCAACTTCAAAACAGTCCCTCAAGGTAACCTCCCTGCTCTGAATTCGTCC 1128
QY 422 IleGlnProAspLeuSerThrThrThrThrThrThrThrThrThrThrThrThrThrThr 441
Db 1129 ATGCAGCCAGATCTG---ACAGTGGACCGGACATACAGCGGACCCCATCTGT---CTGCAG 1182
QY 442 AspGlyProSerProLysPheGlnLeuThrAsnGlyHisLeuLeuSerProLeuGly--- 460
Db 1183 GAC---CCTCTGGACAAGGAGCTCATGACAGAGTCTCACTCTTTAAACCTTTGTCGGAC 1239
QY 460 ----- 460
Db 1240 ATCAAAGTGAAAGTCCAGAGCTCGTTTCATGTTTCCCTGGAGTGCTCGAGAGAGCTGAG 1299
QY 461 -----GlyClyArgHisThrLeuHisHis 468
Db 1300 TACCACGGCAAGAATCATTTCCAGGACTTTTCCCATGGAAACAACACAGCTTTAGTACA 1359
QY 469 SerSerProThrSerGluAlaGluGluPheValSerArgLeuSerThrGlnAsnTyrPhe 488
Db 1360 ATGCATCCACGAATAAATG---CCCTACATCCAAAATCTGTCA----- 1401
QY 489 ArgSerLeuProArgGlyThrSerAsnMetThrTyrGlyThrPheAsnPheLeuGlyGly 508
Db 1402 ---TCACTCCCAAGGACAGAACTGAGGACAACTGGTGTCTTTGGCCATTTAGGGGG 1458
QY 509 ArgLeuMetIleProAsnThrGlyIleSerLeuLeuIleProProAspAlaIleProArg 528
Db 1459 CGCTTAGTATGCCAAATACAGGGGTGAGCTTACTCATACACACAGGTGCCATCCAGAG 1518
QY 529 GlyLysIleTyrGluIleTyrLeuThrLeuHisLysProGluAspValArgLeuProLeu 548
Db 1519 GAGAAATCTTGGAGATTTATATGTCATCAACCAAGGTGAACCC---AGCCTCCAGTCA 1575
QY 549 AlaGlyCysGlnThrLeuLeuSerProIleValSerCysGlyProProGlyValLeuLeu 568
Db 1576 GATGGCTCTGAGTGTCTCTGAGTCTGAAGTCACTGGTGGTCTCTCCAGACATGATCGTC 1635
QY 569 ThrArgProValIleLeuAlaMetAspHisCysGlyGluProSerProAspSerTrpSer 588
Db 1636 ACCACTCCCTTTTCATTTGACATTCGCCGACTGTCAGATGTCAGATTTCTGAGCATTTGAA 1695
QY 589 LeuArgLeuLysLysGlnSerCysGluGlySerTrpGluAspValLeuHisLeuGlyGlu 608
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Db 1696 ATCCATTAAAGAGAGACAGCAGCGCAAAATGGGAGGAAGTATGTCAGTGAAGAT 1755
Qy 609 GluAlaProSerHisLeuTyrTyCysGlnLeuGluAlaSerAlaCysTyrValPheThr 628
Db 1756 GAATCTACATCC-----TGTACTGCTTTTGGACCCCTTTGGCTGTCATGTCCTG 1809
Qy 629 GluGlnLeuGlyArgPheAlaLeuValGlyGluAlaLeuSerValAlaAlaAlaArg 648
Db 1810 GACAGCTTTGGACCTATGCTCACTGGAGAGCAATCACAGAGTGTGCGGTGAAGCAA 1869
Qy 649 LeuLysLeuLeuLeuPheAlaProValAlaCysThrSerLeuGluTyrAsnIleArgVal 668
Db 1870 CTGAAGTGGCGGTTTTGGCTGCTGATGCTGTAACTCCCTGGATTAACAATTCAGAGTT 1929
Qy 669 TyrCysLeuHisAspThrHisAspAlaLeuLysGluValValGlnLeuGluLysGlnLeu 688
Db 1930 TACTGTGTGGACATACCCCTTGTGATTCCTCTGGAGATTTAAACCATTCACCTGCCTGC 1989
Qy 689 GlyGlyGlnLeuIleGlnGluProArgValLeuHisPheLysAspSerTyrHisAsnLeu 708
Db 1990 GGTGGAGAGCTCTCGAAGAACCAAAATGCTGCAATTCAGAGGAATACCTTTAGTCTT 2049
Qy 709 ArgLeuSerIleHisAspValProSerSerLeuTyrPheLysLeuLeuValSerTyr 728
Db 2050 CAGATTTCTGCTTGTATATTCCTCCCAATTCCTCTGGAGATTTAAACCATTCACCTGCCTGC 2109
Qy 729 GlnGluIleProPheTyrHisIleTyrAsnGlyThrGlnArgTyrLeuHisCysThrPhe 748
Db 2110 CAGAAAGTCCCGTCTCCCGGTGTGGTGAAGTAAACCGGAGCCCTGCACTGGCCCTTC 2169
Qy 749 ThrLeuGluArgValSerProSerThrSerAspLeuAlaCysLysLeuTyrValTyrGln 768
Db 2170 TCCCTGGAGCGTTATACGCCCACTACCAACCCAGCTGTCTGCAAAATCTGCAATTCGGCAG 2229
Qy 769 ValGluGlyAspGlyGlnSerPheSerIleAsnPheAsnIleThrLysAspThrArgPhe 788
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Qy 789 AlaGluLeuLeuAlaLeuGluSerGluAlaGlyValProAlaLeuValGlyProSerAla 808
Db 2290 ACCATCACTTCTTCGCACAGAGAGCAGACACTTTCCTCTGCACAGACTGGCCCCCAAGCC 2349
Qy 809 PheLysIleProPheLeuIleArgGlnLysIleSerSerLeuAspProProCysArg 828
Db 2350 TTCAAAATTCCTACTCATCAGACAGCGGATTTGTGCTACATTTGATACCCCAATGCC 2409
Qy 829 ArgGlyAlaAspTyrPheGlyLeuAlaGlnLysLeuHisLeuAspSerHisLeuSerPhe 848
Db 2410 AAAGGCAAGGACTGGCAGATGTTAGCACAGAAAAACAGCATCAACAGGAATTTATCTTAT 2469
Qy 849 PheAlaSerLysProSerProThrAlaMetIleLeuAsnLeuTyrGluAlaArgHisPhe 868
Db 2470 TTCGCTACAAAGATGACCCCATGCTGTCTATTGAACTGTGGAGAGTTCGTCATCAG 2529
Qy 869 ProAsnGlyAsnLeuSerGlnLeuAlaAlaValAlaGlyLeuGlyGlnProAspAla 888
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RESULT 9

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US-09-969-532-13
; Sequence 13, Application US/09969532
; Patent No. 6777232
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; TITLE OF INVENTION: No. 6777232e1 Human Membrane Proteins and Polynucleotides Encodin
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969,532
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; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 2694
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-969-532-13

Alignment Scores:
Pred. No.: 3,06e-165 Length: 2694
Score: 1886.50 Matches: 384
Percent Similarity: 57.55% Conservative: 157
Best Local Similarity: 40.85% Mismatches: 276
Query Match: 39.38% Indels: 123
DB: 4 Gaps: 15
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US-10-624-932C-2 (1-898) x US-09-969-532-13 (1-2694)

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Qy 24 GlyAlaGlnGlnSerAlaThrValAlaAsnProValProGlyAlaAsnProAspLeuLeu 43
Db 103 GGAAGTCAATGGCGAAGCCCTTCCGAAATCCATCCATCAGCT---CTGGGACACTG 159
Qy 44 ProHisPheLeuValGluProGluAspValTyrIleValLysAsnLysProValLeuLeu 63
Db 160 CCTCATTTTATAGAGGAGCCAGATGATGCTTATATATCAAGAGCAACCCCTATTGCACTC 219
Qy 64 ValCysLysAlaValProAlaThrGlnIlePhePheLysCysAsnGlyGluTyrValArg 83
Db 220 AGGTGCAAGCGAGCCAGCCATGTCAGATATTTCTCAATGCAACGCGGAGTGGTCCAT 279
Qy 84 GlnValAspHisValIleGluArgSerThrAspGlySerSerGlyLeuProThrMetGlu 103
Db 280 CAGAACGACGCTCTCTGAAGAGACTCTGCAGAGAGCTCAGGTTTGAAGTCCGCGAA 339
Qy 104 ValArgIleAsnValSerArgGlnValLysValPheGlyLeuGluGluTyrTrp 123
Db 340 GTGTTCAATCAATGTTACTAGCAACAGGTGGAGACTTCCATGGCGCGAGGACTATTGG 399
Qy 124 CysGlnCysValAlaTrpSerSerSerGlyThrThrLysSerGlnLysAlaTyrIleArg 143
Db 400 TGGCAGTGTGTGGCTGGAGCCACCTGGGTACCTTCAAGAGCAGGAAGGCTCTGTGGCG 459
Qy 144 IleAlaArgLeuArgLysAsnPheGluGlnGluProLeuAlaLysGluValSerLeuGlu 163
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Qy 164 GlnGlyIleValLeuProCysArgProGluGluIleProProAlaGluValGluTyr 183
Db 520 GGCATGATTGCTACTGCACTGCCGCCACAGAGGAGTCCCTGTGTCGCGAGTGGAAATGG 579
Qy 184 LeuArgAsnGluAspLeuValAspProSerLeuAspProAsnValTyrIleThrArgGlu 203
Db 580 CTGAAATAATGAAGGCCCATTTGACTCTGAACAAGAGCAAGCAATTTGACCCAGCGGCTGAC 639
Qy 204 HisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysValAla 223
Db 640 CATAACTGATCATCAGCAGGAGCCGCTCTCGAGCTCAGGAATAATTAACCTGATGGCA 699
Qy 224 LysAsnIleValAlaArgArgSerAlaSerAlaAlaValIleValTyrValAsnGly 243
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Qy 244 GlyTyrSerThrTyrThrGluTyrSerValCysSerAlaSerCysGlyArgGlyTyrGln 263
Db 760 AGCTGGGAGTGTGGAGCGAATGTCGTCGTGCACTGCA----- 798
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QY 264 LysArgSerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGly 283
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QY 284 GlnAsnValGlnLysThrAlaCysAlaThrLeuCysProValAspGlySerTrpSerPro 303
Db 798 -----
QY 304 TrpSerLysTrpSerAlaCysGlyLeuAspCysThrHisTrpArgSerArgGluCysSer 323
Db 799 -----
QY 324 AspProAlaProArgHsnGlyGlyGluGluCysGlnGlyThrAspLeuAspThrArgAsn 343
Db 832 GCACCAACCCCGAAATGGGCAAAATCTGTGAAGGTCTAAGCCAGCAATCTGAAGAAC 891
QY 344 CysThrSerAspLeuVal-----GAGTGTGAACATTTGCGGATCCGGAGTGACCA 831
Db 892 TGCACAGATGCTTTTGATCTCTAGATAAAAAACCTCTTCATGAATAAAACCCCAAGC 951
QY 353 AlaSerGlyProGluAspValAlaLeuValGlyLeuValAlaValAlaValCysLeu 372
Db 952 ATTGAGAATCCAGCAGACATTTGTTGACTCGGGCTTG---GGTGTGCGCGTGTGGCC 1008
QY 373 ValLeuLeuLeuValLeuLeuValValLeuValValCysArgLysLysGluGlyLeuAspSer 392
Db 1009 GTTGCACTCTGTGTCATGTGTGTCACCTTTACAGACGGGCGAGAGTGATATGGCGTG 1068
QY 393 AspValAlaAspSerSerLeuLeuThrSerGlyPheGlnProValSerLeuLysProSer 412
Db 1069 GAGCTCATTCACCTCTCTGATTTGACAGGTGGCTTCAGACCTTCAACTTCAAAACAGTC 1128
QY 413 LysAlaAspAsnProHisLeuLeu-----ThrIleGlnProAspLeuSerThrThr 430
Db 1129 CGTCAAGGTAACCTCCCTGCTCTCTGAAATCTGCCATCTGACGACAGATCTG---ACAGTGAGC 1185
QY 431 ThrThrGlnGlySerLeuCysProArgGlnAspGlyProSerProLysPheGlnLeu 450
Db 1186 CGACATACAGCGGAGCCATCTGT---CTCAGGAC---CCTCTGACAAAGGAGCTCATG 1239
QY 451 ThrAsnGlyHisLeuSerProLeuGly----- 460
Db 1240 ACAGAGTCTCTCACTCTTTAACCTTTGTGCGACATCAAGTGAAGTCCAGAGCTCGTTC 1299
QY 460 ----- 460
Db 1300 ATGGTTTCCCTGGGAGTGTCTGAGAGAGCTGAGTACCACGGCAAGAATCATTCAGGACT 1359
QY 461 -----GlyGlyArgHisThrLeuHisSerSerProThrSerGluAlaGluGlu 477
Db 1360 TTTCCCATGGAACCAACACAGCTTTAGTACAAATGATGCCATCCCAAGATAAAATG---CCC 1416
QY 478 PheValSerArgLeuSerThrGlnAsnTyrPheArgSerLeuProArgGlyThrSerAsn 497
Db 1417 TACATCCAAATCTGTCA-----TCACTCCCAACAGGACAGAACTG 1458
QY 498 MetThrTyrGlyThrPheAsnPheLeuGlyGlyArgLeuMetIleProAsnThrGlyIle 517
Db 1459 AGGACAACTGGTGTCTTTGGCCATTTAGGGGGCGCTTAGTAATGCCAAATACAGGGGTG 1518
QY 518 SerLeuLeuLeuProProAspAlaIleProArgGlyLysIleTyrGluIleTyrLeuThr 537
Db 1519 AGCTTACTATACACACGCTGGCATCCCAAGAGAGAAATCTTTGGGAGATTTATATGTCC 1578
QY 538 LeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeuLeuSerPro 557
Db 1579 ATCAACCAAGGTGAACCC---AGCTTCAGTCAGATGGCTCTGAGGTGCTCTCTGAGTCT 1635
QY 558 IleValSerCysGlyProProGlyValLeuLeuThrArgProValIleLeuAlaMetAsp 577
Db 1636 GAAGTCACTGTGGTCTCTCCAGACATGATGTCACCACTCCCTTTGCAATTCAGCATCCCG 1695
QY 578 HisCysGlyGluProSerProAspSerTrpSerLeuArgLeuLysLysGlnSerCysGlu 597

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Db 1756 GGCAAATGGGAGGAGTGTAGTCAGTGAAGATGAATCTACATCC-----TGTACTGC 1809
QY 618 GlnLeuGluAlaSerAlaCysTyrValPheThrGluGlnLeuGlyArgPheAlaLeuVal 637
Db 1810 CTTTGTGAGCCCTTTCGTGTATGTGCTCTCGACAGCTTTTGGGACCTATATGCGCTCACT 1869
QY 638 GlyGluAlaLeuSerValAlaAlaLysArgLeuLysLeuLeuLeuPheAlaProVal 657
Db 1870 GGAAGCCCAATCACAGCTGTCCGTGAAGAACTGAAGTGGCGGTTTTTGGCTGCATG 1929
QY 658 AlaCysThrSerLeuGluTyrAsnIleArgValTyrCysLeuHisAspThrHisAspAla 677
Db 1930 TCTGTAACTCCCTGGATTACAACCTTGAGAGTTTACTGTGTGACAATACCCCTTGTGCA 1989
QY 678 LeuLysGluValValGlnLeuLysGlnLeuGlyGlyGlnLeuLeuGlnGluProArg 697
Db 1990 TTTTCAGAAAGTGGTTTTCAGATGAAGGCATCAAGGTGGACAGCTCTCTGGAAGAACCAAA 2049
QY 698 ValLeuHisPheLysAspSerTyrHisAsnLeuArgLeuSerIleHisAspValProSer 717
Db 2050 TTGCTGCATTTCAAGGGAATACCTTTAGTCTTCAGATTTCTGCTCTGTATATCCCCA 2109
QY 718 SerLeuTrpLysSerLysLeuValSerTyrGlnGluIleProPheTyrHisIleTrp 737
Db 2110 TTCCTCTGGAGAATTAAACCATTCAGCTGCTGCGAGAAAGTCCCGTTCTCCCGGTGTGG 2169
QY 738 AsnGlyThrGlnArgTyrLeuHisCysThrPheThrLeuGluArgValSerProSerThr 757
Db 2170 TGCAGTAAACGGCAGCCCTGCACTGTGCTTCTCCCTGAGCGTTATAGCCCATACC 2229
QY 758 SerAspLeuAlaCysLysLeuTrpValTrpGlnValGluGlyAspGlyGlnSerPheSer 777
Db 2230 ACCAGCTGTCTGCAAAATCTGCATTCGCGAGCTCAAGGCCATGAACAGATCCTCCAA 2289
QY 778 IleAsnPheAsnIleThrLysAspThrArgPheAlaGluLeuAlaLeuGluSerGlu 797
Db 2290 GTGCACATCAATCTAGAGAGTGAACGAGAAACCATCACTTTCTTCGCACAAGAGGAC 2349
QY 798 AlaGlyValProAlaLeuValGlyProSerAlaPheLysIleProPheLeuIleArgGln 817
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QY 818 LysIleIleSerSerLeuAspProProCysArgArgGlyAlaAspTrpArgThrLeuAla 837
Db 2410 CGGATTTGTGTACATTTGATACCCCAATGCCAAAGGCCAAGGACTGGCAGATGTTAGCA 2469
QY 838 GlnLysLeuHisLeuAspSerHisLeuSerPhePheAlaSerLysProSerProThrAla 857
Db 2470 CAGAAAAACAGCATCAACAGGAATTTATCTTATTTGCTACACAAAGTAGCCCATCTGCT 2529
QY 858 MetIleLeuAsnLeuTrpGluAlaArgHisPheProAsnGlyAsnLeuSerGlnLeuAla 877
Db 2530 GTCAATTTGAACCTGTGGGAAGCTCGTCATCAGCATGATGGTGTATCTTGACTCCCTGGCC 2589
QY 878 AlaAlaValAlaGlyLeuGlyGlnProAspAlaGlyLeuPheThrValSerGluAlaGlu 897
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RESULT 10
US-09-969-532-11
; Sequence 11, Application US/09969532
; Patent No. 6777232
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides Encoding
; FILE REFERENCES: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969,532

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; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11

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; LENGTH: 2703
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-969-532-11

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Alignment Scores:		
Pred. No.:	1,91e-164	Length:
Score:	1878.00	Matches:
Percent Similarity:	57.26%	Conservative:
Best Local Similarity:	40.63%	Mismatches:
Query Match:	39.20%	Indels:
DB:	4	Gaps:
		15
		2703

US-10-624-932C-2 (1-898) x US-09-969-532-11 (1-2703)

QY		8	TtpProAlaLeuLeuGlyIleValLeuAlaIalTrpLeuArgGlySer-----23
DB		49	TGGCTCCCGTGGCTGGG-----CTGTGCTTCCTGGCGCAGCGACCGCGGCTGCCGA102
QY		24	GlyAlaGlnGlnSerAlaThrValAlaAlaAenProValProGlyAlaAenProAspLeuLeu43
DB		103	GGACTGCATGGCGAAGCCCTTCCCAGAACCATCCATCCATCAGCT---CCTGGGACACTG159
QY		44	ProHisPheLeuValGluProGluAspValTyrlleVallysAenLysProValLeuLeu63
DB		160	CCTCAITTCATAGAGAGCCAGATGCTTATTATATCAAGAGACAACCCTATTGGCACTC219
QY		64	ValCysLysAlaValProAlaThrGlnIlePhePheLysCysAenGlyGluTrpValArg83
DB		220	AGGTGCAAGCCGAGCGCACCATGCAGATATTTCTCAAATGCAACGGCAGTGCGTCCAT279
QY		84	GlnValAspHisValIleGluArgSerThrAspGlySerSerglyLeuProThrMetGlu103
DB		280	CAGAAGGACGAGCTCTTGAAAGAGACTCTGGACGAGAGCTCAGGTTTTGAAGGTCCGCGAA339
QY		104	ValArgIleAsnValSerArgGlnGlnValGluLysValPheGlyLeuGluTyrrTp123
DB		340	GTGTTCAATCAATGTACTAGGCACAGGTGGAGNCTTCATGGCCCCGAGGACTATTGG399
QY		124	CysGlnCysValAlaTrpSerSerSerglyThrThrylserGlnLysAlaTyrlleArg143
DB		400	TGCCAGTGTGTGGCGTGGAGCCACTGGGTGTACTTCCAAGAGCAGGAAAGGCTCTGTGGCG459
QY		144	IleAlaArgLeuArgLysAsnPheGluGlnGluProLeuAlaLysGluValSerLeuGlu163
DB		460	ATAGCGCTATTACGGANAACCTTTGAACAGACCACAAGAAAGGGAAGTTCCCATTTGA519
QY		164	GlnGlyIleValLeuProCysArgProProdGluGlyIleProAlaGluValGluTrp183
DB		520	GSCATGATTGTACTGCTGCCGCCACCAGAGGGAGTCCCTGCTGCCGAGGTGGATGG579
QY		184	LeuArgAenGluAspLeuValAspProSerLeuAspProhenValTyrlleThrArgGlu203
DB		580	CTGAAAAATGAGAGCCCATGACTCTGAAACAAGCAGACAATGTGACACACCGGCTGAC639
QY		204	HisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAenTyrrCysValAla223
DB		640	CATACTGTATCATCAGGAGCAGCGCTCTCGGACTCAGGAANATTACACTGCATGGCA699
QY		224	LysAenIleValAlaArgArgSerAlaSerAlaAlaValIleValTyrrValAenGly243
DB		700	GCCACATCGTGCCTAAGAGGAGAGCCCTGTCCGCCACTGTGTGGTCTACGTGGATGG759
QY		244	GlyTrpSerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTyrrGln263
DB		760	AGCTGGGAAGTGTGAGCGCAATGTGCTGTGCACTCCA-----798

Qy	264	LysArgSerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGly	283
Db	798	-----	798
Qy	284	GlnAsnValGlnIlysThrAlaCysAlaThrLeuCysProValAspGlySerTrpSerPro	303
Db	798	-----	798
Qy	304	TrpSerIysTrpSerAlaCysGlyLeuAspCysThrHisTrpArgSerArgGluCysSer	323
Db	799	-----GAGTGTGAACATTTGCGGATTCGGGAGTGCACAC	831
Qy	324	AspProAlaProArgAsnGlyGlyGluGlyCysGlnGlyThrAspLeuAspThrArgAsn	343
Db	832	GCACACCCCGGAGAAATGGGGCAAAATCTGTGAAGGTCTAAGCCAGGAATCTGAAAC	891
Qy	344	CysThrSerAspLeuCysValHisSerAlaSerGlyProGluAspValAlaLeuTyrVal	363
Db	892	TGCACAGATGGTCTTTGCATCTTAGGCATTTGGAATGCCAGCGCACATTCCTTTGTACTCG	951
Qy	364	GlyLeuIleAlaValAlaValCysLeuValLeuLeuLeuValLeuIleLeuValTyr	383
Db	952	GGCTTG---GGTGCTGCCGTCTGGCGGTGTCAGTCTCTGGTCATTCGGTGCACCCCTTTAC	1008
Qy	384	CysArgIlysIysGluGlyLeuAspSerAspValAlaAspSerSerIleLeuThrSerGly	403
Db	1009	AGACGGAGCCAGAGTGACTATGGCGTGGACGCTCATTTGACTCTTCTGCAATGACAGGTGGC	1068
Qy	404	PheGlnProValSerIleIysProSerIysAla-----	414
Db	1069	TTCCAGCAGCTTCAACTTCAAAACAGTCCGCTCAAGCCAAAGAATATCATGGAACTAATGATA	1128
Qy	415	-----AspAsnProHisLeuLeu-----ThrIleGlnProAspLeuSer	427
Db	1129	CAAGAAATATCCTTTGGTAACTCCCTGCTCTCTGAATTCGCCATGCGCCAGCATCTG---	1185
Qy	428	ThrThrThrThrThrTyrGlnGlySerLeuCysProArgGlnAspGlyProSerProIys	447
Db	1186	ACAGTGGCGGACATACAGCGGACCCACTGT---CTGCAGGAC---CCTCTGGACAAG	1239
Qy	448	PheGlnLeuThrAsnGlyHisLeuLeuSerProLeuGly-----	460
Db	1240	GAGCTCATGACAGAGTCTCTCACTCTTTAAACCCCTTTGTTCGGACATCAAAAGTGAAGTCCAG	1299
Qy	460	-----	460
Db	1300	AGCTCGTTCATGTTTCCCTGGGAGTGCTCTGAGAGAGCTGAGTACCACGGCAAGATCAT	1359
Qy	461	-----GlyGlyArgHisThrLeuHisHisSerSerProThrSerGlu	474
Db	1360	TCCAGGACTTTTCCCATGGAAACACACAGCTTTTAGTACAATGCATCCAGAAATAAA	1419
Qy	475	AlaGluGluPheValSerArgLeuSerThrGlnAsnTyrPheArgSerLeuProArgGly	494
Db	1420	ATG---CCCTACATCAAAATCTGTCA-----TCACCTCCCCACAAGG	1458
Qy	495	ThrSerAsnMetThrTyrGlyThrPheAsnPheLeuGlyGlyArgLeuMetIleProAsn	514
Db	1459	ACAGAACTGAGGACAACTGGTGTCTTTGGCCATTTAGGGGGGCGCTTAGTAATGCCAAAT	1518
Qy	515	ThrGlyIleSerLeuLeuIleProProAspAlaIleProArgGlyIysIleTyrGluIle	534
Db	1519	ACAGGGGTGAGCTTACTCATACCACAGGTGCCATCCAGAGGAGAGAATTTCTGGGAGATT	1578
Qy	535	TyrLeuThrLeuHisIlysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeu	554
Db	1579	TATATGTTCATCAACCAAGGTGAACCC---AGCCTCCAGTCAGATGGCTCTCAGGTGCTC	1635
Qy	555	LeuSerProIleValSerCysGlyProProGlyValLeuLeuThrArgProValIleLeu	574
Db	1636	CTGAGTCTTGAGTACCTGTGTCTTCAGACATGATCGTCACCACTCCCTTTGCATTG	1695
Qy	575	AlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArgLeuIlysGln	594

Db	1596	ACCATCCGCACTGCGAGATGTCAGTTCTGAGCATTTGGAAATATCCAAATTTAAAGACAGG	1751
Qy	595	SerCysGluGlySerTrpGluAspValLeuHisLeuGlyGluGluAlaProSerHisLeu	614
Db	1756	ACACAGCAGGCGAAATGGAGGAAGTGTGTCAGTGGAGATGAATCTACATCC-----	1809
Qy	615	TyrTyrCysGlnLeuGluAlaSerAlaCysTyrValPheThrGluGlnLeuGlyArgPhe	634
Db	1810	TGTTACTGCGCTTTTGGACCCCTTTGCGGTGTCATGTCCTCGGACAGCTTTGGACCAT	1869
Qy	635	AlaLeuValGlyGluAlaLeuSerValAlaAlaAlaLysArgLeuLysLeuLeuPhe	654
Db	1870	GCGCTCACTGGAGGCCAATCACAGACTGTGCGGTGAAGCACTGAAGGTGGCGGTTTT	1929
Qy	655	AlaProValAlaCysThrSerLeuGluTyrAsnIleArgValTyrCysLeuHisAspThr	674
Db	1930	GGCTGTCATGCTCTAACTCCCTGGATTCAACTGTAGAGTTTACTGTGTGGACAATACC	1989
Qy	675	HisAspAlaLeuLysGluValValGlnLeuGluLysGlnLeuGlyGlyGlnLeuIleGln	694
Db	1990	CTTTGTGCTATTTCAGGAAGTGTTTCAGATGAAGGCAATCAAGGTGACAGCTCCTGGAA	2049
Qy	695	GluProArgValLeuHisPheLysAspSerTyrHisAsnLeuArgLeuSerIleHisAsp	714
Db	2050	GAACCAAAATTGCTGCATTTCAAAGGGAATACCTTTAGTCTTCAGATTTCTGCTCTTGAT	2109
Qy	715	ValProSerSerLeuTrpLysSerLysLeuLeuValSerTyrGlnGluIleProPheTyr	734
Db	2110	ATTCCTCCCATTTCTCTCGAGAAATTAACCAATCTCACTGCCTGCCAGGAAGTCCCGTCTCC	2169
Qy	735	HisIleTrpAsnGlyThrGlnArgTyrLeuHisCysThrPheThrLeuGluArgValSer	754
Db	2170	CGCGTGTGTGCATACCGCGACGCCCTGCACGTGTGCTCTCTCCCTGGAGCGTTATACG	2229
Qy	755	ProSerThrSerAspLeuAlaCysLysLeuTrpValTrpGlnValGluGlyAspGlyGln	774
Db	2230	CCCCTACCAACCCAGCTGTCTGTCGAAATCTGCATTCGGCAGCTCAAAAGCCATGAACAG	2289
Qy	775	SerPheSerIleAsnPheAsnIleThrLysAspThrArgPheAlaGluLeuLeuAlaLeu	794
Db	2290	ATCTCTCAAGTGCAGACATCAATCTTAGAGAGTGAACGAGAAACCATCATCTTCTTCGCA	2349
Qy	795	GluSerGluAlaGlyValProAlaLeuValGlyProSerAlaPheLysIleProPheLeu	814
Db	2350	CAAGAGCAGCAGCACTTTTCCCTGCACAGCTGGCCCCAAAGCCTTCAAAATTCCTACTCC	2409
Qy	815	IleArgGlnLysIleIleSerSerLeuAspProProCysArgArgGlyAlaAspTrpArg	834
Db	2410	ATCAGACAGCGGATTTGTGTACTATTGTATCCCCCAATGCCAACCAAGCAAGGATGGCAG	2469
Qy	835	ThrLeuAlaGlnLysLeuHisLeuAspSerHisLeuSerPhePheAlaSerLysProSer	854
Db	2470	ATGTTAGCAGAAAAACAGACATCAACAGGAATTTATCTTATTTCGCTACACAAAGTAGC	2529
Qy	855	ProThrAlaMetIleLeuAsnLeuTrpGluAlaArgHisPheProAsnGlyAsnLeuSer	874
Db	2530	CCATCTCTGTCAATTTTGAACCTCTGGGGAAGCTCGTCATCAGCATGATGGTGTACTTGAC	2589
Qy	875	GlnLeuAlaAlaAlaValAlaGlyLeuGlyGlnProAspAlaGlyLeuPheThrValSer	894
Db	2590	TCCCTGCGCTGTGCCCTTTGAAGAGATTTGGGAGGACACACAGGAACCTCTCAACATCTTCA	2649
Qy	895	GluAlaGlu	897
Db	2650	GAATCCCGAC	2658

RESULT 11

US-09-969-532-9

; Sequence 9, Application US/09969532

; Patent No. 6777232

GENERAL INFORMATION:

APPLICANT: walke, D. wade

```

; APPLICANT:  Scoville, John
; TITLE OF INVENTION:  No. 677723261 Human Membrane Proteins and Polynucleotides Encoding
; FILE REFERENCE:  LEX-0244-USA
; CURRENT APPLICATION NUMBER:  US/09/969,532
; CURRENT FILING DATE:  2001-10-02
; PRIOR APPLICATION NUMBER:  US 60/237,280
; PRIOR FILING DATE:  2000-10-02
; NUMBER OF SEQ ID NOS:  33
; SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH:  2736
; TYPE:  DNA
; ORGANISM:  homo sapiens
US-09-969-532-9

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Alignment Scores:		
Pred. No.:	1.21e-163	Length:
Score:	1869.50	Matches:
Percent Similarity:	56.71%	Conservative:
Best Local Similarity:	40.25%	Mismatches:
Query Match:	39.02%	Indels:
DB:	4	Gaps:
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		2736

US-10-624-932C-2 (1-898) x US-09-969-532-9 (1-2736)

Qy	8	TtpProAlaLeuLeuGlyIleValLeuAlaAlaTrpLeuArgGlySer-----	23
Db	49	TGGCTCCCGTGGCTGGG-----CTGTGCTTCTGGCGCAGGAGCAGCGGGCTGCCGGA	102
Qy	24	GlyAlaGlnGlnSerAlaThrValAlaAlaAsnProValProGlyAlaAlaAsnProAspLeuLeu	43
Db	103	GGAACTGACATGGCGAAGCCCTTCCCGAATCCATCCATCAGCT---CTGGGACACTG	159
Qy	44	ProHisPheLeuValGluProGluAspValTyrIleValIysAsnIysProoValLeuLeu	63
Db	160	CCTCATTTTCATAGAGGACCGCATGCTTATATATATCAAGAGCAACCCCTATTGGCACTC	219
Qy	64	ValCysLeuAlaValProAlaThrGlnIlePhePheIysCysAsnGlyGluTrpValArg	83
Db	220	AGGTGCNAAGCGAGCGCAGCCATGCAGATATCTTCAANTGCACGCGAGTGGTCCAT	279
Qy	84	GlnValAspHisValIleGluArgSerThrAspGlySerSerGlyLeuProThrMetGlu	103
Db	280	CAGAACGAGCAGCTCTCTGAAGAGACTCTGCAGAGAGCTCAGGTTTGAAGGTCGCGAA	339
Qy	104	ValArgIleAsnValSerArgGlnGlnValGluIysValPheGlyLeuGluGluTyrTrp	123
Db	340	GTGTTCATCAATGTTCATAGGCAACAGGTGGAGGACTTCCATGGCGCCGAGGACTATTGG	399
Qy	124	CysGlnCysValAlaTrpSerSerGlyThrThrLysSerGlnLysAlaTyrIleArg	143
Db	400	TGCCAGTGTGTGGCTGGAGCCACTGGGTACCTCCAAGAGCAGGAAGGCCTCTGTGCGC	459
Qy	144	IleAlaArgLeuArgLysAsnPheGluGlnProLeuAlaIysGluValSerLeuGlu	163
Db	460	ATAGCTTATTTCAGGAAAACTTTGAACAGACCCCAAGGAAGGAAGTTCCCATTTGAA	519
Qy	164	GlnGlyIleValLeuProCysArgProProGluGlyIleProProAlaGluValGluTrp	183
Db	520	GGCATGATTGTACTGCACTGCGGCCCAACAGAGGGAGTCCCTGTGTCGAGGTGGAAATGG	579
Qy	184	LeuArgAsnGluAspLeuValAspProSerLeuAspProAsnValTyrIleThrArgGlu	203
Db	580	CTGAAAAATGAAGAGCCCATTTGACTCTGAAACAGACGAGAACATTTGACACAGCGGCTGAC	639
Qy	204	HisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysValAla	223
Db	640	CATACTGATCATCAGGCAGCAGCGCTCTCGACTCAGGAANAATTACACTGCATGCGCA	699
Qy	224	LysAsnIleValAlaArgArgSerAlaSerAlaValIleValTyrValAsnGly	243
Db	700	GCCAACATCGTGGCTTAAGAGGAGAAGCCGTCTCGGCCACTGTTGTGGTCTACGTGGATGGG	759

Qy	282	GlulGlyGlnAsnValGlnIysThrAlaCysAlaThrLeuCysProValAspGlySerTrp	301
Db	105	-----	105
Qy	302	SerProTrpSerLysTrpSerAlaCysGlyLeuAspCysThrHisTrpArgSerArgGlu	321
Db	106	-----	106
Qy	322	CysSerAspProAlaProArgAsnGlyGlyGluGluCysGlnGlyThrAspLeuAspThr	341
Db	133	TGCACAGCACCACCCCCGAGAAATGGGGCCAAATTCCTGTGAAGGTCTAAGCCAGGAATCT	192
Qy	342	ArgAsnCysThrSerAspLeuCysVal-----	350
Db	193	GAATAACTGCACAGATGGTCTTTGCATCTCTAGATAAAAAACCTTTCATGAATAAAAACCC	252
Qy	351	HisSerAlaSerGlyProGluAspValAlaLeuTyrValGlyLeuIleAlaValAlaVal	370
Db	253	CAAAAGCATTTGAGATGCCAGCGACATTCCTTTGTACTCGGGCTTG---GGTGCTGCCGTC	309
Qy	371	CysLeuValLeuLeuLeuValLeuIleLeuValTyrCysArgLysLysGluGlyLeu	390
Db	310	GTGCCCGTTGCAGTCTCTGGTCTACCTGGTGTCCACCTTTACAGACGGAGCCAGAGTACTAT	369
Qy	391	AspSerAspValAlaAspSerSerIleLeuThrSerGlyPheGlnProValSerIleLys	410
Db	370	GGCTGGACGTCATTGATCTCTTCGATTTGACAGTGCGCTTCCAGACCTTCAACTTCAAA	429
Qy	411	ProSerLysAlaAspAsnProHisLeuLeu-----ThrIleGlnProAspLeuSerThr	428
Db	430	ACAGTCGCGTCAAGGTAACTCCCTGCTCTCGAATTCGCGACGAGCAGATCTG---ACA	486
Qy	429	ThrThrThrThrThrGlnGlySerLeuCysProArgGlnAspGlyProSerProLysPhe	448
Db	487	GTGAGCCGGACATACAGCGGACCCATCTGT---CTGCAGGAC---CCTCTGGACAAGAG	540
Qy	449	GlnLeuThrAsnGlyHisLeuLeuSerProLeuGly-----	460
Db	541	CTCATGACAGAGTCTCACTCTTTAAACCCTTTGTGCGGACATCAAGTGAAGTCCAGAGC	600
Qy	460	-----	460
Db	601	TCGTTTCATGGTTTCCCTGGGAGTGCTCGAGAGAGCTGAGTACCACGCGCAAGAATCATTC	660
Qy	461	-----GlyGlyArgHisThrLeuHisHisSerSerProThrSerSerGluAla	475
Db	661	AGGACTTTTCCCAATGGAAAACAACACAGACTTTAGTACAATGTCATCCAGAAATAAAATG	720
Qy	476	GlulGluPheValSerArgLeuSerThrGlnAsnTyrPheArgSerLeuProArgGlyThr	495
Db	721	---CCCTACATCCAAATCTGTCA-----TCACTCCCCCAAGGACA	759
Qy	496	SerAsnMetThrTyrGlyThrPheAsnPheLeuGlyGlyArgLeuMetIleProAsnThr	515
Db	760	GAACCTGAGGACAACCTGGTGTCTTTGGCCATTTAGGGGGCGCTTTAGTAATGCCAAATACA	819
Qy	516	GlyIleSerLeuLeuIleProProAspAlaIleProArgGlyLysIleTyrGluIleTyr	535
Db	820	GGGTGTAGCTTACTCATACCAACGCGTGCCATCCAGAGGAGAAATCTCTGGAGATTAT	879
Qy	536	LeuThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeuLeu	555
Db	880	ATGTCCATCAACCAAGGTGAACCC---AGCCTCAGTCAGATGGCTCTGAGGTGCTCTCTG	936
Qy	556	SerProIleValSerCysGlyProProGlyValLeuLeuThrArgProValIleLeuAla	575
Db	937	AGTCCTGAAGTCACTGTGGTCTCCAGACATGATCGTCAACCTCCCTCTTGCACTTGACC	996
Qy	576	MetaAspHisCysGlyGluProSerProAspSerTrpSerLeuArgLeuLysLysGlnSer	595
Db	997	ATCCCGCACTGTGCAGATGTCACTGTGAGCATTTGAATTCATTTAAAGACAGAGACA	1056

Qy	596	CysGluClySerTrpGluAspValLeuHisLeuGlyGluGluAlaProSerHisLeuTyr	615
Db	1057	CAGCAGGCGAAATGGGAGGAAGTGAATTCAGTGGGAAGATGAATTCACATCC	
Qy	616	TyrCysGlnLeuGluAlaSerAlaCysTyrValPheThrGlnGlnLeuGlyArgPheAla	635
Db	1111	TACTGCGCTTTTGACCCCTTTGGGTGTCATGTCTCTCGACAGACTTTGGGACCTATGGG	1170
Qy	636	LeuValGlyGluAlaLeuSerValAlaAlaAlaLysArgLeuLysLeuLeuLeuPheAla	655
Db	1171	CTCACTGGAGAGCAATCAAGACTGTGCGTGAAGCAACTGAAGGTGCGGCTTTTGGC	1230
Qy	656	ProValAlaCysThrSerLeuGluTyrAsnIleArgValTyrCysLeuHisAspThrHis	675
Db	1231	TGCATGTCTCTGAATCCCTCGGATTAACAATTGAGAGTTTACTGTGTGGACAATCCCT	1290
Qy	676	AspAlaLeuLysGluValValGlnLeuGluLysGlnLeuGlyGlnLeuLeuGlnGlu	695
Db	1291	TGTGCATTTTCAGAGAGTGGTTTCAGATGAAGGCATCAAGGTGGACAGCTCTCTGGANGAA	1350
Qy	696	ProArgValLeuHisPheLysAspSerTyrHisAsnLeuArgLeuSerIleHisAspVal	715
Db	1351	CCAAATTTGTCATTTCAAAGGGAATCACTTTAGTCTTCAGATTTCTGCTCTGATATT	1410
Qy	716	ProSerSerLeuTrpLysSerLysLeuLeuValSerTyrGlnGluLeuProPheTyrHis	735
Db	1411	CCCCCATTCCTCGGAGATTAAACCATTCACCTGCGCTGCAGAAATCCCGTTCTCCCGC	1470
Qy	736	IleTrpAsnGlyThrGlnArgTyrLeuHisCysThrPheThrLeuGluArgValSerPro	755
Db	1471	GTGTGTGCAGTAACCGGCAGCCCTTGCACTGTGCTTCTCCTCGAGGGTTATACGCC	1530
Qy	756	SerThrSerAspLeuAlaCysLysLeuTrpValTrpGlnValGluGlyAspGlyGlnSer	775
Db	1531	ACTACCACCAGCTGTCTGCAAAATCTCATTCGCGAGCTCAAAGGCCATGAACAGATC	1590
Qy	776	PheSerIleAsnPheAsnIleThrLysAspThrArgPheAlaGluLeuLeuAlaLeuGlu	795
Db	1591	CTCCAAATGAGACATCAATCTCTAGAGAGTGAACAGAGAACCATCACTTTCTTCGCACAA	1650
Qy	796	SerGluAlaGlyValProAlaLeuValGlyProSerAlaPheLysIleProPheLeuIle	815
Db	1651	GAGCAGACGACTTTCCTGCACAGACTGGCCCCAAAGCCTTCAAAATTTCCCTTACTCCATC	1710
Qy	816	ArgGlnLysIleIleSerSerLeuAspProProCysArgArgGlyAlaAspTrpArgThr	835
Db	1711	AGACAGCGGATTGTGCTACATTTGNTATACCCCAATGCCAAGGCAAGGACTGGCAGATG	1770
Qy	836	LeuAlaGlnLysLeuHisLeuAspSerHisLeuSerPhePheAlaSerLysProSerPro	855
Db	1771	TTAGCACAGAAAACAGCATCAACAGGATTTATCTTATTTTCGCTACACAAGTAGTACCCA	1830
Qy	856	ThrAlaMetIleLeuAsnLeuTrpGluAlaArgHisPheProAsnGlyAsnLeuSerGln	875
Db	1831	TCGTGTCATTTTGAACCTGTGGAGAGCTGCTCATCAGCATGATGGTGTATCTTGACTCC	1890
Qy	876	LeuAlaAlaValAlaGlyLeuGlyGlnProAspAlaGlyLeuPheThrValSerGlu	895
Db	1891	CTGGCCTGTGCCCTTGAAGAGATTGGGAGGACACACAGAAACTCTCAACATTTTCAGAA	1950
Qy	896	AlaGlu	897
Db	1951	TCCAG	1956

RESULT 15

US-09-969-532-27

00 03 303 332 27
; Sequence 27, Application US/09969532

; Patent No. 6777232

; GENERAL INFORMATION:

APPLICANT: walke, D. Wade

APPLICANT: Scoville, John

TITLE OF INVENTION: No. 6777232e1 Human Membrane Proteins and Polynucleotides Encoding

FILE REFERENCE: LEX-0244-USA

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; CURRENT APPLICATION NUMBER: US/09/969,532
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 2010
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-969-532-27

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Alignment Scores:

Pred. No.:	2.08e-105	Length:	2010
Score:	1242.50	Matches:	262
Percent Similarity:	53.79%	Conservative:	128
Best Local Similarity:	36.14%	Mismatches:	216
Query Match:	25.93%	Indels:	119
DB:	4	Gaps:	12

US-10-624-932C-2 (1-898) x US-09-969-532-27 (1-2010)

Qy	222	ValAlaLysAsnIleValAlaAargArgSerAlaSerAlaValIleValTyrVal	241
Db	1	ATGGCAGCCAAACATCGTGCTAAGAGGAGAAGCTGTGGCCACTGTTGTGTCTACGTG	60
Qy	242	AsnGlyGlyTrpSerThrTrpThrGlnTrpSerValCysSerAlaSerCysGlyArgGly	261
Db	61	GATGGGAGCTGGGAAGTGTGGAGCAATGGTCCGTGCGATCCA	105
Qy	262	TrpGlnLysArgSerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCys	281
Db	105	-----	105
Qy	282	GlucGlyGlnAsnValGlnLysThrAlaCysAlaThrLeuCysProValAspGlySerTrp	301
Db	105	-----	105
Qy	302	SerProTrpSerLysTrpSerAlaCysGlyLeuAspCysThrHisTrpArgSerArgGlu	321
Db	106	-----GAGTGTGAACATTTGCCGATCCGGAG	132
Qy	322	CysSerAspProAlaProArgAsnGlyGlyGluCysGlnGlyThrAspLeuAspThr	341
Db	133	TGCACAGCACCCCGGAGAAATGGGGCAAAATCTGTGNAGTCTAAGCCAGGAATCT	192
Qy	342	ArgAsnCysThrSerAspLeuCysValHisSerAlaSerGlyProGluAspValAlaLeu	361
Db	193	GA AAACTGCACAGATGGTCTTTGGCATCTGAGCATTCGACGCGACATTTGCTTTG	252
Qy	362	TyrValGlyLeuIleAlaValAlaValCysLeuValLeuLeuLeuValLeuIleLeu	381
Db	253	TACTCGGGTTG---GGTGCTGCCGTGTCGCCGTGCAGTCTCTGGTTCATTGGTGTCA	309
Qy	382	ValTyrCysArgLysGluGlyLeuAspSerAspValAlaAspSerIleLeuThr	401
Db	310	CTTTACAGACGGAGCCAGAGTGACTATGGCGTGACGTCATTGACTCTTCTGCATTG	369
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Qy	415	-----AspAsnProHisLeuLeu-----ThrIleGlnProAsp	425
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Qy 793 AlaLeuGluSerGluAlaGlyValProAlaLeuValGlyProSerAlaPheLysIlePro 812
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1651 TTCGACAAAGAGGACAGCACCTTCCCTGACAGACTGGCCCCAAAGCCTTCAAAATTCCC 1710

Qy 813 PheLeuIleArgGlnLysIleIleSerSerLeuAspProProCysArgArgGlyAlaAsp 832
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1711 TACTCCATCAGACAGCGGATTGTGCTACATTGATACCCCAATGCCAAAGGCAAGGAC 1770

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1771 TGGCAGATGTAGCACAGAAAACAGCATCACAGGATTATCTTATTTGCGCTACACAA 1830

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Qy 873 LeuSerGlnLeuAlaAlaValAlaGlyLeuGlyGlnProAspAlaGlyLeuPheThr 892
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Job time : 579 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 8, 2005, 09:12:06 ; Search time 3771 Seconds
(without alignments)
1543.656 Million cell updates/sec

Title: US-10-624-932C-2
Perfect score: 4791
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Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 7297361 seqs, 3241162794 residues

Total number of hits satisfying chosen parameters: 14594722

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

Command line parameters:

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Database :

- Published Applications NA:*
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 - 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
 - 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
 - 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
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 - 16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
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 - 21: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq:*
 - 22: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
 - 23: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq:*
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 - 25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
 - 26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4791	100.0	2752	10	US-09-918-779-1 Sequence 1, Appli
2	4791	100.0	2752	18	US-10-624-932-1 Sequence 1, Appli
3	4698.5	98.1	2881	10	US-09-970-944-1 Sequence 15, Appl
4	4638	96.8	2697	16	US-10-240-154-15 Sequence 1, Appli
5	4638	96.8	3014	10	US-09-933-261-1 Sequence 1, Appli
6	4638	96.8	3014	14	US-10-256-702-1 Sequence 1, Appli
7	4413	92.1	3561	20	US-10-643-795A-77 Sequence 77, Appl
8	4413	92.1	3561	21	US-10-948-518-77 Sequence 77, Appl
9	4413	92.1	3580	17	US-10-311-623-13 Sequence 13, Appl
10	2710	56.6	1787	10	US-09-933-261-2 Sequence 2, Appli
11	2710	56.6	1787	14	US-10-256-702-2 Sequence 2, Appli
12	2572.5	53.7	3866	21	US-10-764-420-2213 Sequence 2213, Ap
13	2563.5	53.5	2860	17	US-10-087-684-1 Sequence 1, Appli
14	2563.5	53.5	2860	17	US-10-087-684-3 Sequence 3, Appli
15	2563.5	53.5	2860	17	US-10-087-684-1 Sequence 1, Appli
16	2563.5	53.5	2860	17	US-10-218-779-1 Sequence 3, Appli
17	2558.5	53.4	3485	9	US-09-816-828-18 Sequence 18, Appl
18	2558.5	53.4	3884	14	US-10-028-072-145 Sequence 145, App
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29	2558.5	53.4	3884	14	US-10-143-114-145 Sequence 145, App
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ALIGNMENTS

RESULT 1
US-09-918-779-1
; Sequence 1, Application US/09918779
; Publication No. US20030064369A1
; GENERAL INFORMATION:
; APPLICANT: Taupier, Raymond
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Rastelli, Luca
; APPLICANT: Spaderna, Steven
; APPLICANT: Shimkets, Richard
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Sytek, Kimberly
; APPLICANT: Shenoy, Suresh
; APPLICANT: Li, Li
; APPLICANT: Gusev, Vladimir
; APPLICANT: Grosse, William

APPLICANT: Alsobrook, John
APPLICANT: Lepley, Denise
APPLICANT: Burgess, Catherine
APPLICANT: Gerlach, Valerie
APPLICANT: Ellerman, Karen
APPLICANT: MacDougall, John
APPLICANT: Stone, David
APPLICANT: Smithson, Glenda
TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-074 US
CURRENT APPLICATION NUMBER: US/09/918,779
CURRENT FILING DATE: 2001-07-30
PRIORITY APPLICATION NUMBER: 60/221,409
PRIORITY FILING DATE: 2000-07-28
PRIORITY APPLICATION NUMBER: 60/222,840
PRIORITY FILING DATE: 2000-08-04
PRIORITY APPLICATION NUMBER: 60/223,752
PRIORITY FILING DATE: 2000-08-08
PRIORITY APPLICATION NUMBER: 60/223,762
PRIORITY FILING DATE: 2000-08-08
PRIORITY APPLICATION NUMBER: 60/223,770
PRIORITY FILING DATE: 2000-08-08
PRIORITY APPLICATION NUMBER: 60/223,769
PRIORITY FILING DATE: 2000-08-08
PRIORITY APPLICATION NUMBER: 60/225,146
PRIORITY FILING DATE: 2000-08-14
PRIORITY APPLICATION NUMBER: 60/225,392
PRIORITY FILING DATE: 2000-08-15
PRIORITY APPLICATION NUMBER: 60/225,470
PRIORITY FILING DATE: 2000-08-15
PRIORITY APPLICATION NUMBER: 60/225,697
PRIORITY FILING DATE: 2000-08-16
PRIORITY APPLICATION NUMBER: 60/263,662
PRIORITY FILING DATE: 2001-02-01
PRIORITY APPLICATION NUMBER: 60/281,645
PRIORITY FILING DATE: 2001-04-05
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn ver. 2.1
SEQ ID NO 1
LENGTH: 2752
TYPE: DNA
ORGANISM: Homo sapiens
US-09-918-779-1

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Score: 4791.00 Matches: 898
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-624-932C-2 (1-898) x US-09-918-779-1 (1-2752)

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Db 106 CGCGGCTCGGGTGGCCAGAGAGTGCCACCGTGGCCNACCAGTGGCTGTGGCCNACCCG 165
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RESULT 2

US-10-624-932-1
; Sequence 1, Application US/10624932
; Publication No. US20040096877A1

GENERAL INFORMATION:

; APPLICANT: Taupier, Raymond
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Rastelli, Luca
; APPLICANT: Spaderna, Steven
; APPLICANT: Shimkets, Richard
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Spytek, Kimberly
; APPLICANT: Shenoy, Suresh
; APPLICANT: Li, Li
; APPLICANT: Gusev, Vladimir
; APPLICANT: Grosse, William
; APPLICANT: Alebrook, John
; APPLICANT: Lepley, Denise
; APPLICANT: Burgess, Catherine
; APPLICANT: Gerlach, Valerie
; APPLICANT: Ellerman, Karen
; APPLICANT: MacDougall, John
; APPLICANT: Stone, David
; APPLICANT: Smithson, Glenda

; TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same

; FILE REFERENCES: 21402-074 US

; CURRENT APPLICATION NUMBER: US/10/624,932

; CURRENT FILING DATE: 2003-07-21

; PRIOR APPLICATION NUMBER: 09/918,779

; PRIOR FILING DATE: 2001-07-03

; PRIOR APPLICATION NUMBER: 60/221,409

; PRIOR FILING DATE: 2000-07-28

; PRIOR APPLICATION NUMBER: 60/222,840

; PRIOR FILING DATE: 2000-08-04

; PRIOR APPLICATION NUMBER: 60/223,752

; PRIOR FILING DATE: 2000-08-08

; PRIOR APPLICATION NUMBER: 60/223,762

; PRIOR FILING DATE: 2000-08-08

; PRIOR APPLICATION NUMBER: 60/223,770

; PRIOR FILING DATE: 2000-08-08

; PRIOR APPLICATION NUMBER: 60/223,769

; PRIOR FILING DATE: 2000-08-08

; PRIOR APPLICATION NUMBER: 60/225,146

; PRIOR FILING DATE: 2000-08-14

; PRIOR APPLICATION NUMBER: 60/225,392

; PRIOR FILING DATE: 2000-08-15

; PRIOR APPLICATION NUMBER: 60/225,470

; PRIOR FILING DATE: 2000-08-15

; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 61

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1

; LENGTH: 2752

; TYPE: DNA

; ORGANISM: Homo sapiens

; US-10-624-932-1

Alignment Scores:

Pred. No.:	0	Length:	2752
Score:	4791.00	Matches:	898
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	18	Gaps:	0
US-10-624-932c-2 (1-898) x US-10-624-932-1 (1-2752)			
Qy	1	MetAlaValArgProGlyLeuTrpProAlaLeuLeuGlyIleValLeuAlaAaTrpLeu	20
Db	46	ATGGCCGTCGCCGCCGCGCTGTGGCAGCGCTCTCTGGCATAGTCTCGCGCGTGGCTC	105
Qy	21	ArgGlySerGlyAlaGlnGlnSerAlaThrValAlaAaenProValProGlyAlaAaenPro	40
Db	106	CGCGGCTCGGGTGCACAGAGAGTGCACCGCTGGCCAAACCCAGTGGCTGGTGCACCCG	165
Qy	41	AspLeuLeuProHisPheLeuValGluProGluAspValTyrIleValLysAaenLysPro	60
Db	166	GACCTGCTTCCCACTTCTCTGGTGGAGCCCGAGATGTGTACATCTGTCAAGAACAGCCA	225
Qy	61	ValLeuLeuValCysLysAlaValProAlaThrGlnIlePhePheLysCysAaenGlyGlu	80
Db	226	GTGCTGCTGTGTCAAGCGCTGCCCGCCACGCAGATCTTCTCAAGTGCACAGGGAG	285
Qy	81	TrpValArgGlnValAspHisValIleGluArgSerThrAspGlySerSerGlyLeuPro	100
Db	286	TGGGTGCGCCAGGTGGACCAACGTGATCGAGCGAGCACAGACGGGAGCAGTGGGCTGCC	345
Qy	101	ThrMetGluValArgIleAaenValSerArgGlnGlnValGluLysValPheGlyLeuGlu	120
Db	346	ACCATGAGGTTCGCATTATGTCTCAAGCAGCAGGTCCAGAGGTTCGGGCTGGAG	405
Qy	121	GluTyrTrpCysGlnCysValAlaTrpSerSerGlyThrThrLysSerGlnLysAla	140
Db	406	GAATACTGGTCCAGTGGCATGTGAGTCTCTCGGGCACCAACCAAGAGTCAAGAGGCC	465
Qy	141	TyrIleArgIleAlaArgLeuArgLysAaenPheGluGlnGluProLeuAlaLysGluVal	160
Db	466	TACATCCGCATAGCCAGATTGCCAGAACTTCAGCAGAGAGCGCTGGCCAAAGAGGTG	525
Qy	161	SerLeuGluGlnGlyIleValLeuProCysArgProGluGlyIleProProAlaGlu	180
Db	526	TCCTTGAGCAGGGCATCGTGTCTGCTGCCCTGCCAGCGAGGGCATCCCTCCAGCGGAG	585
Qy	181	ValGluTrpLeuArgAaenGluAspLeuValAspProSerLeuAspProAaenValTyrIle	200
Db	586	GTGGAGTGGCTCCGGAACGAGGACCTGGTGGACCCCGTCCCTGGACCCCAATGTATACATC	645
Qy	201	ThrArgGluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAaenTyrThr	220
Db	646	ACGCGGAGCACAGCTGGTGGTGGCAGAGCCCGCTTGTCTACACGCGCAACTACACC	705
Qy	221	CysValAlaLysAaenIleValAlaArgArgSerAlaSerAlaAlaValIleValTyr	240
Db	706	TGGTGGCCAAAGAACATCTGGGCACGTCCGCGCAGCGCTCCGCTGCTGTCTATCTCTAC	765
Qy	241	ValAaenGlyGlyTrpSerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArg	260
Db	766	GTGAACGGTGGTGGTGCAGCTGGACCGAGTGGTCTGCTGTCAGCGCGCAGCTGTGGGCGC	825
Qy	261	GlyTrpGlnLysArgSerArgSerCysThrAsnProAlaProLeuAaenGlyAlaPhe	280
Db	826	GGCTGGCAGAAACGGAGCCGGAGCTGCACCAACCCCGCGCTCTCAACGGGGCGCTTTC	885
Qy	281	CysGluGlyGlnAaenValGlnLysThrAlaCysAlaThrLeuCysProValAspGlySer	300
Db	886	TGTGAGGGGCGAATGTCCAGAAAAACAGCCTGGCGCCACCCTGTGCCAGTAGAGCGGAGC	945
Qy	301	TrpSerProTrpSerLysTrpSerAlaCysGlyLeuAspCysThrHisTrpArgSerArg	320
Db	946	TGGAGCCCGTGGAGCAAGTGGTGGCGCTGTGGGTGGACTGCGACCCCACTGGCGGAGCGGT	1005
Qy	321	GluCysSerAspProAlaProArgAaenGlyGlyGluGluCysGlnGlyThrAspLeuAsp	340
Db	1006	GAGTGTCTGTACCCAGCACCCCGCAACGGAGGGGAGAGTGGCCAGGGCACTGTACCTGGAC	1065
Qy	341	ThrArgAaenCysThrSerAspLeuCysValHisSerAlaSerGlyProGluAspValAla	360
Db	1066	ACCGCAACTGTACACAGTGCACCTCTGTGTACACAGTGTCTTGGCCCTGAGGAGTGGCC	1125
Qy	361	LeuTyrValGlyLeuIleAlaValAlaValCysLeuValLeuLeuLeuValLeuIle	380
Db	1126	CTCTATGTGGGCTCATCGCGGTGGCGCTGTGCTGTCTGTCTGTCTGTCTGTCTCATC	1185
Qy	381	LeuValTyrCysArgLysLysGluLysLeuAspSerAspValAlaAspSerSerIleLeu	400
Db	1186	CTCGTTTATTTGCCGGAAGAGGAGGGGCTGGACTCAGATGTGGCTGACTGCTCATTTCTC	1245
Qy	401	ThrSerGlyPheGlnProValSerIleLysProSerLysAlaAspAaenProHisLeuLeu	420
Db	1246	ACCTCAGGCTTCCAGCCGCTCAGCATCAAGCCAGCAAGAGCAGACACCCCATCTGTCTC	1305
Qy	421	ThrIleGlnProAspLeuSerThrThrThrThrTyrThrTyrGlnGlySerLeuCysProArg	440
Db	1306	ACCATCCAGCGGACCTCAGCACCAACCACTAGCCAGGGCAGTCTCTGTCCCGG	1365
Qy	441	GlnAspGlyProSerProLysPheGlnLeuThrAaenGlyHisLeuLeuSerProLeuGly	460
Db	1366	CAGGATGGGCGCCAGCCCCAAGTTCCAGCTCACCAATGGGCGACCTGTACAGCCCCCTGGGT	1425
Qy	461	GlyGlyArgHisThrLeuHisHisSerSerProThrSerGluAlaGluGluPheValSer	480
Db	1426	GGCGGCGCCGCACACACTGCACACACACTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCC	1485
Qy	481	ArgLeuSerThrGlnAaenTyrPheArgSerLeuProArgGlyThrSerAaenMetThrTyr	500
Db	1486	CGCTCTCCACCCAGAACTACTTCCGCTCCCTGCCCGGAGGACCAACAGCATGACCTAT	1545
Qy	501	GlyThrPheAsnPheLeuGlyArgLeuMetIleProAsnThrGlyIleSerLeuLeu	520
Db	1546	GGGACCTTCAACTTCTCTGGGGGCGGGCTGATGATCCCTAATACAGGTATCAGCCCTCCTC	1605
Qy	521	IleProProAspAlaIleProArgGlyLysIleTyrGluIleTyrLeuThrLeuHisLys	540
Db	1606	ATCCCCCAGATGCCATACCCCGAGGGAAGATCTATGAGATCTACCTCAGCTGCACAG	1665
Qy	541	ProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeuLeuSerProIleValSer	560
Db	1666	CCGGAAGAGCTGAGGTTCGCCCTAGCTGGCTGTTCAGACCTGTGAGTCCCATCTGTAGC	1725
Qy	561	CysGlyProProGlyValLeuLeuThrArgProValIleLeuAlaMetAspHisCysGly	580
Db	1726	TGTGGACCCCTGGCGCTCTGTCTCACCCGCGCAGTCTCTGGCTATGACCACTGTGGG	1785
Qy	581	GluProSerProAspSerTrpSerLeuArgLeuLysLysGlnSerCysGluGlySerTrp	600
Db	1786	GAGCCCGCCCTGCACAGCTGGAGCTTGCGCTCAAAAAGCAGCTGTCGCGAGGCGCAGCTGG	1845
Qy	601	GluAspValLeuHisLeuGlyGluAlaProSerHisLeuTyrTyrCysGlnLeuGlu	620
Db	1846	GAGGATGTCTGCACCTGGCGGAGGAGGCGCCCTCCACCTCTACTACTGCCAGCTGGAG	1905
Qy	621	AlaSerAlaCysTyrValPheThrGluGlnLeuGlyArgPheAlaLeuValGluAla	640
Db	1906	GCCAGTGTCTGTACGTCTTCCCGAGCAGCTGGGCGCTTTTGCCCTGTGGAGAGGCC	1965
Qy	641	LeuSerValAlaAlaAlaLysArgLeuLysLeuLeuLeuPheAlaProValAlaCysThr	660
Db	1966	CTCAGGCTGTCTGCCCAAGCGCTCAAGCTGCTTCTGTGGCGCGGTGGCGCTGCACC	2025
Qy	661	SerLeuGluTyrAaenIleArgValTyrCysLeuHisAspThrHisAspAlaLeuLysGlu	680
Db	2026	TCCCTCGAGTCAACATCCGGGTCTACTGCTGTCATGACACCCACCATGCTCAAGGAG	2085
Qy	681	ValValGlnLeuGluLysGlnLeuGlyGlyGlnLeuIleGlnLeuProArgValLeuHis	700

Db 2086 GTGGTGCAGCTGGAGAGCAGCTGGGGGACAGCTGATCCAGGAGCCACCGGCTCTGCAC 2145
Qy 701 PheLysAspSerTyrHisAsnLeuArgLeuSerIleHisAspValProSerSerLeuTyr 720
Db 2146 TTCAGGACAGTATACCAACACTGGCCCTATCCATCCACGATGTGCCAGCTCCCTGTGG 2205
Qy 721 LysSerLysLeuValSerTyrGlnGluIleProPheTyrHisIleTyrAsnGlyThr 740
Db 2206 AAGAGTAAGCTCCCTGTGTCAGCTACAGGAGATCCCTTTTATCATCATCTGGAATGGCAG 2265
Qy 741 GlnArgTyrLeuHisCysThrPheThrLeuGluArgValSerProSerThrSerAspLeu 760
Db 2266 CAGCGGTACTTGCACATGCACCTTCCCTGGAGGGTGTTCAGCCCGCAGCACTAGTGCAGCTG 2325
Qy 761 AlaCysLysLeuTyrValTyrGlnValGluGlyAspGlyGlnSerPheSerIleAsnPhe 780
Db 2326 GCCTGCAAGCTGTGGGTGTGCAGGTGGAGGGCCAGCGGAGAGCTTCAGCATCAACTTC 2385
Qy 781 AsnIleThrLysAspThrArgPheAlaGluLeuLeuAlaLeuGluSerGluAlaGlyVal 800
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Qy 801 ProAlaLeuValGlyProSerAlaPheLysIleProPheLysIleArgGlnLysIleIle 820
Db 2446 CCAGCCCTGTGGGGCCCGCAGTCCCTTCAAGATCCCTTCTCTCATTCGCGCAGAGATAATT 2505
Qy 821 SerSerLeuAspProProCysArgArgGlyAlaAspTyrArgThrLeuAlaGlnLysLeu 840
Db 2506 TCCAGCTGGAGCCACACCTGTAGGCGGGGTGCCACTGGCGGAGCTCTGGGCCCAAGAACTC 2565
Qy 841 HisLeuAspSerHisLeuSerPheAlaSerLysProSerProThrAlaMetIleLeu 860
Db 2566 CACCTGGACAGCATCTCAGCTCTTTGGCTCCAGGCCAGCCCAAGCATGATCTCTC 2625
Qy 861 AsnLeuTyrGluAlaArgHisPheProAsnGlyAsnLeuSerGlnLeuAlaAlaVal 880
Db 2626 AACCTGTGGAGGCGCGCACTTCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTG 2685
Qy 881 AlaGlyLeuGlyGlnProAspAlaGlyLeuPheThrValSerGluAlaGlyCys 898
Db 2686 GCTGGAGTGGGCCAGCCAGCTGGGCTCTTTCACAGTGTGGAGGCTGAGTGC 2739

RESULT 3

US-09-970-944-1
; Sequence 1, Application US/09970944
; Publication No. US20030204052A1
; GENERAL INFORMATION:
; APPLICANT: Herrman, John L
; APPLICANT: Rastelli, Luca
; APPLICANT: Shimkets, Richard A
; TITLE OF INVENTION: No. US20030204052A1el Proteins and Nucleic Acids Encoding Same an
; FILE REFERENCE: 21402-138
; CURRENT APPLICATION NUMBER: US/09/970,944
; CURRENT FILING DATE: 2002-05-02
; PRIOR FILING DATE: 60/237,862
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-970-944-1

Alignment Scores:

Pred. No.: 0 Length: 2881
Score: 4698.50 Matches: 888
Percent Similarity: 98.89% Conservatives: 2
Best Local Similarity: 98.67% Mismatches: 7
Query Match: 98.07% Indels: 3
DB: 10 Gaps: 3

US-10-624-932C-2 (1-898) x US-09-970-944-1 (1-2881)
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Qy 21 ArgGlySerGlyAlaGlnGlnSerAlaThrValAlaAsnProValProGlyValAsnPro 40
Db 147 CGCGGCTCGGGTGGCCAGCAGAGTCCACCGTGGCCAAACCAAGTGCCTTGTGTCACACCG 206
Qy 41 AspLeuLeuProHisPheLeuValGluProGluAspValTyrIleValLysAsnLysPro 60
Db 207 GACCTGCTTCCCCACTTCTTGGTGGAGCCCGGAGATGTGTACATCGTCAAGAACCAAGCCA 266
Qy 61 ValLeuLeuValCysLysAlaValProAlaThrGlnIlePhePheLysCysAsnGlyGlu 80
Db 267 GTGCTGCTTGTGTCAAGGCGCTGCCCGCCACGCGAGATCTTCTTCAAGTGCACCGGGAG 326
Qy 81 TrpValArgGlnValAspHisValIleGluArgSerThrAspGlySerSerGlyLeuPro 100
Db 327 TGGTGGCCCGGCTGGACCGATCGAGCGCAGCAGACAGCGGAGCAGTGTGTAGCCG 386
Qy 101 ThrMetGluValArgIleAsnValSerArgGlnGlnValGluLysValPheGlyLeuGlu 120
Db 387 ACCATGGAGGTCCGCATTATGCTCAAGGCGAGCGAGTCCGAGAGGTTCGGGCTGGAG 446
Qy 121 GluTyrTrpCysGlnCysValAlaTyrPheSerSerSerGlyThrThrLysSerGlnLysAla 140
Db 447 GAATACTGTGGTGGCCAGTGGCATGTGATCGAGCGCAGCAGCAGCGGAGTCAAGAGTCAAGAGCC 506
Qy 141 TyrIleArgIleAlaArgLeuArgLysAsnPheGluGlnGluProLeuAlaLysGluVal 160
Db 507 TACATCCGCTATAGCAGATTTCGCAAGACTTCAGCAGGAGCGCTGGCCCAAGAGGTG 566
Qy 161 SerLeuGluGlnGlyIleValLeuProCysArgProGluGlyIleProProAlaGlu 180
Db 567 TCCTTGGAGCAGGCGCATGCTGCTGCTCCCGTCCACCGGAGGCGCATCCCTCCAGCCGAG 626
Qy 181 ValGluTyrLeuArgAsnGluAspLeuValAspProSerLeuAspProAsnValTyrIle 200
Db 627 GTGGAGTGGCTCCGGAAACGAGGACCTGTGTGGAGCCGCTCCCTGGACCCCAATGTATACATC 686
Qy 201 ThrArgGluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThr 220
Db 687 ACCGCGGAGCAGACCTGTGTGTGGTGGCAGCGCCGCTCTGTGACAGCGCAACTACACC 746
Qy 221 CysValAlaLysAsnIleValAlaArgArgSerAlaSerAlaAlaValIleValTyr 240
Db 747 TGGTGGCCCAAGAACATCGTGGCACGCTGGCGCAGCGCTCCGCTGCTGTCATCGTCTAC 806
Qy 241 ValAsnGlyGlyTyrPheThrThrThrGluTyrSerValCysSerAlaSerCysGlyArg 260
Db 807 GTGAACGGTGGGTGGTGCAGCTGGACCGAGTGGTCCGCTCTGACAGCGCCAGCTGTGGCGGC 866
Qy 261 GlyTyrGlnLysArgSerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPhe 280
Db 867 GGCTGGCAGAACGAGCGCGGAGCTGCACCAACCGCGGCTCTTCAACGGGGGCGCTTTC 926
Qy 281 CysGluGlyGlnAsnVal---GlnLysThrAlaCysAlaThrLeuCysProValAspGly 299
Db 927 TGTGAGGGGCGAGAAATGCCATGACCGCAGCTCTCTCTCTGCTGTGTCTGTGGAGCGC 986
Qy 300 SerTyrSerProTyrPheSerLysTyrSerAlaCysGlyLeuAspCysThrHisTyrArgSer 319
Db 987 AGCTGGAGCCCGTGGAGCAAGTGTGTGGCTGTGGGTGGAGTGCACCCACCGGAGGAGTGCAGCGGAGC 1046
Qy 320 ArgGluCysSerAspProAlaProArgAsnGlyGlyGluCysGlnGlyThrAspLeu 339
Db 1047 CGTGAAGTGTCTGACCCAGCACCACCGGAGGAGGAGTGCAGCGGAGTGCAGCGGAGC 1106
Qy 340 AspThrArgAsnCysThrSerAspLeuCysValHisSerAlaSerGlyProGluAspVal 359

Db 1107 GACACCGCAACTGTACCAAGTACCTCTGTGTACACAGTGTCTTGGCCCTGAGGAGCTG 1166
Qy 360 AlaLeuTyrValGlyLeuIleAlaValAlaValAlaValAlaValAlaValAlaValAlaVal 379
Db 1167 GCCTCTATGTGGGCTCATCGCGCTGTGGCTGTGGCTGTGGCTGTGGCTGTGGCTGTGGCT 1226
Qy 380 IleLeuValTyrCysArgLysGlyLeuAspSerAspValAlaAspSerSerIle 399
Db 1227 ATCTCTGTTATGCCGGAAGAGGGGTTGACTCAGATGTGGCTGACTCGTCAAT 1286
Qy 400 LeuThrSerGlyPheGlnProValSerIleLysProSerLysAlaAspAsnProHisLeu 419
Db 1287 CTCACCTCAGGCTTCCAGCGCTGAGCATCAAGCCAGCAAGAGAGAGAGAGAGAGAGAGAG 1346
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Qy 440 ArgGlnAspGlyProSerProLysPheGlnLeuThrAsnGlyHisLeuLeuSerProLeu 459
Db 1404 CGGAGGATGGCCCGCCAGCCCAAGTTCCAGCTCACCNAATGGGACCTGCTCAGCCCCCTG 1463
Qy 460 GlyGlyArgHisThrLeuHisHisSerSerProThrSerGluAlaGluGluPheVal 479
Db 1464 GGTGGCGCGCCACACACACACACAGCTCTCCCACTCTGAGGCGGAGAGTTGCTC 1523
Qy 480 SerArgLeuSerThrGlnAsnTyrPheArgSerLeuProArgGlyThrSerAsnMetThr 499
Db 1524 TCCCGCTCTCCACCCAGAACTACTTCCGCTCCCTGCGCCGAGGACACAGCAACATGACC 1583
Qy 500 TyrGlyThrPheAsnPheLeuGlyArgLeuMetIleProAsnThrGlyIleSerLeu 519
Db 1584 TATGGGACCTTCAACTTCTCGGGGGCGGCTGATGATCCCTAATACAGGTATCAGCCCT 1643
Qy 520 LeuIleProAspAlaIleProArgGlyLysIleTyrGluIleTyrLeuThrLeuHis 539
Db 1644 CTCATCCCCCAGATGCCATACCCGAGGGAAGATCTATGAGATCTACCTCAGCTGCAC 1703
Qy 540 LysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeuLeuSerProIleVal 559
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Qy 560 SerCysGlyProProGlyValLeuLeuThrArgProValIleLeuAlaMetAspHisCys 579
Db 1764 AGCTGTGACCCCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1823
Qy 580 GlyGluProSerProAspSerTrpSerLeuArgLeuLysGlnSerCysGlyLys 599
Db 1824 GGGAGGCCAGCCCTGACAGCTGGAGCTGCGGCTCAAAAAGCAGTCTGTCGAGGGGAGC 1883
Qy 600 TrpGlu---AspValLeuHisLeuGlyGluAlaProSerHisLeuTyrTyrCysGln 618
Db 1884 TGGAGCAGGATGTGTGACCTTGGGCGAGGAGGCGCCCTCCACCTCTACTACTGCGCAG 1943
Qy 619 LeuGluAlaSerAlaCysTyrValPheThrGluGlnLeuGlyArgPheAlaLeuValGly 638
Db 1944 CTGGAGCCAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2003
Qy 639 GluAlaLeuSerValAlaAlaAlaLysArgLeuLysLeuLeuPheAlaProValAla 658
Db 2004 GAGGCCCTCAGCGTGGCTGCGCCAGCGCTCAAGCTGCTTCTGTTTGGCGCGGTGGCC 2063
Qy 659 CysThrSerLeuGluTyrAsnIleArgValTyrCysLeuHisAspThrHisAspAlaLeu 678
Db 2064 TGACCTCTCCCTCGAGTACAAATCCCGGCTCTACTGCTGCTGCTGCTGCTGCTGCTGCTG 2123
Qy 679 LysGluValValGlnLeuGluLysGlnLeuGlyGlyGlnLeuIleGlnGluProArgVal 698
Db 2124 AAGAGGTGTGAGCTGGAGAGAGCTGGGGGAGCAGTGTATCCAGGAGCCACCGGCTC 2183
Qy 699 LeuHisPheLysAspSerTyrHisAsnLeuArgLeuSerIleHisAspValProSerSer 718
Db 2184 CTGCACCTTCAAGGACAGTTACCAACCTCGCGCTATCCATCCAGATGTGCGCCAGCTCC 2243

Qy 719 LeuTrpLysSerLysLeuLeuValSerTyrGlnGluIleProPheTyrHisIleTrpAsn 738
Db 2244 CTGTGAAGAGTAAAGTCTCTGTGACGTACCAAGAGATCCCCCTTTATCATCATCTGGAAT 2303
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Qy 759 AspLeuAlaCysLysLeuTrpValTrpGlnValGluGlyAspGlyGlnSerPheSerIle 778
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Qy 779 AsnPheAsnIleThrLysAspThrArgPheAlaGluLeuLeuAlaLeuGluSerGluAla 798
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Db 2484 GGGTCCAGCCCTGTGGGCCCGCAGTCTTCAGATCCCTTCCTCATTCGCGCAGAG 2543
Qy 819 IleIleSerSerLeuAspProProCysArgArgGlyAlaAspTrpArgThrLeuAlaGln 838
Db 2544 ATAATTTCCAGCTGACCCACCTGTAGCGGGGTGCCACTGCGGACTCTGGCCAG 2603
Qy 839 LysLeuHisLeuAspSerHisLeuSerPhePheAlaSerLysProSerProThrAlaMet 858
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Qy 859 IleLeuAsnLeuTrpGluAlaArgHisPheProAsnGlyAsnLeuSerGlnLeuAlaAla 878
Db 2664 ATCTCAACTGTGGAGGGGGGCACTTCCCAACGGCACTCAGCCAGCTGGCTGCA 2723
Qy 879 AlaValAlaGlyLeuGlyGlnProAspAlaGlyLeuPheThrValSerGluAlaGluCys 898
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RESULT 4

US-10-240-154-15
; Sequence 15, Application US/10240154
; Publication No. US20030175741A1
; GENERAL INFORMATION:
; APPLICANT: Cochran et al.
; TITLE OF INVENTION: SCHIZOPHRENIA RELATED GENES
; FILE REFERENCE: CKFW-P01-006
; CURRENT APPLICATION NUMBER: US/10/240,154
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: PCT/GB01/01486
; PRIOR FILING DATE: 2001-04-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 2697
; TYPE: DNA
; ORGANISM: Rattus sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2697)
US-10-240-154-15

Alignment Scores:
Pred. No.: 0 Length: 2697
Score: 4338.00 Matches: 862
Percent Similarity: 97.88% Conservative: 17
Best Local Similarity: 95.99% Mismatches: 19
Query Match: 96.81% Indels: 0
DB: 16 Gaps: 0

US-10-624-932C-2 (1-898) x US-10-240-154-15 (1-2697)

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Db 1 ATGGCCGTCCGGCCCGGCTGTGGCCAGTGTCTTCTGGCATAGTCTCTCGCCGCTGCTT 60


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Qy 761 AlaCysLysLeuTrpValTrpGlnValGluGlyAspGlyGlnSerPheSerIleAsnPhe 780
      |||:::|||||
Db 2281 GCCTGCAAGGTGTGGGTGTGGCAGGTGGAGGGAGATGGGCAGAGCTTCAACATCAACTTC 2340
      |||:::|||||
Qy 781 AsnIleThrLysAspThrArgPheAlaGluLeuAlaGluLeuGluSerGluAlaGlyVal 800
      |||:::|||||
Db 2341 AACATCACTAAGGACACAAGGTTTGTGTAATTGTGGCTCTGGAGAGTGAAGGGGGGTC 2400
      |||:::|||||
Qy 801 ProAlaLeuValGlyProSerAlaPheIleValPheIleProPheLeuIleArgGlnIleIle 820
      |||:::|||||
Db 2401 CCAGCCCTGTGGGCCCCAGTGCCTTCAAGATCCCCCTTCATTCGGCAAAAGATCATC 2460
      |||:::|||||
Qy 821 SerSerLeuAspProProCysArgArgGlyAlaAspTrpArgThrLeuAlaGlnLysLeu 840
      |||:::|||||
Db 2461 GCCAGTCTGACCCACCTGCAGCGGGGGCGGAGCTGGGAGAACTCTAGGCCAGAACTT 2520
      |||:::|||||
Qy 841 HisLeuAspSerHisLeuSerPhePheAlaSerIlyProSerProThrAlaMetIleLeu 860
      |||:::|||||
Db 2521 CACCTGGACAGCATCTTAGCTTCTTTTGCCTCCAAGCCCAAGCCCTACAGCCATGATCCTC 2580
      |||:::|||||
Qy 861 AsnLeuTrpGluAlaArgHisPheProAsnGlyAsnLeuSerGlnLeuAlaAlaVal 880
      |||:::|||||
Db 2581 AACCTATGGAGGACAGGCACTTCCCCACGGCAACCTCGGCCAGCTGGCAGAGCTGTG 2640
      |||:::|||||
Qy 881 AlaGlyLeuGlyGlnProAspAlaGlyLeuPheThrValSerGluAlaGluCys 898
      |||:::|||||
Db 2641 GCCGGACTGGGCCAACCAAGATGCTGGCCTCTTCAACGGTGTGGAGGCCGAGTGT 2694
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RESULT 5
US-09-933-261-1
; Sequence 1, Application US/09933261
; Publication No. US20030040046A1
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; Leonardo, E. David
; Hink, Lindsey
; Masu, Masayuki
; Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/933,261
; FILING DATE: 20-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/808,982
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3014 base pairs
; TYPE: nucleic acid
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; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-933-261-1

Alignment Scores:
Pred. No.: 0 Length: 3014
Score: 4638.00 Matches: 862
Percent Similarity: 97.88% Conservatives: 17
Best Local Similarity: 95.99% Mismatches: 19
Query Match: 96.81% Indels: 0
DB: 10 Gaps: 0

US-10-624-932C-2 (1-898) x US-09-933-261-1 (1-3014)

Qy 1 MetAlaValArgProGlyLeuTrpProAlaLeuLeuGlyIleValLeuAlaAaTtpLeu 20
Db 1 ATGGCCGTTCGGCCCGCCCTGTGGCCAGTGTCTCTGGGCATAGTCTCTGCCGCGCTGGCTT 60
Qy 21 ArgGlySerGlyValaglnGlnSerAlaThrValAlaAsnProValProGlyAlaAaPro 40
Db 61 CGTGGTTTCGGGTGCCCCAGCAGAGTGCCACGGTGGCCAATCCAGTGCCTGGTGCACACCCC 120
Qy 41 AspLeuLeuProHisPheLeuValGluProGluAspValTyrIleValLysAsnLysPro 60
Db 121 GACCTGCTGCCACACTTCTGGTAGAGCTGTGGCTGCCACCCAGATCTTCTTCAAGTGCATATGGGAA 180
Qy 61 ValLeuLeuValCysLysAlaValProAlaThrGlnIlePhePheLysCysAsnGlyGlu 80
Db 181 GTGTTGTTGGTGTGCAAGGCTGTGGCTGCCACCCAGATCTTCTTCAAGTGCATATGGGAA 240
Qy 81 TrpValArgGlnValAspHisValIleGluArgSerThrAspGlySerSerGlyLeuPro 100
Db 241 TGGGTCCGCCAGGTGCATCACGTAATTGAACGCGCAGCACGACAGCAGCAGCGGATGGCCA 300
Qy 101 ThrMetGluValArgIleAsnValSerArgGlnGlnValGluLysValPheGlyLeuGlu 120
Db 301 ACCATGGAGGTCCGTATCAACGTTATCGAGCGCAGCAGGTAGAGAAAGTGTTTGGGCTGGAG 360
Qy 121 GluTyrTrpCysGlnCysValAlaTrpSerSerSerGlyThrThrLysSerGlnLysAla 140
Db 361 GAATACTGTGGTCCAGTGTGTGGCATGGAGCTCTCTGGGTACCAACCAAAAGTCAGAGGCC 420
Qy 141 TyrIleArgIleAlaArgLeuArgLysAsnPheGluGlnGluProLeuAlaLysGluVal 160
Db 421 TACATCCGATTGCTTATTTGGCAAGAACTTTGAGCAGAGGACCACTGGCCAAAGGAAGTG 480
Qy 161 SerLeuGluGlnGlyIleValLeuProCysArgProProGluGlyIleProProAlaGlu 180
Db 481 TCACGTGGAGCAAGGCATTGTACTTGTGCGCCCCCAGAGGAATCCCCCAGCTGAG 540
Qy 181 ValGluTrpLeuArgAsnGluAspLeuValAspProSerLeuAspProAsnValTyrIle 200
Db 541 GTGGAGTGGCTTCGAATGAGGACCTCTGTGGACCCCTCTCCATCCCAATGTGTACATC 600
Qy 201 ThrArgGluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThr 220
Db 601 ACGCGGGAGCACAGCCTAGTGTGCTCAGGCCCGCTGGCCGACACGCGCAACTACACC 660
Qy 221 CysValAlaLysAsnIleValAlaArgArgSerAlaSerAlaAlaValIleValTyr 240
Db 661 TGTGTGGCAAGAAACATCTAGCCCTGCGCAAGCACCTCTGTGACGGGTCAATGTGTTAT 720
Qy 241 ValAsnGlyGlyTrpSerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArg 260
Db 721 GTGAACGGTGGGTGGTTCGACGTGGACTGAGTGGTCCGTCTGCAGCCAGCTGTGGCGGT 780
Qy 261 GlyTrpGlnLysArgSerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPhe 280
Db 781 GGCTGGCAAAACGGAGCGGAGCTGCACCAACCCCGCACCTCTCAACGGGGCGGCTTC 840
Qy 281 CysGluGlyGlnAsnValGlnLysThrAlaCysAlaThrLeuCysProValAspGlySer 300
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SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/256,702

FILING DATE: 27-Sep-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/933,261

FILING DATE: 20-Aug-2001

APPLICATION NUMBER: 08/808,982

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: OSMAN, RICHARD A

REGISTRATION NUMBER: 36,627

REFERENCE/DOCKET NUMBER: UC96-217

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 343-4341

TELEFAX: (415) 343-4342

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 3014 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-10-256-702-1

Alignment Scores:

Pred. No.:	0	Length:	3014
Score:	4638.00	Matches:	862
Percent Similarity:	97.88%	Conservative:	17
Best Local Similarity:	95.99%	Mismatches:	19
Query Match:	96.81%	Indels:	0
DB:	14	Gaps:	0

US-10-624-932C-2 (1-898) x US-10-256-702-1 (1-3014)

Qy	1	MetAlaValArgProGlyLeuTrpProAlaLeuLeuGlyLeuValLeuAlaTrpLeu	20
Db	1	ATGGCGCTCGGCGCGCGCTGTGGCCAGTGTCTCTGGGCATAGTCTCGCGCTGGCTT	60
Qy	21	AtqGlySerGlyAlaGlnSerAlaThrValAlaAsnProValProGlyAlaAsnPro	40
Db	61	CGTGGTTGGGTGCCAGAGAGTGCCAGCGTGCCCAATCCAGTGGCGCGGTGCAACCCC	120
Qy	41	AspLeuLeuProHisPheLeuValGluProGluAspValTyrIleValLysAsnLysPro	60
Db	121	GACCTGCTGCCCCACTTCTCGTGTAGAGCTGTGAGGACGTGTACATTGTCAAGAACAGCG	180
Qy	61	ValLeuLeuValCysLysAlaValProAlaThrGlnIlePhePheLysCysAsnGlyGlu	80
Db	181	GTGTTGTTGGTGTGCAAGGCTGTGCTGCCACCCAGATCTTCTCAAGTGCATGGGGAA	240
Qy	81	TrpValArgGlnValAspHisValIleGluAtqSerThrAspGlySerSerGlyLeuPro	100
Db	241	TGGGTCCGCAGGTCCATCAGTAATTAACCGCAGCAGCAGCAGCAGCGAATGGCA	300
Qy	101	ThrMetGluValArgIleAsnValSerArgGlnGlnValGluLysValPheGlyLeuGlu	120
Db	301	ACCATGGAGGTCCGTATACAGTATCGAGGACGAGTATGAGAAAGTGTGGGCTGGAG	360
Qy	121	GluTyrTrpCysGlnCysValAlaTrpSerSerSerGlyThrThrLysSerGlnLysAla	140
Db	361	GAATACTGGTGCCAGTGTGTGGCATGGAGCTCTCGGGTACCACCAAAAGTCAGAAAGGC	420
Qy	141	TyrIleArgIleAlaArgLeuArgLysAsnPheGluGlnGluProLeuAlaLysGluVal	160
Db	421	TACATCCGGATTGCCATTATTTGCCAAGAACTTTTGACAGAGGACCTGGCCAAAGGATG	480
Qy	161	SerLeuGluGlnGlyIleValLeuProCysArgProProGluGlyIleProProAlaGlu	180
Db	481	TCACTGGAGCAAGGCATTGTACTACTTGTTCGCCCCCAGAGGAATCCCCCAGCTGAG	540

Qy	181	ValGluTrpLeuArgAsnGluAspLeuValAspProSerLeuAspProAsnValTyrIle	200
Db	541	GTGGAGTGGCTTCGAAATGAGGACCTCGTGGACCCCTCCCTCGATCCCAATGTGTATC	600
Qy	201	ThrArgGluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThr	220
Db	601	ACGCGGAGCAGACAGCTTAGTGTGCTCAGGCGCGCTGGCGACACGGCCAACTACACC	660
Qy	221	CysValAlaLysAsnIleValAlaArgArgSerAlaSerAlaAlaValIleValTyr	240
Db	661	TGTGTGCCCAAGAACATCGTAGCCCGTCCCGAAGCACCTCTGCAGCGCTCATTTTAT	720
Qy	241	ValAsnGlyGlyTrpSerThrTrpGluTrpSerValCysSerAlaSerCysGlyArg	260
Db	721	GTCAACGCTGGGTGGTTCGACGTGAGTGGTTCGCTGCAGCCCGACGCTGTGGCGCT	780
Qy	261	GlyTrpGlnLysArgSerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPhe	280
Db	781	GGCTGCGAAGACGGAGCGGAGCTGCACACCCCGCACCTCTCAACGGGGCGCTTC	840
Qy	281	CysGluGlyGlnAsnValGlnLysThrAlaCysAlaThrLeuCysProValAspGlySer	300
Db	841	TGTGAGGCGCAGAAATGTCAGAAAAACAGCCTGCGCCACTCTGTGCCAGTGGATGGAGC	900
Qy	301	TrpSerProTrpSerLysTrpSerAlaCysGlyLeuAspCysThrHisTrpArgSerArg	320
Db	901	TGGAGTTCGTGGAGTAAGTGGTCAGCCTGTGGCTTGACTGCACCCACTGGCGGAGCCGC	960
Qy	321	GluCysSerAspProAlaProArgAsnGlyGlyGluGluCysGlnGlyThrAspLeuAsp	340
Db	961	GAGTGTCTTCAGCCAGCACCCCGCAATGGAGTGGAGGTGCGGGTGTGACCTGGAC	1020
Qy	341	ThrArgAsnCysThrSerAspLeuCysValHisSerAlaSerGlyProGluAspValAla	360
Db	1021	ACCGCAACTGTACCACTGACCTCTGCGCTGCACACCGCTTCTTGGCCCCGAGGACGTGCT	1080
Qy	361	LeuTyrValGlyLeuIleAlaValAlaValCysLeuValLeuLeuLeuValLeuIle	380
Db	1081	CTCTACATCGGCTTGTGCTGTGGCTGTGCTCTTCTTGTGTGTCGCTTGA	1140
Qy	381	LeuValTyrCysArgLysLysGlyLeuAspSerAspValAlaAspSerSerIleLeu	400
Db	1141	CTCATTTACTGTGCGAAGAGAGGGCTGGACTCGATGTGGCCGACTGCTCCATCTTC	1200
Qy	401	ThrSerGlyPheGlnProValSerLysProSerLysAlaAspAsnProHisLeuLeu	420
Db	1201	ACCTCGGCTTCCAGCTGTGAGCATCAAGCCAGCAAGCAGCAACCCACCTGCTC	1260
Qy	421	ThrIleGlnProAspLeuSerThrThrThrThrThrThrThrThrThrThrThrThr	440
Db	1261	ACCATCCAGCCAGACCTCAGCACCCACTACACCTACAGGCGCAGTCTATGTTTCGAGG	1320
Qy	441	GlnAspGlyProSerProLysPheGlnLeuThrAsnGlyHisLeuLeuSerProLeuGly	460
Db	1321	CAGATGAGCCAGCCCGCCCAAGTTCAGCTCTCTAATGGTCACTGCTCAGCCACTGGGG	1380
Qy	461	GlyGlyArgHisThrIleHisHisSerSerProThrSerGluAlaGluGluPheValSer	480
Db	1381	AGTGGCGGCATACGTTGCACACAGCTCACCCACTCTGAGGCTGAGGACTTCGTCTCC	1440
Qy	481	ArgLeuSerThrGlnAsnTyrPheArgSerLeuProArgGlyThrSerAsnMetThrTyr	500
Db	1441	CGCCTCTCCACCAAACTACTTTGTGTTCCCTGCGCGCGGCGCCAGCAACATGGGCTAC	1500
Qy	501	GlyThrPheAsnPheLeuGlyArgLeuMetIleProAsnThrGlyIleSerLeuLeu	520
Db	1501	GGGACCTTCACTTCTCGGGGCGGCTGATGATCCCTAATACGGGGATCAGCTCTCC	1560
Qy	521	IleProProAspAlaIleProArgGlyLysIleTyrGluIleTyrLeuThrLeuHisLys	540
Db	1561	ATACCCCGGATGCCATCCCGGAGAAAGATCTACGAGATCTACCTCACACTGCAAG	1620
Qy	541	ProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeuLeuSerProIleValSer	560

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Db 1621 CCAGAAGACGTGAGGTTGCCCTAGCTGGCTGTCCAGACCCCTGCTGAGTCCAGTGGTTAGC 1680
Qy 561 CysGlyProProGlyValLeuLeuThraArgProValIleLeuAlaMetAspHisCysGly 580
Db 1681 TGTGGGCCCCCAGGAGTCTGCTCACCAGGCGAGTCTATCCCTGGAATGGACCACTGTGGA 1740
Qy 581 GluProSerProAspSerTrpSerLeuArgLeuLeuValysGlnSerCysGluGlySerTrp 600
Db 1741 GAGCCAGCCCTGACAGCTGGAGTCTGGGCTCTAAAAGAGCTCTCTGGAGGGGAGTTGG 1800
Qy 601 GluAspValLeuHisLeuGlyGluAlaProSerHisLeuTrpTrpCysGlnLeuGlu 620
Db 1801 GAGGATGCTGTCACCTTGTGGTGGAGGAGTCACTTCCCACTCTACTACTGCGAGTGGAG 1860
Qy 621 AlaSerAlaCysTrpValPheThrGlnGlnLeuGlyArgPheAlaLeuValGlyAla 640
Db 1861 GCCGGGCGCTGTATGCTTCCAGGAGCAGCTGGGCGCTTGGCCCTGGTGGAGAGGCC 1920
Qy 641 LeuSerValAlaAlaAlaLysArgLeuLeuLeuLeuPheAlaProValAlaCysThr 660
Db 1921 CTAGCGTGGCTGCCACCAAGGCGCTCAGGCTCTCTGTTGCTCCGCTGGCTGTACG 1980
Qy 661 SerLeuGluTrpAsnIleArgValTrpCysLeuHisAspThrHisAspAlaLeuLysGlu 680
Db 1981 TCCCTTGAGTACACATCCGAGTGTACTGCTACACGACACCCACGAGCGCTCTCAAGGAG 2040
Qy 681 ValValGlnLeuGluLysGlnLeuGlyGlyGlnLeuIleGlnGluProArgValLeuHis 700
Db 2041 GTGGTGAGCTGGAGAGCAGCTAGGTAGTGAGCAGCTGATCCAGGAGCGCTCGCTGCAC 2100
Qy 701 PheLysAspSerTrpHisAsnLeuArgLeuSerIleHisAspValProSerSerLeuTrp 720
Db 2101 TTCAAGACAGTTACCAACCTACGCTCTCCATCCAGCAGCTGCCAGCTCTCTGTGG 2160
Qy 721 LysSerLysLeuLeuValSerTrpGlnGluIleProPheTrpHisIleTrpAsnGlyThr 740
Db 2161 AAGAGCAAGTACTTGTGAGTACAGGAGATCCCTTTTACCAATCTGGAAGCGCAC 2220
Qy 741 GlnArgTrpLeuHisCysThrPheThrLeuGluArgValSerProSerThrSerAspLeu 760
Db 2221 CACGATATCTGCACTGCACCTTCCACCTGAGCGCATCAACGCGCACACGAGCGACTG 2280
Qy 761 AlaCysLysLeuTrpValTrpGlnValGluGlyAspGlyGlnSerPheSerIleAsnPhe 780
Db 2281 GCCTGCAAGGTGTGGGTGTGGCAGGTGAGGAGATGGGAGAGCTTCAACATCACTTC 2340
Qy 781 AsnIleThrLysAspThrArgPheAlaGluLeuAlaLeuGluSerGluAlaGlyVal 800
Db 2341 AACATCACTAAGGACACAAGTTTGTGTAATTGTTGCTCTGGAGAGTGAAGGGGGGTC 2400
Qy 801 ProAlaLeuValGlyProSerAlaPheLysIleProPheLeuIleArgGlnLysIleIle 820
Db 2401 CCAGCCCTGTGGGCCCCAGTGTCAAGATCCCTTCCATTCGCGCAAAAGATCATC 2460
Qy 821 SerSerLeuAspProProCysArgArgGlyAlaAspTrpArgThrLeuAlaGlnLysLeu 840
Db 2461 GCCAGTCTGAGCCACCCTTGAGCCGGGGCGGCGACTGGAGAACTCTAGCCCAAGAACT 2520
Qy 841 HisLeuAspSerHisLeuSerPhePheAlaSerLysProSerProThrAlaMetIleLeu 860
Db 2521 CACCTGGACAGCCATCTTAGCTTCTTCCAGCCCGAGCCCTACAGCCATGATCCTC 2580
Qy 861 AsnLeuTrpGluAlaArgHisPheProAsnGlyAsnLeuSerGlnLeuAlaAlaVal 880
Db 2581 AACCTATGGGAGGCACGGCACCTTCCCCAACGGCAACCTCGGCCAGCTGGCAGCAGCTGTG 2640
Qy 881 AlaGlyLeuGlyGlnProAspAlaGlyLeuPheThrValSerGluAlaGluCys 898
Db 2641 GCCGAGTGGGCCAACAGATGCTGGCTCTTTCAGCGTGTGGAGGCCGAGTGT 2694
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RESULT 7

US-10-643-795A-77

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; Sequence 77, Application US/10643795A
; Publication No. US20040241703A1
; GENERAL INFORMATION:
; APPLICANT: FREDERIC J. DESAUVAGE
; APPLICANT: GRETCHEN FRANTZ
; APPLICANT: KENNETH J. HILLAN
; APPLICANT: PAUL POLAKIS
; APPLICANT: ANDREW POLSON
; APPLICANT: VICTORIA SMITH
; APPLICANT: SUSAN D. SPENCER
; APPLICANT: THOMAS D. WU
; APPLICANT: ZEMIN ZHANG
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF TUMOR
; FILE REFERENCE: P5026R1-US
; CURRENT APPLICATION NUMBER: US/10/643,795A
; CURRENT FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: US 60/404,809
; PRIOR FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/405,645
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/413,192
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: US 60/419,008
; PRIOR FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/426,847
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/484,959
; PRIOR FILING DATE: 2003-07-02
; NUMBER OF SEQ ID NOS: 158
; SEQ ID NO 77
; LENGTH: 3561
; TYPE: DNA
; ORGANISM: Homo sapien
; US-10-643-795A-77
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Alignment Scores:
Pred. No.: 0 Length: 3561
Score: 4413.00 Matches: 840
Percent Similarity: 93.65% Conservative: 1
Best Local Similarity: 93.54% Mismatches: 1
Query Match: 92.11% Indels: 56
DB: 20 Gaps: 1
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US-10-624-932C-2 (1-898) x US-10-643-795A-77 (1-3561)

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Qy 1 MetAlaValArgProGlyLeuTrpProAlaLeuLeuGlyIleValLeuAlaAlaTrpLeu 20
Db 4 ATGGCGGTCCGGCCCGCCCTGTGGCAGCGCTCTGGGCATAGTCTCTCGCGCTTGGCTC 63
Qy 21 ArgGlySerGlyAlaGlnGlnSerAlaThrValAlaAsnProValProGlyAlaAsnPro 40
Db 64 CGCGGCTCGGGTCCCGCAGCAGAGTGCCACCGTGGCCCAACCCAGTGGCTGTGCCAACCCG 123
Qy 41 AspLeuLeuProHisPheLeuValGluProGluAspValTrpIleValLysAsnLysPro 60
Db 124 GACCTGCTTCCCCCTCTCTGGTGGAGCCCGAGAGTGTACATGCTCAAGAACAGCCCA 183
Qy 61 ValLeuLeuValCysLysAlaValProAlaThrGlnIlePhePheLysCysAsnGlyGlu 80
Db 184 GTGCTGCTTGTGTGCAAGGCGGTGGCCGCGCCAGCAGATCTTCTTCAAGTCAACGGGGAG 243
Qy 81 TrpValArgGlnValAspHisValIleGluArgSerThrAspGlySerSerGlyLeuPro 100
Db 244 TGGGTGCGCCAGGTGGACCACTGTGATCGAGCGCAGCACACGCGGAGCAGTGGGCTGCC 303
Qy 101 ThrMetGluValArgIleAsnValSerArgGlnGlnValGluLysValPheGlyLeuGlu 120
Db 304 ACCATGGAGGTCCGCATTATGTTCTCAAGCAGCAGGTGCGAAGAGTGTTCGGGCTGGAG 363
Qy 121 GluTrpTrpCysGlnCysValAlaAlaTrpSerSerGlyThrThrLysSerGlnLysAla 140
Db 364 GAATACTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 423
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QY 141 TyrIleArgIleAlaArgLeuArgLysAsnPheGluGlnGluProLeuAlaLysGluVal 160
DB 424 TACATCCGATACCTATTATTCGCCAAGAACTTCGAGCAGGAGCCGCTGGCCAAAGAGGTG 483
QY 161 SerLeuGluGlnGlyIleValLeuProCysArgProProGluGlyIleProProAlaGlu 180
DB 484 TCCCTGGAGCAGGGCATCGTGTCTGCCCTGCCGTCCACCGAGGGCATCCCTCCAGCCGAG 543
QY 181 ValGluTrpLeuArgHenGluAspLeuValAspProSerSerLeuAspProHenValTyrIle 200
DB 544 GTGGAGTGGCTCCGGAACAGGACCTGGTGGACCCGCTCCCTGACCCCAATGTATACATC 603
QY 201 ThrArgGluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThr 220
DB 604 ACCGGGAGCAGACCTGGTGGTGCACACAGGCCCGCTTGTCTACACGGCCAACTACACC 663
QY 221 CysValAlaLysAsnIleValAlaArgArgSerAlaSerAlaAlaValIleValTyr 240
DB 664 TGGTGGCCNAGAACATCGTGGCAGCGTCCGCGCAGGCCCTCCGCTGTCTGTATCGTCTAC 723
QY 241 ValAsnGlyGlyTrpSerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArg 260
DB 723 ----- 723
QY 261 GlyTrpGlnLysArgSerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPhe 280
DB 723 ----- 723
QY 281 CysGluGlyGlnAsnValGlnLysThrAlaCysAlaThrLeuCysProValAspGlySer 300
DB 724 -----GTGGACGGCAGC 735
QY 301 TrpSerProTrpSerLysTrpSerAlaCysGlyLeuAspCysThrHisTrpArgSerArg 320
DB 736 TGGAGCCCGTGGAGCAAGTGGTGGCTGTGGCTGGACTGCACCCACTGGCGGAGCCGT 795
QY 321 GluCysSerAspProAlaProArgAsnGlyGlyGluGluCysGlnGlyThrAspLeuAsp 340
DB 796 GAGTGTCTGTACCCAGACCCCGCAACGGAGGGGAGGTGCCAGGGCACTGACCTGGAC 855
QY 341 ThrArgAsnCysThrSerAspLeuCysValHisSerAlaSerGlyProGluAspValAla 360
DB 856 ACCCGCACTGTACAGTAGTACCTCTGTGTACACACTGTCTTGGCCCTGAGGAGCTGGCC 915
QY 361 LeuTyrValGlyLeuIleAlaValAlaValCysLeuValLeuLeuLeuValLeuIle 380
DB 916 CTCTATGTGGCCCTCATCGCCGTGGCCGTCTGCCTGTGCTGTGCTGTGTCTCATC 975
QY 381 LeuValTyrCysArgLysLysGluGlyLeuAspSerAspValAlaAspSerSerIleLeu 400
DB 976 CTCGTTTATTCGCGAAGAGGAGGGGCTGGACTCAGATGTGGCTGACTGTCCATTCTC 1035
QY 401 ThrSerGlyPheGlnProValSerIleLysProSerLysAlaAspAsnProHisLeuLeu 420
DB 1036 ACCTCAGGCTTCAGGCCGCTCAGCATCAGCCAGCCAGCAGACAAACCCCATCTGCTC 1095
QY 421 ThrIleGlnProAspLeuSerThrThrThrThrThrTyrTrpGlnGlySerLeuCysProArg 440
DB 1096 ACCATCAGCCGACCTCAGCACCAACCCACCTACCAGGGCAGTCTCTGTCCCCGG 1155
QY 441 GlnAspGlyProSerProLysPheGlnLeuThrAsnGlyHisLeuLeuSerProLeuGly 460
DB 1156 CAGATGGGGCCAGCCCAAGTTCCAGCTCACCATTCCAAATGGGCACCTGTCTAGCCCCCTGGGT 1215
QY 461 GlyGlyArgHisThrLeuHisHisSerSerProThrSerGluAlaGluGluPheValSer 480
DB 1216 GGGCGGCCACACACTGCACACACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCC 1275
QY 481 ArgLeuSerThrGlnAsnTyrPheArgSerLeuProArgGlyThrSerAsnMetThrTyr 500
DB 1276 CGCCTCTCCACCCAGAACTACTTCGCTCCCTGCCCGGAGCCACGACCAATGACCTAT 1335

QY 501 GlyThrPheAsnPheLeuGlyGlyArgLeuMetIleProAsnThrGlyIleSerLeuLeu 520
DB 1336 GGGACCTTCAACTTCTTCGGGGGCCCGGCTGATATCCCTAATACAGGAATCAGCCCTCCTC 1395
QY 521 IleProProAspAlaIleProArgGlyLysIleTyrGluIleTyrLeuThrLeuHisLys 540
DB 1396 ATCCCCCAGATGCCATACCCCGAGGGAAGATCTATGAGATCTACTCTCAGCTGCACAAG 1455
QY 541 ProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeuLeuSerProIleValSer 560
DB 1456 CCGAAGACGTGAGGTGGCCCTAGCTGTGTGTGTCAGACCTGTGTGAGTCCCATCGTTAGC 1515
QY 561 CysGlyProGlyValLeuLeuThrArgProValIleLeuAlaMetAspHisCysGly 580
DB 1516 TGTGGACCCCTGGCGCTCTGTCTACCCGCGCAGTCATCTGTGCTATGGACCACTGTGGG 1575
QY 581 GluProSerProAspSerTrpSerLeuArgLeuLysLysGlnSerCysGluGlySerTrp 600
DB 1576 GAGCCACCCCTGACAGCTGGAGCTGCGCCTCAAAAGCAGTCGTGGGAGGAGCAGCTGG 1635
QY 601 GluAspValLeuHisLeuGlyGluGluAlaProSerHisLeuTyrTyrCysGlnLeuGlu 620
DB 1636 GAGGATGTGTGCACCTGGCGAGGAGGCGCCCTCCACCTCTACTACTGCCAGCTGGAG 1695
QY 621 AlaSerAlaCysTyrValPheThrGluGlnLeuGlyArgPheAlaLeuValGlyGluAla 640
DB 1696 GCAGTGGCTGTGTACGTCTTCCCGAGCAGCTGGCGCGCTTGTCCCTGTGGGAGAGGCC 1755
QY 641 LeuSerValAlaAlaAlaLysArgLeuLysLeuLeuLeuPheAlaProValAlaCysThr 660
DB 1756 CTCAGGCTGGCTGGCCCAAGCGCTCAAGCTGCTTCTGTGTGGCGGGTGGCTGCACC 1815
QY 661 SerLeuGluTyrAsnIleArgValTyrCysLeuHisAspThrHisAspAlaLeuLysGlu 680
DB 1816 TCCTCGAGTACAACTCCGGGTCTACTGCTGTCATGACACCCACCATGCACTCAAGGAG 1875
QY 681 ValValGlnLeuGluLysGlnLeuGlyGlyGlnLeuIleGlnGluProArgValLeuHis 700
DB 1876 GTGGTGCAGCTGGAGAAGCAGCTGGGGGACAGCTGATCCAGAGGCCAGGGTCTTGAC 1935
QY 701 PheLysAspSerTyrHisAsnLeuArgLeuSerIleHisAspValProSerSerLeuTrp 720
DB 1936 TTCAAGACAGTTACCAACCTTGGCGCTATCCATCCAGATGTGCCAGCTCCCTGTGG 1995
QY 721 LysSerLysLeuLeuValSerTyrGlnGluIleProPheTyrHisIleTrpAsnGlyThr 740
DB 1996 AAGAGTAAAGTCTCTGTCTCAGCTACCAGGAGATCCCTTTTATCACATCTGGATGCGACG 2055
QY 741 GlnArgTyrLeuHisCysThrPheThrLeuGluAtqValSerProSerThrSerAspLeu 760
DB 2056 CAGCGGTACTTGGACCTGCACCTTACCCTGGAGCGTGTGAGCCCGAGCTAGTGACCTG 2115
QY 761 AlaCysLysLeuTrpValTrpGlnValGluGlyAspGlyGlnSerPheSerIleAsnPhe 780
DB 2116 GCCTGCAAGCTGTGGGTGTGGCAGGTGGAGGGCGACGGCAGAGCTTCAGCATCAACTTC 2175
QY 781 AsnIleThrLysAspThrArgPheAlaGluLeuLeuAlaLeuGluSerGluAlaGlyVal 800
DB 2176 AACATCACCAAGGACACAAGGTTTGTCTGAGCTGTGGCTGTGGAGAGTGAAGCGGGGTC 2235
QY 801 ProAlaLeuValGlyProSerAlaPheLysIleProPheLeuIleArgGlnLysIleIle 820
DB 2236 CAGCCCTCGTGGGCCCCAGTGCCTTCAAGATCCCTTCTCATTCGGCAGAGATTAAT 2295
QY 821 SerSerLeuAspProProCysArgArgGlyAlaAspTrpArgThrLeuAlaGlnLysLeu 840
DB 2296 TCCAGCCTTGAGCCACCCCTGTAGGGGGGTGCCGACTGGCGGACTCTGGCCCAAGAAATC 2355
QY 841 HisLeuAspSerHisLeuSerPhePheAlaSerLysProSerProThrAlaMetIleLeu 860
DB 2356 CACCTGGAGAGCATCTCAGCTTCTTTGCTTCCAGCCCGAGCCCAAGCCATGATCCTC 2415
QY 861 AsnLeuTrpGluAlaArgHisPheProAsnGlyAsnLeuSerGlnLeuAlaAlaVal 880

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Db 2416 AACCTGTGGAGCGCGGCACCTTCCCAACGCGCAACCTCAGCCAGCTGGCTGCAGCAGTG 2475
Qy 881 AlaGlyLeuGlyGlnProAspAlaGlyLeuPheThrValSerGluAlaGluCys 898
Db 2476 CTTGACTGGGCCAGCCAGACGCTGGCCCTCTTACAGTGTCCGAGGCTGAGTGC 2529

RESULT 8
US-10-948-518-77
; Sequence 77, Application US/10948518
; Publication No. US20050064492A1
; GENERAL INFORMATION:
; APPLICANT: FREDERIC J. DESAUVAGE
; APPLICANT: GRETCHEN FRANTZ
; APPLICANT: KENNETH J. HILLAN
; APPLICANT: PAUL POLAKIS
; APPLICANT: ANDREW POLSON
; APPLICANT: VICTORIA SMITH
; APPLICANT: SUSAN D. SPENCER
; APPLICANT: THOMAS D. WU
; APPLICANT: ZEMIN ZHANG
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TREATMENT OF TUMOR
; FILE REFERENCE: P5026R1-US
; CURRENT APPLICATION NUMBER: US/10/948,518
; CURRENT FILING DATE: 2004-09-22
; PRIOR APPLICATION NUMBER: US/10/643,795
; PRIOR FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: US 60/404,809
; PRIOR FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/405,645
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/413,192
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: US 60/419,008
; PRIOR FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/426,847
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/484,959
; PRIOR FILING DATE: 2003-07-02
; NUMBER OF SEQ ID NOS: 158
; SEQ ID NO 77
; LENGTH: 3561
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-948-518-77

Alignment Scores:
Pred. No.: 0 Length: 3561
Score: 4413.00 Matches: 840
Percent Similarity: 93.65% Conservative: 1
Best Local Similarity: 93.54% Mismatches: 1
Query Match: 92.11% Indels: 56
DB: 21 Gaps: 1

US-10-624-932C-2 (1-898) x US-10-948-518-77 (1-3561)

Qy 1 MetAlaValArgProGlyLeuTrpProAlaLeuLeuGlyLeuValLeuAlaAAlaTrpLeu 20
Db 4 ATGGCCGTCCGGCCCGCGCTGTGGCCAGCGCTCTGGGCATAGTCTCGCCGCTTGGCTC 63
Qy 21 ArgGlySerGlyAlaGlnGlnSerAlaThrValAlaAsnProValProGlyAlaAsnPro 40
Db 64 CGCGGCTCGGTGCCCCAGCAGAGTGCCACCGTGCCCAACCCAGTGGCTGGTGCACCCG 123
Qy 41 AspLeuLeuProHisPheLeuValGluProGluAspValTyrLeuValAsnLysPro 60
Db 124 GACCTGCTTCCCACTTCTCGTGGAGCCCGAGGATGTGTACATCGTCAAGAAACAAGCCA 183
Qy 61 ValLeuLeuValCysLysAlaValProAlaThrGlnPhePheLysCysAsnGlyGlu 80
Db 184 GTGCTGCTTGTGTCAAGGCGCGTCCCGCCACCGCAGATCTTCTTCAAGTGCACCGGGAG 243
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Qy 81 TrpValArgGlnValAspHisValIleGluArgSerThrAspGlySerSerGlyLeuPro 100
Db 244 TGGGTGGCCAGGTGGACACGCTGATCGAGCGCAGCAGACGAGCGGAGCAGTGGCTGCCC 303
Qy 101 ThrMetGluValArgIleAsnValSerArgGlnGlnValGluLysValPheGlyLeuGlu 120
Db 304 ACCATGGAGGTCCGCATTAAATGTCTCAAGGCAGCAGGTTCGAGAAAGGTGTTTCGGGTGAG 363
Qy 121 GluTyrTrpCysGlnCysValAlaTrpSerSerGlyThrThrLysSerGlnLysAla 140
Db 364 GAATACTGGTCCAGTGGCATGGAGCTCTCCGGGCACCAACAGAGTCAGAAGGCC 423
Qy 141 TyrIleArgIleAlaArgLeuArgLysAsnPheGluGlnGluProLeuAlaLysGluVal 160
Db 424 TACATCCGATAGCTATTGTCGCAAGAACTTCGAGCAGGAGCCGCTGGCCCAAGAGGTG 483
Qy 161 SerLeuGluGlnGlyIleValLeuProCysArgProProGluGlyIleProProAlaGlu 180
Db 484 TCCCTGGAGCAGGCGCATCGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 543
Qy 181 ValGluTrpLeuArgAsnGluAspLeuValAspProSerLeuAspProAsnValTyrIle 200
Db 544 GTGGAGTGGCTCCGGAACAGGAGCTGTGGACCCGCTGCTGGACCCCAATGTATATACATC 603
Qy 201 ThrArgGluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThr 220
Db 604 ACGCGGAGCAGCAGCTGGTGGTGGCAGACGCGCCGCTTGTGACACGCGCCCACTACACC 663
Qy 221 CysValAlaLysAsnIleValAlaArgArgSerAlaSerAlaAlaValIleValTyr 240
Db 664 TGCCTGGCCCAAGAACTCGTGGCAGCTGCGCGCAGCGCTCCGCTGCTGCTGCTGCTGCTAC 723
Qy 241 ValAsnGlyGlyTrpSerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArg 260
Db 723 ----- 723
Qy 261 GlyTrpGlnLysArgSerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPhe 280
Db 723 ----- 723
Qy 281 CysGluGlyGlnAsnValGlnLysThrAlaCysAlaThrLeuCysProValAspGlySer 300
Db 724 -----GTGACGCGCAGC 735
Qy 301 TrpSerProTrpSerLysTrpSerAlaCysGlyLeuAspCysThrHisLeuTrpAspSerArg 320
Db 736 TGGAGCCCGTGGAGCAAGTGGTGGCTGTGGGCTGGAGCTGCACCCACTGCGCGGAGCGGT 795
Qy 321 GluCysSerAspProAlaProArgAsnGlyGlyGluGluCysGlnGlyThrAspLeuAsp 340
Db 796 GAGTGTCTTCACCCAGCAGCAGCCGCAACGAGGAGGAGGAGTGCACGCGCAGCTGACCTGGAC 855
Qy 341 ThrArgAsnCysThrSerAspLeuCysValHisSerAlaSerGlyProGluAspValAla 360
Db 856 ACCCGCAACTGTATACAGTACCTCTGTGTACACACTGCTTCTGGCCCTGAGGAGCGTGCC 915
Qy 361 LeuTyrValGlyLeuIleAlaValAlaValCysLeuValLeuLeuLeuValLeuIle 380
Db 916 CTCTATGTGGGCTCATCGCCGCTGGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTCATC 975
Qy 381 LeuValTyrCysArgLysLysGluLysAspSerAspValAlaAspSerSerIleLeu 400
Db 976 CTGTTTTATTGCGGAAGAGGAGGCGCTGAGCTCAGATGTGGCTGACTCGTCCATTCTC 1035
Qy 401 ThrSerGlyPheGlnProValSerIleLysProSerLysAlaAspAsnProHisLeuLeu 420
Db 1036 ACCTCAGGCTTCCAGCCGCTCAGCATCAGCCCAAGCAAGCAGACACCCCATCTGCTC 1095
Qy 421 ThrIleGlnProAspLeuSerThrThrThrThrThrThrThrThrThrThrThrThrThr 440
Db 1096 ACCATCAGCGGAGCTCAGCACACCAACCACTTACCAGGCGAGTCTCTGTGCCCCGG 1155
Qy 441 GlnAspGlyProSerProLysPheGlnLeuThrAsnGlyHisLeuLeuSerProLeuGly 460
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Db 1156 CAGGATGGCCGACCCCAAGTTCCAGCTCACCATGGGCACCTGTCCAGCCCTCGGT 1215
Qy 461 GlyArgHisThrLeuHisHisSerSerProThrSerGluAlaGluGluPheValSer 480
Db 1216 GCGCGCCGACACACACTGCACACAGCTCTCCACCTCTCAGGCGGAGGATTCGTCTCC 1275
Qy 481 ArgLeuSerThrGlnAsnTyrPheArgSerLeuProArgGlyThrSerAsnMetThrTyr 500
Db 1276 CGCTCTCCACCCAGAACTACTTCCTCCCTCCCTGCGCGGACCCAGCAACATGACCTAT 1335
Qy 501 GlyThrPheAsnPheLeuGlyGlyArgLeuMetIleProAsnThrGlyIleSerLeu 520
Db 1336 GGGACCTTCAACTTCTTCGGGGGGCGGCTGATGATCCCTAATACAGGAATCAGCCCTCCTC 1395
Qy 521 IleProProAspAlaIleProArgGlyIleYrGluIleTyrLeuThrLeuHisLys 540
Db 1396 ATCCCCCAGATGCCATACCCCGAGGGAAGATCTATGAGATCTACCTCAGCTGCACAAG 1455
Qy 541 ProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeuLeuSerProIleValSer 560
Db 1456 CCGGAAGACGTGAGTTGGCCCTAGCTGGCTGTCCAGACCCCTGCTGAGTCCCATCGTTAGC 1515
Qy 561 CysGlyProProGlyValLeuLeuThrArgProValIleLeuAlaMetAspHisCysGly 580
Db 1516 TGTGGACCCCTGGCGTCTCTACCCGGCCAGTCATCTGGCTATGGACCACTGTGGG 1575
Qy 581 GluProSerProAspSerTrpSerLeuArgLeuLysGlnSerCysGluGlySerTrp 600
Db 1576 GAGCCACGCCCTGACAGCTGGAGCGCTCAAAAGCAGTCGTGCGAGGGCAGCTGG 1635
Qy 601 GluAspValLeuHisLeuGlyGluAlaProSerHisLeuTyrTyrCysGlnLeuGlu 620
Db 1636 GAGGATGTGTGCACTGGCGGAGGAGCGCCCTCCACCTCTACTACTGCCAGCTGGAG 1695
Qy 621 AlaSerAlaCysTrpValPheThrGluGlnLeuGlyArgPheAlaLeuValGlyGluAla 640
Db 1696 GCCAGTGCCTGCTACGTCCTACCGAGCAGCTGGCGCGCTTGGCCCTGTGGAGAGGCC 1755
Qy 641 LeuSerValAlaAlaAlaLysArgLeuLysLeuLeuPheAlaProValAlaCysThr 660
Db 1756 CTCAGCTGGCTGCGCCAAAGCGCTCAAGCTGCTTCTGTTTGGCGCGTGGCTGCACC 1815
Qy 661 SerLeuGluTyrAsnIleArgValTyrCysLeuHisAspThrHisAspAlaLeuLysGlu 680
Db 1816 TCCTTCAGTACAACTCCCGGCTCTACTGCTGTCATGACACCCACGATGCACCTCAAGGAG 1875
Qy 681 ValValGlnLeuGluLysGlnLeuGlyGlnLeuIleGlnGluProArgValLeuHis 700
Db 1876 GTGGTGAGCTGGGAAGCAGCTGGGGGGACAGCTGATCCAGAGCCACGGGCTCTGCAC 1935
Qy 701 PheLysAspSerTyrHisAsnLeuArgLeuSerIleHisAspValProSerSerLeuTrp 720
Db 1936 TTCAGGACAGTTTACCAACCTTGGCGCTATTCATCCACGATGTGCCAGCTCCCTGTGG 1995
Qy 721 LysSerLysLeuLeuValSerTyrGlnGluIleProPheTyrHisIleTrpAsnGlyThr 740
Db 1996 AAGAGTAAGCTCTTGTTCAGCTACCAAGGAGATCCCTTTTATCACATCTGGAAATGGCAGC 2055
Qy 741 GlnArgTyrLeuHisCysThrPheThrLeuGluArgValSerProSerThrSerAspLeu 760
Db 2056 CAGGGTACTTGTGACTGCACCTTCACTCCCTGAGGGTGTGAGCCCGCAGCATAGTGACCTG 2115
Qy 761 AlaCysLysLeuTrpValTrpGlnValGluGlyAspGlyGlnSerPheSerIleAsnPhe 780
Db 2116 GCCTGCAAGCTGTGGGTGTGGCAGGTGGAGGGCGACGGGCGAGAGCTTCAGCATCAACTTC 2175
Qy 781 AsnIleThrLysAspThrArgPheAlaGluLeuLeuAlaLeuGluSerGluAlaGlyVal 800
Db 2176 AACATCAACCAAGGACACAAAGTTTGTGTGAGCTGTGCTGTGAGAGTGAAGCGGGGCTC 2235
Qy 801 ProAlaLeuValGlyProSerAlaPheLysIleProPheLeuIleArgGlnLysIleIle 820

Db 2236 CCAGCCCTGGTGGGCCCCAGTCCTTCAAGATCCCTTCTCATTCCGCGCAGAGATAATT 2295
Qy 821 SerSerLeuAspProCysArgArgGlyAlaAspTrpArgThrLeuAlaGlnLysLeu 840
Db 2296 TTCAGCTGTGACCCACCTGTAGCGGGTGCAGACTGTGGCGGACTCTGGCCCAAGAACTC 2355
Qy 841 HisLeuAspSerHisLeuSerPhePheAlaSerLysProSerProThrAlaMetIleLeu 860
Db 2356 CACCTGGACAGCCATCTCAGCTTCTTTTGGCTCCAAAGCCAGCCCGCATGATCCTC 2415
Qy 861 AsnLeuTrpGluAlaArgHisPheProAsnGlyAsnLeuSerGlnLeuAlaAlaVal 880
Db 2416 AACCTGTGGAGCGCGGCACTTCCCAACAGGCACTCAGCCAGCTGGCTGCAGCAGTG 2475
Qy 881 AlaGlyLeuGlyGlnProAspAlaGlyLeuPheThrValSerGluAlaGluCys 898
Db 2476 GCTGAGCTGGCCAGCAGCGCTGCGCTCTTCCACAGTGTGGAGGCTGAGTGC 2529

RESULT 9

US-10-311-623-13
; Sequence 13, Application US/10311623
; Publication No. US20040023244A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.; GRIFFIN, Jennifer A.
; APPLICANT: KALLICK, Deborah A.; TRIBOULEY, Catherine M.
; APPLICANT: YUE, Henry; NGUYEN, Danniell B.
; APPLICANT: TANG, Y. Tom; LAL, Preeti G.
; APPLICANT: POLICKY, Jennifer L.; AZIMZAI, Yalda
; APPLICANT: LU, Dying Aina M.; GRAUL, Richard C.
; APPLICANT: YAO, Monique G.; BURFORD, Neil
; APPLICANT: HAPALIA, April J. A.; BAUGHN, Mariah R.
; APPLICANT: BANDMAN, Olga; ARVIZO, Chandra S.
; APPLICANT: YANG, Junming; XU, Yuming
; APPLICANT: GANDHI, Ameena R.; WARREN, Bridget A.
; APPLICANT: DING, Li; SANJANWALA, Madhusudan M.
; APPLICANT: DUGGAN, Brendan M.; LU, Yan
; TITLE OF INVENTION: RECEPTORS
; FILE REFERENCE: PF-0793 USN
; CURRENT APPLICATION NUMBER: US/10/311,623
; CURRENT FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: US 01/19942
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/214,027
; PRIOR FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: US 60/228,045
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/255,104
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PERL Program
; SEQ ID NO 13
; LENGTH: 3580
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040023244A1 6052371CB1
US-10-311-623-13

Alignment Scores:
Pred. No.: 0 Length: 3580
Score: 4413.00 Matches: 840
Percent Similarity: 93.65% Conservative: 1
Best Local Similarity: 93.54% Mismatches: 1
Query Match: 92.11% Indels: 56
DB: 17 Gaps: 1

US-10-624-932C-2 (1-898) x US-10-311-623-13 (1-3580)

Qy 1 MetAlaValArgProGlyLeuTrpProAlaLeuLeuGlyIleValLeuAlaIleTrpLeu 20
Db 4 ATGGCGCTCCGGCCCGCTGTGGCAGCGCTCTCTGGCATAGTCTCTCGCGCTTGGCTC 63

Qy 21 ArgGlySerGlyAlaGlnGlnSerAlaThrValAlaAsnProValProGlyAlaAsnPro 40
Db 64 CGCGCTCGGGTCCGACAGAGTGCACCGTGGCCAAACCCAGTGGCTGGTGCACCCG 123
Qy 41 AspLeuLeuProHisPheLeuValGluProGluAspValTyrIleValLysAsnLysPro 60
Db 124 GACCTGCTTCCCACTTCCCTGGTGAGGCCCGAGGATGTATCATCGTCAAGAACAGGCCA 183
Qy 61 ValLeuLeuValCysLysAlaValProAlaThrGlnIlePhePheLysCysAsnGlyGlu 80
Db 184 GTGCTGCTTGTGTCAGAGCCGTCGCCCGCCAGCAGATCTTCTTCAAGTGCAACGGGAG 243
Qy 81 TrpValArgGlnValAspHisValIleGluArgSerThrAspGlySerSerGlyLeuPro 100
Db 244 TGGGTGGCCAGGTGGACACCGTATCGAGCGCAGCACAGACGGGAGCAGTGGGCTGCC 303
Qy 101 ThrMetGluValArgIleAsnValSerArgGlnGlnValGluLysValPheGlyLeuGlu 120
Db 304 ACCATGGAGGTCCGATTAATGTCTCAAGGCAGCAGGTTCGAGAGGTGTTCGGGCTGGAG 363
Qy 121 GluTyrTrpCysGlnCysValAlaTrpSerSerGlyThrThrLysSerGlnLysAla 140
Db 364 GAATACTGGTGCCAGTGGTGGATGGAGCTCTCGGGCACCACCAAGAGTCAAGAGGCC 423
Qy 141 TyrIleArgIleAlaArgLeuArgLysAsnPheGluGlnGluProLeuAlaLysGluVal 160
Db 424 TACATCCGCATAGCTATTTGGCAAGAACTTCGAGCAGGAGCGCTGGCCCAAGAGGTG 483
Qy 161 SerLeuGlnGlnIleValLeuProCysArgProProGluGlyIleProProAlaGlu 180
Db 484 TCCCTGGAGCAGGGCATGTGCTGCCCTGGCTCCACCGGAGGGCATCCCTCCAGCCGAG 543
Qy 181 ValGluTrpLeuArgAsnGluAspLeuValAspProSerLeuAspProAsnValTyrIle 200
Db 544 GTGGAGTGGCTCCGGACAGGAGACTGTGGTGGACCCGCTCCCTGGACCCCAATGTATATCATC 603
Qy 201 ThrArgGluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThr 220
Db 604 ACGGGGAGCAGACGCTGGTGGTGGCAGCGCCGCTTGTGACAGCGCCCAACTACACC 663
Qy 221 CysValAlaLysAsnIleValAlaArgArgSerAlaSerAlaAlaValIleValTyr 240
Db 664 TGGGTGGCCAAAGAACATGTGGACGTGGCGCAGCGCTCCGCTGTGTGTATCATCGTCTAC 723
Qy 241 ValAsnGlyGlyTyrTrpSerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArg 260
Db 723 ----- 723
Qy 261 GlyTrpGlnLysArgSerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPhe 280
Db 723 ----- 723
Qy 281 CysGluGlyGlnAsnValGlnLysThrAlaCysAlaThrLeuCysProValAspGlySer 300
Db 724 -----GTGGACGGCAGC 735
Qy 301 TrpSerProTrpSerLysTrpSerAlaCysGlyLeuAspCysThrHisTrpArgSerArg 320
Db 736 TGGAGCCCGTGGACCAAGTGTGGCTGTGGCTGTGGCTGTGGCTGTGGCTGTGGCTGTGG 795
Qy 321 GluCysSerAspProAlaProArgAsnGlyGlyGluGluCysGlnGlyThrAspLeuAsp 340
Db 796 GAGTGTCTGACCCAGCACCCCGCAACGGAGGGGAGGAGTGGCCAGGGCACTGACCTGGAC 855
Qy 341 ThrArgAsnCysThrSerAspLeuCysValHisSerAlaSerGlyProGluAspValAla 360
Db 856 ACCCGCAACTGTACAGTACCTCTGTGTATACACTGCTTCTGGCCCTGAGGACGTGGCC 915
Qy 361 LeuTyrValGlyLeuIleAlaValAlaValCysLeuValLeuLeuLeuValLeuIle 380
Db 916 CTCTATGTGGGCCCTCATCGCGGTGGCGTGTGGCTGTGGCTGTGGCTGTGGCTGTGG 975
Qy 381 LeuValTyrCysArgLysLysGluGlyLeuAspSerAspValAlaAspSerSerIleLeu 400

Db 976 CTGCTTTATTCCCGAAGAGGAGGGCTGGACTCAGATGTGGCTGACTCGTCCATCTC 1035
Qy 401 ThrSerGlyPheGlnProValSerIleAspSerLysAlaAspAsnProHisLeuLeu 420
Db 1036 ACCTCAGGCTTCCAGCCCGTTCAGCATCAAGCCCAAGCAGACAACCCCATCTGCTC 1095
Qy 421 ThrIleGlnProAspLeuSerThrThrThrThrTyrGlnGlySerLeuCysProArg 440
Db 1096 ACCATCCAGCGGAGCTTCAGCACCAACCAACCACTTACAGGGCAGTCTCTGTCCCGG 1155
Qy 441 GlnAspGlyProSerProLysPheGlnLeuThrAsnGlyHisLeuLeuSerProLeuGly 460
Db 1156 CAGGATGGGCCCGCCAGCTTCCAGCTCACCATAATGGSCACCTGTCTCAGCCCCCTGGGT 1215
Qy 461 GlyGlyArgHisThrLeuHisHisSerSerProThrSerGluAlaGluGluPheValSer 480
Db 1216 GCGGGCCGCGCACACACTGCACCAAGCTCTCCACCTCTGAGGCCGAGGATTCGTCTCC 1275
Qy 481 ArgLeuSerThrGlnAsnTyrPheArgSerLeuProArgGlyThrSerAsnMetThrTyr 500
Db 1276 CGCTCTCCACCCAGAACTACTTCCGCTCCCTGCGCCGAGGACCAAGCAATGACCTAT 1335
Qy 501 GlyThrPheAsnPheLeuGlyArgLeuMetIleProAsnThrGlyIleSerLeuLeu 520
Db 1336 GSGACCTTCAACTTCTCGGGGGCCGCTGATGATCCCTAATACAGGAATCAGCTCTCCTC 1395
Qy 521 IleProAspAlaIleProArgGlyIleTyrGluIleTyrLeuThrLeuHisLys 540
Db 1396 ATCCCCCAGATGCCATACCCCGAGGAGAGATCTATGAGATCTACCTCAGCTGCACAA 1455
Qy 541 ProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeuLeuSerProIleValSer 560
Db 1456 CCGAGACGTGAGTTGGCCCTAGCTGGCTGTGAGACCTCTGAGTCCCATCGTTAGC 1515
Qy 561 CysGlyProProGlyValLeuLeuThrArgProValIleLeuAlaMetAspHisCysGly 580
Db 1516 TGTGGACCCCTGGCTGCTGCTCACCAGCCAGTATCTGCTGGCTATGGACCATGTGGG 1575
Qy 581 GluProSerProAspSerTrpSerLeuArgLeuLysLysGlnSerCysGluGlySerTrp 600
Db 1576 GAGCCAGCCCTGACAGCTGGAGCTTGGCTGCTCAAAAGCAGTCTGTCGAGGGCAGCTGG 1635
Qy 601 GluAspValLeuHisLeuGlyGluAlaProSerHisLeuTyrTyrCysGlnLeuGlu 620
Db 1636 GAGATGTGCTGCACCTGGGCGAGGAGGCCCTCCACCTCTACTACTGCCAGCTGGAG 1695
Qy 621 AlaSerAlaCysTyrValPheThrGluGlnLeuGlyArgPheAlaLeuValGlyGluAla 640
Db 1696 GCCAGTGGCTGCTACGCTTTCACCGAGCAGCTGGGCGCTTTGGCCCTGGTGGAGAGGCC 1755
Qy 641 LeuSerValAlaAlaLysArgLeuLysLeuLeuLeuPheAlaProValAlaCysThr 660
Db 1756 CTGAGGTGGCTGCGCCCAAGCGCTCAAGCTGCTTGTGTGGCGCGTGGCTGCACC 1815
Qy 661 SerLeuGluTyrAsnIleArgValTyrCysLeuHisAspThrHisAspAlaLeuLysGlu 680
Db 1816 TCCCTCGAGTACAAATCCGGGTCTACTGCTGCTGATGACACCCAGCATGCACTCAAGAG 1875
Qy 681 ValValGlnLeuGluLysGlnLeuGlyGlyGlnLeuIleGlnGluProArgValLeuHis 700
Db 1876 GTGGTGCAGCTGGAGAGCAGCTGGGGGAGCAGCTGATCCAGGAGCCACGGTCTCTGCAC 1935
Qy 701 PheLysAspSerTyrHisAsnLeuArgLeuSerIleHisAspValProSerSerLeuTrp 720
Db 1936 TTCAGGACAGATTACCAACCTTGCCTATCCATCCAGCATGTGCCAGCTCCCTGTGG 1995
Qy 721 LysSerLysLeuLeuValSerTyrGlnGluIleProPheTyrHisIleTrpAsnGlyThr 740
Db 1996 AAGAGTAAGCTCTTGTGAGTACCAAGAGATCCCTTTTATCACAATCTGGAATGGCAGC 2055
Qy 741 GlnArgTyrLeuHisCysThrPheThrLeuGluArgValSerProSerThrSerAspLeu 760

Db 2056 CAGCGGTACTTGCACTGCACCTTCAACCTGGAGCGTGTGAGCCCCAGCACCTAGTACCTG 2115
QY 761 AlaCysLysLeuTrpValTrpGlnValGluGlyAspGlyGlnSerPheSerIleAsnPhe 780
Db 2116 GCCTGCAAGCTGTGGGTGTGGCAGGTGGAGGGCGAGGGGAGAGCTTACGATCAACTTC 2175
QY 781 AsnIleThrLysAspThrArgPheAlaGluLeuLeuAlaLeuGluSerGluAlaGlyVal 800
Db 2176 AACATCACCAGGACACAGAGTTTGTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGTC 2235
QY 801 ProAlaLeuValGlyProSerAlaPheLysIleProPheLeuIleArgGlnLysIleIle 820
Db 2236 CAGACCTGTGGTGGCCCGCAGTGCCTTCAGATCCCTTCTCATTCGGCAGAGATAT 2295
QY 821 SerSerLeuAspProProCysArgArgGlyAlaAspTrpArgThrLeuAlaGlnLysLeu 840
Db 2296 TCCAGAGCTGACCCAGCCCTGTAGCGGGGTGCGGACTTGGCGGACTCTGGGCCAGAACTC 2355
QY 841 HisLeuAspSerHisIleSerPhePheAlaSerLysProSerProThrAlaMetIleLeu 860
Db 2356 CACTGTGACAGCCATCTCAGCTTCTTTGGCTTCCAAAGCCCGAGCCCCACAGCCATGATCCCT 2415
QY 861 AsnLeuTrpGluAlaArgHisPheProAsnGlyAsnLeuSerGlnLeuAlaAlaVal 880
Db 2416 AACCTGTGGAGGGCGGCGACTTCCCAACGGCACTCAGCCAGCTGGCTGCAGCAGTG 2475
QY 881 AlaGlyLeuGlyGlnProAspAlaGlyLeuPheThrValSerGluAlaGluCys 898
Db 2476 GCTGGAGTGGCCAGCAGACGCTGGCTTTCACAGTGTGGAGGCTGAGTGC 2529

RESULT 10

US-09-933-261-2

; Sequence 2, Application US/09933261

; Publication No. US20030040046A1

; GENERAL INFORMATION:

; APPLICANT: Tessier-Lavigne, Marc

; Leonardo, E. David

; Hink, Lindsey

; Masu, Masayuki

; Kazuko, Keino-Masu

; TITLE OF INVENTION: Netrin Receptors

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

; STREET: 268 BUSH STREET, SUITE 3200

; CITY: SAN FRANCISCO

; STATE: CALIFORNIA

; COUNTRY: USA

; ZIP: 94104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/933,261

; FILING DATE: 20-Aug-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/808,982

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: OSMAN, RICHARD A

; REGISTRATION NUMBER: 36,627

; REFERENCE/DOCKET NUMBER: UC96-217

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 343-4341

; TELEFAX: (415) 343-4342

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1787 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-933-261-2

Alignment Scores:

Pred. No.: 3 61e-276 Length: 1787
Score: 2710.00 Matches: 544
Percent Similarity: 97.50% Conservative: 1
Best Local Similarity: 97.32% Mismatches: 11
Query Match: 56.56% Indels: 9
DB: 10 Gaps: 0

US-10-624-932C-2 (1-898) x US-09-933-261-2 (1-1787)

QY 343 AsnCysThrSerAspLeuCysValHisSerAlaSerGlyProGluAspValAlaLeuTyr 362
Db 3 AACTGTACAGTGACCTCTG-GTACACACTGCTTCTGGCCCTGAGGACGTGGCCCTCTAT 61
QY 363 ValGlyLeuIleAlaValAlaValCysLeuValLeuLeuLeuValLeuVal 382
Db 62 GTGGGCTCATCGCCGTGGCTGCTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 121
QY 383 TyrCysArgLysLysGluGlyLeuAspSerAspValAlaAspSerSerIleLeuThrSer 402
Db 122 TATTGCGGAGAGAGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTCACCCTCA 181
QY 403 GlyPheGlnProValSerIle-LysProSerLysAlaAspAsnProHisLeuLeuThrI 422
Db 182 GGCTTCCAGCCGCTCAGCATCTAAGCCAGCAAGCAGACAACCCCATCTGCTCACCAT 241
QY 422 eGlnProAspLeuSerThrThrThrThrThrThrThrThrThrThrThrThrThrThr 442
Db 242 CCAGCCGAGCCTCAGCACCAACCACCACTACACAGGGCAGTCTCTGTCCCGGAGGAG 301
QY 442 pGlyProSerProLysPheGlnLeuThrAsnGlyHisLeuLeuSerProLeuGlyGlyG 462
Db 302 TGGGCCAGCCGCCAGTTCCAGCTCACCATTGGGCACCTGTCTCAGCCCCCTGGGTGGCG 361
QY 462 yArgHisThrLeuHisHisSerSerProThrSerGluAlaGluGluPheValSerArgLe 482
Db 362 CGGCCACACACTGCACACACAGCTCTCCACCTCTGAGGGCGAGGAGTTCGTCTCCGCGCT 421
QY 482 uSerThrGlnAsnTyrPheArgSerLeuProArgGlyThrSerAsnMetThrTyrGlyTh 502
Db 422 CTCACCCAGAACTACTTCCGCTCCCTGCCCGGAGGACACAGCAACATGACCTATGGAC 481
QY 502 rPheAsnPheLeuGlyArgLeuMetIleProAsnThrGlyIleSerLeuLeuIlePr 522
Db 482 CTTCAACTTCTCGGGGGCGGCTGATGATCCCTAATACAGGAATCAGCCTCTCATCCC 541
QY 522 oProAspAlaIleProArgGlyLysIleTyrGluIleTyrLeuThrLeuHisLysProGl 542
Db 542 CCAGATATGCCATACCCCGAGGGAAGATATATGAGATCTACCTCAGCGTGCACAAAGCGGA 601
QY 542 uAspValArgLeuProLeuAlaGlyCysGlnThrLeuLeuSerProIleValSerCysGl 562
Db 602 AGACGTGAGGTGCCCCCTAGCTGGCTGTGAGACCCCTGAGTCCCATCTGTTAGCTGTGG 661
QY 562 yProGlyValLeuLeuThrArgProValIleLeuAlaMetAspHisCysGlyGluPr 582
Db 662 ACCCCCTGGGCTCTGCTCACC CGGCGCAGTCTCTGGCTATGAGACCATGTGGGAGCC 721
QY 582 oSerProAspSerTrpSerLeuArgIleLysLysGlnSerCysGluGlySerTrpGluAs 602
Db 722 CAGCCCTGACAGCTGGAGGCTGGCCCTCAAAAAAGCAGTCTGTGCGAGGAGC-TGGGAGGA 780
QY 602 pValLeuHisLeuGlyGluGluAlaProSerHisLeuTyrCysGlnLeuGluAlaSe 622
Db 781 TGT-CTGACACCTGGGCGAGAGGGCCCTCCCACTCTACTCTGCTGAGTGGAGGCGAG 839
QY 622 rAlaCysTyrValPheThrGluGlnLeuGlyArgPheAlaLeuValGlyGluAlaLeuSe 642


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Qy 502 rPheAenPheLeuGlyGlyArgGleuMetIleProAenThrGlyIleSerLeuLeuIlePr 522
Db 482 CTTCAACTTCTCGGGGGCGGGCTGATGATCCCTAATACAGGAATCAGCCCTCTCATPCC 541
Qy 522 oProAapAlaIleProArgGlyLysIleTyrgluIleTyrluLeuThrLeuHisLysProGl 542
Db 542 CCAGATGCCATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAGCGGA 601
Qy 542 uAapValArgLeuProLeuAlaGlyCysGlnThrLeuLeuLeuSerProIleValSerCysGl 562
Db 602 AGACGTGAGGTTCGCCCTAGCTGGCTGTGCAGACCCCTGCTGAGTCCCATCGTTAGCTGTGG 661
Qy 562 yProProGlyValLeuLeuThrArgProValIleLeuAlaMetAspHisCysGlyGluPr 582
Db 662 ACCCCCTGGCGCTCTGCTACCCGGCCGAGTCATCTCGGCTATGGACCATGTGGGAGGCC 721
Qy 582 oSerProAapSerTrpSerLeuArgLeuLysLysGlnSerCysGluGlySerTrpGluAs 602
Db 722 CAGCCCTGACAGCTGGAGCCTGGCCCTCAAAAGACAGTGTGTGAGGGAGC-TGGAGGA 780
Qy 602 pValLeuHisLeuGlyGluGluAlaProSerHisLeuTyrrTyrrCysGlnLeuGluAlaSe 622
Db 781 TGT-CTGACCTGGCGAGGAGCGGCCCTCCACCTCTACTACTGCGAGCTGGAGGCCAG 839
Qy 622 rAlaCysTyrrValPheThrGluGlnLeuGlyArgPheAlaLeuValGlyGluAlaLeuSe 642
Db 840 TGCCTGCTACGTCTTACCAGAGCAGTGGGCCCTTGTGCCCTGGTGGGAGAGGCCCTCAG 899
Qy 642 rValAlaAlaAlaLysArgLeuLysLeuLeuLeuPheAlaProValAlaCysThrSerLe 662
Db 900 CGTGGCTGCCGCCNAGCGCCTCAAGCTGCTTCTGTTGGCCGGTGGCTGCACCTCCCT 959
Qy 662 uGluTyrrAsnIleArgValTyrrCysLeuHisAspThrHisAspAlaLeuLysGluValVa 682
Db 960 CGAGTACAAACATCCGGGTCTACTGCTGTCATGACACCCACGATGCCTCAAGGAGGTGT 1019
Qy 682 lGlnLeuGluLysGlnLeuGlyGlnLeuIleGlnGluProArgValLeuHisPheLys 702
Db 1020 GCAGCTGGGAAGAGCAGCTGGGGGACAGCTGATCCAGAGGCCACGGGTCTCTGCACATT-AA 1078
Qy 702 sAapSerTyrrHisAsnLeuArgLeuSerIleHisAspValProSerSerLeuTrpLysSe 722
Db 1079 GGACAGTTACCAACACTGCC-CTATC-ATCCAGATGTGCCAGCTCCCTGTGGAGAG 1136
Qy 722 rLysLeuLeuValSerTyrrGlnGluIleProPheTyrrHisIleTrpAsnGlyThrGlnAr 742
Db 1137 TAAGCTCCTTGTGAGCTTACCAGGAGATCCCTTTTATCATCATCTGGAATGGCAGCGC 1196
Qy 742 gTyrrLeuHisCysThrPheThrLeuGluArgValSerProSerThrSerAspLeuAlaCy 762
Db 1197 GTACTTGCATGCACTTCACTTACCTGGAGCGGTGTGAGCCCGACGACTAGTACCTGGCGCTG 1256
Qy 762 sLysLeuTrpValTrpGlnValGluGlyAspGlyGlnSerPheSerIleAsnPheAsnIl 782
Db 1257 CAAGCTGTGGGTGGCAGGTGGAGGGCGAGCGGCAGAGCTTCAGCATCAACTTCAACAT 1316
Qy 782 eThrLysAspThrArgPheAlaGluLeuLeuAlaLeuGluSerGluAlaGlyValProAl 802
Db 1317 CACCAAGGACACAAAGTTTCTCAGCTGTGGTCTGTGAGAGTGAAGCGGGGGTCCGAGC 1376
Qy 802 aLeuValGlyProSerAlaPheLysIleProPheLeuIleArgGlnLysIleIleSerSe 822
Db 1377 CTGGGTGGGCCCCAGTTCAGATPCCCTTCTCATTCGGGAGAGATAATTTCCAG 1436
Qy 822 rLeuAapProProCysArgArgGlyAlaAapTrpArgThrLeuAlaGlnLysLeuHisLe 842
Db 1437 CCTGGACCCACCTGTAGGCGGGGTGCCGACTGGCGAGCTCTGGCCACAGAACTCCACCT 1496
Qy 842 uAapSerHisLeuSerPhePheAlaSerLysProSerProThrAlaMetIleLeuAsnLe 862
Db 1497 GGACAGCATCTCAGCTTCTTTGCTTCAAGCCGAGCCCGCCACAGCCCATGATCTCAACCT 1556
Qy 862 uTrpGluAlaArgHisPheProAenGlyAsnLeuSerGlnLeuAlaAlaValAlaGl 882
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Db 1557 GTGGGAGGCGGGCAGCTTCCCAACGGCAACCTCAGCAGCTGCTGCAGCAGTGGCTGG 1616
Qy 882 yLeuGlyGlnProAapAlaGlyLeu-PheThrVal-SerGluAlaGluCys 898
Db 1617 GACTGGCCAGCAGGACGGTGGCTTCTTTCACAGTGTTCGAGGCTGAGTGC 1667

RESULT 12
US-10-764-420-2213
; Sequence 2213, Application US/10764420
; Publication No. US20050084872A1
; GENERAL INFORMATION:
; APPLICANT: Lum, Pek Yee
; APPLICANT: Ian, Yejun
; TITLE OF INVENTION: Methods For Determining Whether An Agent
; TITLE OF INVENTION: Possesses A Defined Biological Activity
; FILE REFERENCE: ROSA122057
; CURRENT APPLICATION NUMBER: US/10/764,420
; CURRENT FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: US 60/442,797
; PRIOR FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: US 60/474,413
; PRIOR FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 3683
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2213
; LENGTH: 3866
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-764-420-2213

Alignment Scores:
Pred. No.: 4,32e-261 Length: 3866
Score: 2572.50 Matches: 505
Percent Similarity: 68.80% Conservative: 150
Best Local Similarity: 53.05% Mismatches: 236
Query Match: 53.69% Indels: 61
DB: 21 Gaps: 15

US-10-624-932C-2 (1-898) x US-10-764-420-2213 (1-3866)
Qy 1 MetAlaValArgProGlyLeuTrpProAlaLeuLeuGlyIleValLeuAlaAlaTrp--- 19
Db 417 ATGAGGCGCGGAGCGGGGTGGGAGCGCGCTGCTGCTGGCGCTGCTGCTTCTGGGAT 476
Qy 20 -----LeuArgGly-----SerGlyAlaGlnGlnSerAlaThrValAlaAsn 33
Db 477 CCGACACCGAGCCTAGCAGGCGTTGACTCTGCTGGCCAG-----GTGCTCCCAGAC 527
Qy 34 ProValProGlyAlaAsnProAapLeuLeuProHisPheLeuValGluProGluAapVal 53
Db 528 TCCTACCCATCAGCCCTCGGAGCAGCTGCCGTACTTCTATTGGGCCACAGGACGCC 587
Qy 54 TyrrIleValLysAsnLysProValLeuLeuValCysLysAlaValProAlaThrGlnIle 73
Db 588 TACATCGTAAAGAACCAAGCCAGTGGAACTGCACTGCAGAGCCTTCCCTGCCACGAGATC 647
Qy 74 PhePheLysCysAsnGlyGluTrpValArgGlnValAspHisValIleGluArgSerThr 93
Db 648 TACTTCAAGTGTAAATGCGAGTGGGTGAGCCAGCAATGACCACGTCACACAGGAGAGCCTG 707
Qy 94 AspGlySerSerGlyLeuProThrMetGluValArgIleAsnValSerArgGlnGlnVal 113
Db 708 GATGAGGCCACAGCCTTGGCGGTGCGAGAGGTGCAGATCGAGGTGTACGCGCAGCAAGTG 767
Qy 114 GluLysValPheGlyLeuGluTyrrTyrrCysGlnCysValAlaAlaTrpSerSerGly 133
Db 768 GAGAAACTCTTCGGGCTCGAGGACTACTGTGTGCAGTGTGCTGCGCTGGAGCTCTTCGGGA 827
Qy 134 ThrThrLysSerGlnLysAlaTyrrIleArgIleAlaArgLeuArgLysAsnPheGluGln 153
Db 828 ACTACCAAGAGTCGCGGAGCCTACATCCGCACTTGCCTACTTTCGCAAGAACTTTTGACCAG 887
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154 GluProLeuAlaLysGluValSerLeuGluGlnGlyIleValLeuProCysArgProPro 173
| | | | | : : : : :
Db GAGCTCTGGCCAGGAGTACCTTGGATCATGAGTCTCTGCACTGCGGCCACCG 947

174 GluGlyIleProProAlaGluValGluTrpLeuArgAsnGluAspLeuValAspProSer 193
| | | | | : : : : :
Db GAGGAGTGGCTGTGGCTGAGTGAATGGCTCAAGATGAAGATGTCAATTGACCCCGCT 1007

194 LeuAspProAsnValTyrIleThrArgGluHisSerLeuValValArgGlnAlaArgLeu 213
| | | | | : : : : :
Db CAGGACACTAATCTCTCTGCTCACCATTGACCACCACTCATCCGCGCAGCGCGCTC 1067

214 AlaAspThrAlaAsnTyrThrCysValAlaLysAsnIleValAlaArgArgSerAla 233
| | | | | : : : : :
Db TCAGACGGCCCACTACACCTGTGTGGCCAGGAATATCGTGGCCAGGCGCGGAGCACC 1127

234 SerAlaAlaValIleValTyrValAsnGlyTyrTrpSerThrTrpGluTrpSerVal 253
| | | | | : : : : :
Db CGGCCACAGTCATCGTCTATGTGAATGGAGCTGGTCCAGTGGCCAGAGTGGTCAACC 1187

254 CysSerAlaSerCysGlyArgGlyTyrGlnLysArgSerArgSerCysThrAsnProAla 273
| | | | | : : : : :
Db TGTTCCAATCGCTGTGGCCGAGGCTGGCAGAGCGTACTCGGACCTGCACCAATCCAGCC 1247

274 ProLeuAsnGlyIleAlaPheCysGluGlyGlnAsnValGlnLysThrAlaCysAlaThr 293
| | | | | : : : : :
Db CCACTCAATGAGGGCTCTCTGTGAGGGAAGGCTTCCAGAGACAGCTTGCACACC 1307

294 LeuCysProValAspGlySerTrpSerProTrpSerLysTrpSerAlaCysGlyLeuAsp 313
| | | | | : : : : :
Db GTGTGCCAGTGGATGAGCGGTGAGCGTGGACGAGTGGAGCAAGTGGTCTGCGCTGCAGCACAG 1367

314 CysThrHisTrpArgSerArgGluCysSerAspProAlaProArgAsnGlyIleGluGlu 333
| | | | | : : : : :
Db TGTGCGCACTGGCGAGCGGAGTGGATGCGACCGCCACCGCCAGAACGGAGGCGGTGAC 1427

334 CysGlnGlyThrAspLeuAspThrArgAsnCysThrSerAspLeuCysVal----- 350
| | | | | : : : : :
Db TGCAGGGGAGCTACTTGCATCCAGNACTGCATGATGGGCTGTGGTGTGCTGAATCAG 1487

351 -----HisSerAlaSerGlyProGluAspValAlaLeuTyr 362
| | | | | : : : : :
Db AGAACTCTAAACGACCCCTAAAGCCACCCCTGGAGACATCGGGAGATGTGGCACTGTAC 1547

363 ValGlyLeu-----IleAlaValAlaValCysLeuValLeuLeuValLeuLeu 381
| | | | | : : : : :
Db GCAGGCTTGTGGTGGCGCTCTTTGTGGTGTAGCGTCTCATGGCGGAGGAGTGATC 1607

382 ValTyrCysArgLysGlyLeuAspSerAspValAlaAspSerSer-----IleLeu 400
| | | | | : : : : :
Db GTATACCGGAGAACTGCCGGGACTTCGACACGACGACATCACCGACTCTCTGCGGCCCTC 1667

401 ThrSerGlyPheGlnProValSerIleLysProSerLysAlaAspAsnProHisLeuLeu 420
| | | | | : : : : :
Db ACTGGTGGCTTCCACCTGTCAACTTCAAGACTGCAAGGCCCAACACCCCGCAGCTCTG 1727

421 -----ThrIleGlnProAspLeuSerThrThrThrThrThrThrThrThrThrThr 438
| | | | | : : : : :
Db CACCCGCTCCGCTCCAGACTTAACGGCCAGTGGCTGGCACTACCGCGGCGCTGTGTAT 1787

439 ProArgGlnAspGlyProSerProLysPheGlnLeuThrAsnGlyHisLeuLeuSerPro 458
| | | | | : : : : :
Db GCGTGCAGGACTCC---GCCGACAGATCCCGCATGACTAATTCGCGCTGCTGGATCCC 1844

459 LeuGlyGlyArgHisThrLeuHisSerSer----- 470
| | | | | : : : : :
Db CTGCCAGCCTCAAGATCAAGGTCTATAACTCCAGCACCATCGGTCTGGGTCTGGCGCTG 1904

471 -----ProThrSerGluAlaGluLupheVal 479
| | | | | : : : : :
Db GCTGATGAGCGGACCTGCTGGGTGTCTCTCCCGCGGCGACGTACCCAGGCGGATTC--- 1961

480 SerArgLeuSerThrGlnAsnTyrPheArgSer----- 490
| | | | | : : : : :
Db TCCCGGACACCCCATTTCTTCGACCTGGCAGTCCAGCCTTGGTCCAGCACCTCTCTG 2021

491 ---LeuProArgGlyThrSerAsnMetThrTyrGlyThrPheAsnPheLeuGlyGlyArg 509
| | | | | : : : : :
Db GGCTCTAGCTCGGACCCAGCAGCAGTGTACGCGGCACCTTTGGTGTGGAGGAAGG 2081

510 LeuMetIleProAsnThrGlyIleSerLeuLeuIleProProAspAlaIleProArgGly 529
| | | | | : : : : :
Db CTGAGCTCCCGGCAAGGGGTGAGCTGTGTGTACCAATGGAGGCATTTCCCGAGGC 2141

530 LysIleTyrGluIleTyrLeuThrLeuHisLysProGluAspValArgLeuProLeuAla 549
| | | | | : : : : :
Db AAGTTCTATGACCTGTATCTACATATCAACAGGCCGGAAGCACC---CTCCACTTCA 2198

550 ---GlyCysGlnThrLeuLeuSerProIleValSerCysGlyProProGlyValLeuLeu 568
| | | | | : : : : :
Db GAAGGTTCACAGACAGTATTGAGCCCTCGGTGACCTGTGGGCCACAGGCTACTCTG 2258

569 ThrArgProValIleLeuAlaMetAspHisCysGlyGluProSerProAspSerTrpSer 588
| | | | | : : : : :
Db TGCAGCTGTGTGCTCTACCGTCCCCCTGTCTGAACTCATCGTGGAGACTGGATC 2318

589 LeuArgLeuLysLysGlnSerCysGluGlySerTrpGluAspValLeuHisLeuGlyGlu 608
| | | | | : : : : :
Db TTTTCAGCTCAAGACCCAGGCCCATCAGGCCACTGGGAGGAGTGGTGCATTTGATGAG 2378

609 GluAlaProSerHisLeuTyrTyrCysGlnLeuGluAlaSerAlaCysTyrValPheThr 628
| | | | | : : : : :
Db GAGACCTCAACACACCTGTCTGTCAGCTGGAGGCTAAGTCTCTGCACATCTCTGCTG 2438

629 GluGlnLeuGlyArgPheAlaLeuValGlyGluAlaLeuSerValAlaAlaLysArg 648
| | | | | : : : : :
Db GACCACTGGGTCTCTACGATTTCATGGGCGAGTCTACTCTCGCTCTGCAAGTCAAGCGG 2498

649 LeuLysLeuLeuLeuPheAlaProValAlaCysThrSerLeuGluTyrAsnIleArgVal 668
| | | | | : : : : :
Db CTCAGCTGGCCATCTTCGCCCCCAGCCCTCTGCACCTCCCTGGAGTATAGCTCAGGGTC 2558

669 TyrCysLeuHisAspThrHisAspAlaLeuLysGluValValGlnLeuGluLysGlnLeu 688
| | | | | : : : : :
Db TACTGTCTGGAGGACACACCTGTAGCAGTGAAGGAGTCTCTGGAGCTGGAGGACTCTG 2618

689 GlyGlyGlnLeuIleGlnGluProArgValLeuHisPheLysAspSerTyrHisAsnLeu 708
| | | | | : : : : :
Db GGTGGCTACTTGGTGGAGGAGCCCAAGCTTGTCTTTAAGGACAGTTACCAACACTA 2678

709 ArgLeuSerIleHisAspValProSerSerLeuTrpLysSerLysLeuLeuValSerTyr 728
| | | | | : : : : :
Db CGCTCTCTCCATGACATCCCTCCATGCCCTCCAGCTGGAGGAGCAACTACTTGGCCAGTAC 2738

729 GlnGluIleProPheTyrHisIleTrpAsnGlyThrGlnArgTyrLeuHisCysThrPhe 748
| | | | | : : : : :
Db CAGGAGATTCCTTCTACCACTGTGGAATGGCAGCAGAGAGCCCTGCATCGACTCTTC 2798

749 ThrLeuGluArgValSerProSerThrSerAspLeuAlaCysLysLeuLeuTrpValTrpGln 768
| | | | | : : : : :
Db ACCCTGAGAGGCATAGCTGGCTCCACGGAGTTCACCTGTAAAGTCTGGCTGGCGGAG 2858

769 ValGluGlyAspGlyGlnSerPheSerIleAsnPheAsnIleThrLysAspThrArgPhe 788
| | | | | : : : : :
Db GTCGAGGGGAGGCCAGATTTTCCAGCTGCACACACGTTGGCC---GAGACGCTGCT 2915

789 AlaGlnLeuLeuAlaLeuGluSerGluAlaGly-----ValProAlaLeuValGlyPro 806
| | | | | : : : : :
Db GGCTCCCTGGATGTCTCTGCTCTGCTGCGCGCAATGCCATCACCCAGCTGGAGCCC 2975

807 SerAlaPheLysIleProPheLeuIleArgGlnLysIleSerSerLeuLeuAspPro 826
| | | | | : : : : :
Db TATGCTTCAAGATACCCCTGTCCATCCGCCAAAGATCTGCAGACGCTGGAGCGCCCC 3035

827 CysArgGlyAlaAspTrpArgThrLeuAlaGlnLysLeuHisLeuAspSerHisLeu 846
| | | | | : : : : :
Db

Db 3036 GATCCGGGGGCAACGACTGGAGCTGTGGCGCAGAACTGTCCATGGACCGGTACCTA 3095
Qy 847 SerPhePheAlaSerLysProSerProThrAlaMetIleLeuAsnLeuTrpGluAlaArg 866
Db 3096 AACTACTTCGCCACCAAGAGTAGTCCACAGGTGTCTATCTAGACCTCTGGGAAGCTCGG 3155
Qy 867 HisPheProAsnGlyAsnLeuSerGlnLeuAlaAlaValAlaGlyLeuGlyGlnPro 886
Db 3156 CAACAGGATGACGGGACCTCAACAGCTGGCCAGTGCCTTGGAGGAGATGGGCAAGAGT 3215
Qy 887 AspAlaGlyLeuPheThrValSerGluAlaGluCys 898
Db 3216 GAGATGCTGGTAGCCATGGCCACAGATGGCGATTGC 3251

RESULT 13

US-10-087-684-1
; Sequence 1, Application US/10087684
; Publication No. US20040029116A1
; GENERAL INFORMATION:
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: MacDougall, John R.
; APPLICANT: Millet, Isabelle
; APPLICANT: Ellerman, Karen
; APPLICANT: Stone, David J.
; APPLICANT: Grosse, William M.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Li, Li
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Mishra, Vishnu
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Rastelli, Luca
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Miller, Charles E.
; APPLICANT: Gangolli, Esha A.
; TITLE OF INVENTION: PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-214 CIP
; CURRENT APPLICATION NUMBER: US/10/087,684
; CURRENT FILING DATE: 2003-03-10
; PRIOR APPLICATION NUMBER: 60/253,834
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 60/250,926
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 60/264,180
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/274,194
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/313,656
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/327,456
; PRIOR FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 220
; SOFTWARE: Curaseqlist version 0.1
; SEQ ID NO 1
; LENGTH: 2860
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (59) .. (2857)
US-10-087-684-1

Alignment Scores:

Pred. No.: 2,46e-260 Length: 2860

Score: 2563.50 Matches: 501
Percent Similarity: 69.08% Conservative: 147
Best Local Similarity: 53.41% Mismatches: 245
Query Match: 53.51% Indels: 45
DB: 17 Gaps: 15
US-10-624-932c-2 (1-898) x US-10-087-684-1 (1-2860)
Qy 1 MetAlaValArgProGlyLeuTrpProAlaLeuLeuGlyIleValLeuAlaAlaTrp--- 19
Db 59 ATGGGGGCCCGAGCGAGCTGGGGCGCGCTGCTGTGGCACTGTCTCTGGAC 118
Qy 20 -----LeuArgGlySerGlyAlaGlnGln---SerAlaThrValAlaAsnProValPro 36
Db 119 CCGAGGCTGAGCCAAGCAGCGACATGATCTGGCAGCGAGGTGCTCCTGACTCTTCCCG 178
Qy 37 GlyAlaAsnProAspLeuLeuProHisPheLeuValGluProGluAspValTyrIleVal 56
Db 179 TCAGCGCCAGCAGAGCGGTGCTTCTTCTGAGAGCCACAGAGCGCTTACATTGTG 238
Qy 57 LysAsnLysProValLeuLeuValCysLysAlaValProAlaThrGlnIlePhePheLys 76
Db 239 AAGAACAAAGCTGTGGAGCTCGCTGCCGCGCTTCCGCCACACAGATCTACTTCAAG 298
Qy 77 CysAsnGlyGluTrpValArgGlnValAspHisValIleGluArgSerThrAspGlySer 96
Db 299 TGCACCGCGAGTGGGTGAGCCAGACGACACGCTCACAGGAAGCGCTTGGATGAGGCC 358
Qy 97 SerGlyLeuProThrMetGluValArgIleAsnValSerArgGlnGlnValGluLysVal 116
Db 359 ACCGCTCTGGGGTGGCGAGGTGCAGATCGAGTGTCCGGCAGCAGGTGGAGGAGCTC 418
Qy 117 PheGlyLeuGluGluTyrTrpCysGlnCysValAlaTrpSerSerSerGlyThrLys 136
Db 419 TTTGGCTGGAGGATTACTGGTCCAGTGTGGCTCGCTGGAGTCTCCGGGACACCAAG 478
Qy 137 SerGlnLysAlaTyrIleArgIleAlaArgLeuArgLysAsnPheGluGlnGluProLeu 156
Db 479 AGTCGCCGAGCTTACGTCCGATCGCTTCTCTCAGTGGCCGCGCGCGAGGGGGTG 538
Qy 157 AlaLysGluValSerLeuGluGlnGlyIleValLeuProCysArgProGluGlyIle 176
Db 539 GGCACAGAGGTGCCCTTGGACCATGAGTTCCTCTCAGTGGCCGCGCGAGGGGGTG 598
Qy 177 ProProAlaGluValGluTrpLeuArgAsnGluAspLeuValAspProSerLeuAspPro 196
Db 599 CTTGTGGCGAGGTGGAATGGTCAAGAATGAGGATGTATCGACCCACCCAGGACACC 658
Qy 197 AsnValTyrIleThrArgGluHisSerLeuValValArgGlnAlaArgLeuAlaAspThr 216
Db 659 AACTTCTGTCTACCATCGACCAACCTCATCTCCGCGAGCGCGCTGTCTGGACACT 718
Qy 217 AlaAsnTyrThrCysValAlaLysAsnIleValAlaArgArgSerAlaSerAlaAla 236
Db 719 GCCAACTATACCTGCTGGCCAGAACATCGTGGCCAAAGCGCGAGCACCCTGCCACC 778
Qy 237 ValIleValTyrValAsnGlyGlyTrpSerThrTrpThrGluTrpSerValCysSerAla 256
Db 779 GTCATGCTCTACGTGAATGGCTCCAGTGGCGAGAGTGGTGCACCCCTCTCCCAAC 838
Qy 257 SerCysGlyArgGlyTrpGlnLysArgSerArgSerCysThrAsnProAlaProLeuAsn 276
Db 839 CGCTGTGGCGAGGCTGGGAGAACGCCACCCGAGCTTGCACCAACCCCGCTTCACTCAAC 898
Qy 277 GlyGlyAlaPheCysGluGlyGlnAsnValGlnLysThrAlaCysAlaThrLeuCysPro 296
Db 899 GGAGGGGCGCTTCTGCGAGGCGCCAGGCATTCACAAGACCGCTGTCACCATCTGCCCA 958
Qy 297 ValAspGlySerTrpSerProTrpSerLysTrpSerAlaCysGlyLeuAspCysThrHis 316
Db 959 GTCGATGGGGCGTGGACGAGTGGCAAGTGGTTCAGCTGACGCTGACGAGCTGTGCCCCAC 1018
Qy 317 TrpArgSerArgGluCysSerAspProAlaProArgAsnGlyGlyGluGluCysGlnGly 336


```
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Zernhuesen, Bryan D.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Miller, Charles E.
; APPLICANT: Gangolli, Baha A.
; TITLE OF INVENTION: PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-214 CIP
; CURRENT APPLICATION NUMBER: US/10/087,684
; CURRENT FILING DATE: 2003-03-10
; PRIOR APPLICATION NUMBER: 60/253,834
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 60/250,926
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 60/264,180
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/274,194
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/313,656
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/327,456
; PRIOR FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 220
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 3
; LENGTH: 2860
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (59)..(2857)
US-10-087-684-3

Alignment Scores:
Pred. No.: 2,46e-260 Length: 2860
Score: 2563.50 Matches: 501
Percent Similarity: 69.08% Conservative: 147
Best Local Similarity: 53.41% Mismatches: 245
Query Match: 53.51% Indels: 45
DB: 17 Gaps: 15

US-10-624-932C-2 (1-898) x US-10-087-684-3 (1-2860)

QY 1 MetAlaValArgProGlyLeuTrpProAlaLeuLeuGlyLeValLeuAlaAlaTrp--- 19
DB 59 ATGGGGCCCGAGCGAGAGTCGGGGCGCGCTGCTGGCACTGGCTGCTCTCTGGAC 118
QY 20 -----LeuArgGlySerGlyAlaGlnGln---SerAlaThrValAlaAenProValPro 36
DB 119 CCAGGCTGAGCCAGCAGGACATGATTCTGGCAGCGAGGTGCTCCTGACTCTCTCCCG 178
QY 37 GlyAlaAenProAspLeuLeuProHisPheLeuValGluProGluAspValTrileVal 56
DB 179 TCAGCGCCAGCAGAGCGCTGCCCTACTCTCTGAGGAGCCACAGGAGCGCTACATTGTG 238
QY 57 LysAenLysProValLeuLeuValCysLysAlaValProAlaThrGlnLilePhePheLys 76
DB 239 AAGAACAGCCTGTGAGCTTCGCTGCGCGCCTTCCCGCCACACAGATCTACTTCAAG 298
QY 77 CysAenGlyLutTrpValArgGlnValAspHisValIleGluArgSerThrAspGlySer 96
DB 299 TGCAACGGCGAGTGGGTGACCCAGAGACACACGTACACAGAGGAGGCTGGATGAGGCC 358
QY 97 SerGlyLeuProThrMetGluValArgIleAsnValSerArgGlnGlnValGluLysVal 116
DB 359 ACCGGCTGCGGGTGGCGAGGTGCAGATTCAGGTGTGCGGCGCAGCAGGTGGAGGAGCTC 418
QY 117 PheGlyLeuGluLutTrpCysGlnCysValAlaTrpSerSerSerGlyThrThrLys 136
DB 419 TTTGGGCTGGAGGATTACTGGTCCAGTGGCTGGAGTCCGAGGACACACCAAG 478
QY 137 SerGlnLysAlaTrileArgIleAlaArgLeuArgLysAenPheGluGlnGluProLeu 156
DB 1550 ACATACCTTAGCAGATTTCGCCCGGGGACACCCACTTCTTCTGCACCTGCGCAGCGCAGCCTC 1609

479 AGTCGCGGAGCCCTACGTCCGCACTACCTACCTGCGCAAGAACTTCGATCAGGAGCCCTCTG 538
157 AlaLysGluValSerLeuGlnGlyIleValLeuProCysArgProGluGlyIle 176
539 GGCAGGAGGTGCCCTCGACCATGAGTTCTCTCAGTGCCTCCGCCCGCGGAGGGGTG 598
177 ProProAlaGluValGluTrpLeuArgAenGluValAspLeuValAspProSerLeuLeuAspPro 196
599 CTTGTGGCGGAGTGGATGGCTCAAGATGAGGATGTATCGACACCCACCCACACACC 658
197 AsnValTrpIleThrArgGluHisSerLeuValValArgGlnAlaArgLeuAlaAspThr 216
659 AACTTCTGCTACCATCGACCACTCATCTCGGCGAGCCCGCTCTGGGACACT 718
217 AlaAsnTrpThrCysValAlaLysAenIleValAlaArgArgSerAlaSerAlaAla 236
719 GCCAACTATACCTGCGTGCCAAAGACATCGTGCCAAACGCCGAGGACCACTGCCACC 778
237 ValIleValTrpValAsnGlyTrpSerThrTrpThrGluTrpSerValCysSerAla 256
779 GTCATCTGTAGTGAATGGCGCTGTCGAGAGAGTGGTGCAGAGTGGTGCAGCTGCTCCAAC 838
257 SerCysGlyArgGlyTrpGlnLysArgSerArgSerCysThrAsnProAlaProLeuAsn 276
839 CGCTGTGGCGGAGCTGGCAGAGCGCACCGGACCTGCACCAACCCCGCTCCACTCAAC 898
277 GlyGlyAlaPheCysGluGlnAenValGlnLysThrAlaCysAlaThrLeuCysPro 296
899 GGAGGGCCCTTCTCGAGGGCCAGGCAATTCAGAGAGCGCTGCACCACTCATCTGCCCA 958
297 ValAspGlySerTrpSerProTrpSerLysTrpSerAlaCysGlyLeuAspCysThrHis 316
959 GTCGATGGGGCGTGGAGGAGTGGCAAGTGGTGCAGCTGCAGCACTGAGTGTGCCAC 1018
317 TrpArgSerArgGluCysSerAspProAlaProArgAsnGlyGlyGluGluCysGlnGly 336
1019 TGGCGTAGCGCGAGTGCATGGCGCCGCCACCCACAGCGGAGCGCTGACTGCAGCGGG 1078
337 ThrAspLeuAspThrArgAenCysThrSerAspLeuCysValHis---SerAlaSerGly 355
1079 ACCTGCTCGACTCTAAGAACTGCACAGATGGGCTGTGCATGCAACTGGAGGCGCTCAGGG 1138
356 ProGluAspValAlaLeuTrpValGlyLeu---IleAlaValAlaValCysLeuValLeu 374
1139 -----GATGCGCGCTGTATGCGGGCTGCTGGTGCCATCTCGTGTGCTGGGCATC 1192
375 LeuLeuLeuValLeuIleLeuValTrpCysArgLysLysGluGlyLeuAspSerAspVal 394
1193 CTCATGGCGTGGGGGTGGTGTGTACCGCCCACTGCCGTGACTTCGACACAGACATC 1252
395 AlaAspSerSer---IleLeuThrSerGlyPheGlnProValSerLysProSerLys 413
1253 ACTGACTCATCTGCTCCCTGACTGTGTGTTCACCCCGTCAACTTTAAGACGCGCAAG 1312
414 AlaAspAsnProHisLeuLeu-----ThrIleGlnProAspLeuSerThrThrThr 431
1313 CCAGTAACCCGAGCTCTTACACCCCTCTGCGCTCTGACCTGACGCGCAGCGCGCGC 1372
432 ThrTrpGlnGlySerLeuCysProArgGlnAspGlyProSerProLysPheGlnLeuThr 451
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1430 AACTCTCTCTGTGTGACCCCTTACCCAGCTTAAAGTCAAGGTCAAGTCTACAGCTCCAGCACC 1489
472 Thr-----SerGluAlaGluPheValSerArgLeuSerThrGln 485
1490 ACCGGCTCTGGGCGCAGGCTGGCAGTGGGGCTGACCTGCTGGGGGTCTTCCGCCCTGGC 1549
486 AsnTrp-----PheArgSer----- 490
1550 ACATACCTTAGCAGATTTCGCCCGGGGACACCCACTTCTTCTGCACCTGCGCAGCGCAGCCTC 1609
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Qy 504 AsnPheLeuGlyGlyArgLeuMetIleProAsnThrGlyIleSerLeuLeuIleProPro 523
Db 1670 GGCTGCTGGGTGGGAGCTCAGCATCCCGGACAGGGGTGAGCTTCTGCTGGTCCCAAT 1729
Qy 524 AspAlaIleProArgGlyIleTyrGluIleTyrLeuThrLeuHisLysProGluAsp 543
Db 1730 GGAGCCATTCACAGGCAAGTTCTACAGATGATATCTACTCATCAACAGGCGAAGT 1789
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Db 1907 AGTCCCTGACTGATCTTTCAGCTCAAGACCCAGGCCCCACAGGGCCACTGGGAGGAG 1966
Qy 603 ValLeuHisLeuGlyGluAlaProSerHisLeuTyrTyrCysGlnLeuGluAlaSer 622
Db 1967 GTGGTGACCTTGGATGAGGAGACCTGAACACACCTCTACTGCGAGCTGGAGCCGAG 2026
Qy 623 AlaCysTyrValPheThrGluGlnLeuGlyArgPheAlaLeuValGlyGluAlaLeuSer 642
Db 2027 GCCTGTACATCTCTGAGCAGCTGGGACCTACGTTTTCAGGGCGAGTCTTATTCC 2086
Qy 643 ValAlaAlaLysArgLeuLysLeuLeuPheAlaProValAlaCysThrSerLeu 662
Db 2087 CGCTCAGCAGTCAGCGGCTCTCAGTGGCTCTTGGCCGCCCTCTGACCTCCCTG 2146
Qy 663 GluTyrAsnIleArgValTyrCysLeuHisAspThrHisAspAlaLeuLysGluValVal 682
Db 2147 GAGTACAGCTCCGGTCTACTGCTGGAGGACAGCCTGTAGCAGTGAAGAGGTGCTG 2206
Qy 683 GlnLeuGluLysGlnLeuGlyGlyGlnLeuIleGlnGluProArgValLeuHisPheLys 702
Db 2207 GAGCTGGAGCGACTCTGGGCGGATCTTGTGGAGGAGCGGAAACCGCTAATGTTCAAG 2266
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; Publication No. US2004002922A1
; GENERAL INFORMATION:
; APPLICANT: Edinger, Shlomit
; APPLICANT: MacDougall, John
; APPLICANT: Millet, Isabelle
; APPLICANT: Ellerman, Karen
; APPLICANT: Stone, David
; APPLICANT: Gerlach, Valerie
; APPLICANT: Grosse, William
; APPLICANT: Alsbrook II, John
; APPLICANT: Lepley, Denise
; APPLICANT: Rieger, Daniel
; APPLICANT: Burgess, Catherine
; APPLICANT: Casman, Stacie
; APPLICANT: Spytek, Kimberly
; APPLICANT: Boldog, Ferenc
; APPLICANT: Li, Li
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Mishra, Vishnu
; APPLICANT: Patturajan, Meera
; APPLICANT: Shenoy, Suresh
; APPLICANT: Rastelli, Luca
; APPLICANT: Tchernev, Velizar
; APPLICANT: Vernet, Corine
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Malyankar, Uriel
; APPLICANT: Guo, Xiaojia
; APPLICANT: Miller, Charles
; APPLICANT: Gangolli, Baha
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-214
; CURRENT APPLICATION NUMBER: US/10/218,779
; PRIOR FILING DATE: 2002-08-14
; PRIOR FILING DATE: 2002-08-14
; PRIOR FILING DATE: 60/253,834
; PRIOR FILING DATE: 2000-11-29
; PRIOR FILING DATE: 2000-11-30
; PRIOR FILING DATE: 60/264,180
; PRIOR FILING DATE: 2001-01-25
; PRIOR FILING DATE: 60/313,656
; PRIOR FILING DATE: 2001-08-20
; PRIOR FILING DATE: 60/327,456
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2860
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-218-779-1
Alignment Scores:
Pred. No.: 2,46e-260 Length: 2860
Score: 2563.50 Matches: 501
Percent Similarity: 69.08% Conservatives: 147
Best Local Similarity: 53.41% Mismatches: 245
Query Match: 53.51% Indels: 45
DB: 17 Gaps: 15


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Qy 683 GlnLeuGluLysGlnLeuGlyGlnLeuLeuGlnGlnProArgValLeuHisPheLys 702
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
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Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
2564 ACCACCCAGCTGGGACCTTATGCCTTCAAGATCCCACTGCTCCATCCGCCAGAGATATGC 2623
Qy 821 SerSerLeuAspProProCysArgArgGlyAlaAspTrpArgThrLeuAlaGlnLysLeu 840
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2744 GACCTCTGGAGAGCTTGCAGCAGAGCGATGGGACCTCAACAGCCTGGCGAGTGCCTTG 2803
Qy 881 AlaGlyLeuGlyGlnProAspAlaGlyLeuPheThrValSerGluAlaGluCys 898
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
2804 GAGGAGATGGCAAGAGTGAGATGCTGCTGCTGGCCACCAGCGGGGACTGC 2857
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Search completed: August 8, 2005, 20:14:24
Job time : 3876 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 8, 2005, 02:39:30 ; Search time 10019 Seconds
(without alignments)
3411.689 Million cell updates/sec

Title: US-10-624-932c-2

Perfect score: 4791

Sequence: 1 MAVRPLGWPALLGIVLAWL.....AVAGLGQPDAGLFTVSEAC 898

Scoring table: BLOSUM62

Xgapop 10.0, Xgapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-UNITS=bites -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pct -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10624932@cgn 1 1 5180 @runat_03082005_110053_3214 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:
1: gb_est1:*
2: gb_est2:*
3: gb_hcc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gses1:*
9: gb_gses2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2767.5	57.8	3790	3 AK031655	AK031655 Mus muscu
2	2747	57.3	2802	9 AY406491	AY406491 Homo sapi
3	2733	57.0	2791	9 AY406493	AY406493 Mus muscu
4	2572.5	53.7	3866	3 AK018177	AK018177 Mus muscu
5	2342.5	48.9	2532	9 AY411749	AY411749 Mus muscu
6	2326.5	48.6	2532	9 AY411747	AY411747 Homo sapi
7	2244	46.8	2802	9 AY406492	AY406492 Pan trogl
8	2111	44.1	2775	9 AY401471	AY401471 Mus muscu
9	2104	43.9	2775	9 AY401469	AY401469 Homo sapi

10	1917.5	40.0	2532	9	AY411748	AY411748 Pan trogl
11	1884.5	39.3	1532	3	BC033727	BC033727 Homo sapi
12	1591.5	33.2	2507	9	AY401470	AY401470 Pan trogl
13	1524	31.8	1852	3	CR598115	CR598115 full-leng
14	1402	29.3	1034	4	BI758231	BI758231 603029876
15	1349	28.2	818	4	BI818609	BI818609 603033362
16	1274.5	26.6	874	5	BQ689148	BQ689148 AGENCOURT
17	1270	26.5	788	1	AI951556	AI951556 wv36f04.X
18	1269	26.5	788	6	CA317532	CA317532 UI-M-FW0-
19	1268.5	26.5	889	5	BQ691915	BQ691915 AGENCOURT
20	1252	26.1	756	5	BU612387	BU612387 UI-M-EW0-
21	1252	26.1	796	5	EX348193	EX348193 BX348193
22	1206	25.2	1175	2	BF530640	BF530640 602071931
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ALIGNMENTS

RESULT 1

AK031655

LOCUS

DEFINITION

AK031655 3790 bp mRNA linear HTC 03-APR-2004
Mus musculus 13 days embryo male testis cDNA, RIKEN full-length
enriched library, clone:6030473H24 product:unc5 homolog (C.
elegans) 3, full insert sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

AK031655 3790 bp mRNA linear HTC 03-APR-2004
Mus musculus 13 days embryo male testis cDNA, RIKEN full-length
enriched library, clone:6030473H24 product:unc5 homolog (C.
elegans) 3, full insert sequence.
AK031655 GI:26327502
HTC; CAP trapper.
Mus musculus (house mouse)
Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
9279253
10349636
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374
11042159
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsuina, T., Tashiro, H., Itoh, M.,
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Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Kozaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 Riken integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer
 Genome Res. 10 (11), 1757-1771 (2000)
 20530913
 11076861

REFERENCE
AUTHORS
4
The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.

TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
REFERENCE 5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE	JOURNAL	REFERENCE	AUTHORS
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs	Nature 420, 563-573 (2002)	6 (bases 1 to 3790)	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akaira, S., Tanaka, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Havaashizumi, Y.


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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
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Percent Similarity: 73.17% Conservative: 154
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DB: 9 Gaps: 10

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Genomic survey sequence.
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VERSION AY406493.1 GI:39762467
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REFERENCE 1 (bases 1 to 2791)
AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 2791)
AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
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Db      1486 CTCATCCAAATGTTCACCCAGATGACCCAGATGCTTGTGTAGAGATGAGGCCCTTAACTT 1545
QY      489 -----ArgSerLeuProArgGlyThr-----SerAsnMetThrTyrGlyThrPheAs 504
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QY      504 nPheLeuGlyGlyArgLeuMetIleProAsnThrGlyIleSerLeuLeuIleProProAs 524
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QY      524 pAlaIleProArgGlyLysIleTyrGluIleTyrLeuThrLeuHisLysPheProLysVa 544
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QY      584 oAspSerTrpSerLeuArgLeuLysLysGlnSerCysGluGlySerTrpGluAspVal 604
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QY      604 uHisLeuGlyGluAlaProSerHisLeuTyrTyrCysGlnLeuGluAlaSerAlaCy 624
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QY      624 sTyrValPheThrGluGlnLeuGlyArgPheAlaLeuValGlyGluAlaLeuSerVal 644
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Db      2026 AGTGCCAAAGCGCTTTAAACTGGCCATCTTTGGGCCCTCTGTCTGTCTTCCCTGGAGTA 2085
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QY      684 uGluLysGlnLeuGlyGlnLeuIleGlnGluProArgValLeuHisPheLysAspSe 704
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QY      704 rTyrHisAsnLeuArgLeuSerIleHisAspValProSerSerLeuTrpLysSerLysLe 724
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Db      2266 GCTGGCTAAGATATCAGAAATTCATTTTACCACATCTGAGTGGCTCTCAAGAAACCT 2325
QY      744 uHisCysThrPheThrLeuGluArgValSerProSerThrSerAspLeuAlaCysLysLe 764
Db      2326 CCAGTGCACCTTCACTCTGGAAGACTCAGCCTAAACACAGATGGAATGTTTGTGCAACT 2385
QY      764 uTrpValTrpGlnValGluGlyAspGlyGlnSerPheSerIleAsnPheAsnIleThrLy 784
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QY      784 sAspThrArgPheAlaGluLeuAlaLeuGluSerGluAlaGlyValProAlaLeuVa 804
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TITLE
Functional annotation of a full-length mouse cDNA collection
REFERENCE
Nature 409, 695-690 (2001)
AUTHORS
The PANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

HSLASTEFTCKVCVROVEGEQIFQLHTTLAETPAGSLDALCSAPNAITQLPYAF
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ORIGIN

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DEFINITION genomic survey sequence.
ACCESSION AY411749
VERSION AY411749.1 GI:39767717
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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1 (bases 1 to 2532)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferrera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
Science 302 (5652), 1960-1963 (2003)
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
2 (bases 1 to 2532)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferrera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
<1..>2532
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ORIGIN
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Score: 2342.50 Matches: 454
Percent Similarity: 69.78% Conservative: 137
Best Local Similarity: 53.60% Mismatches: 205
Query Match: 48.89% Indels: 51
DB: 9 Gaps: 12
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QY 119 LeuGluGluTyrTrpCysGlnCysValAlaTrpSerSerGlyThrThrLysSerGln 138
Db 61 CTCGAGGACTACTGGTGCCAGTGGTGGCTTGGAGCTCTTCGGGAACTACCAAGATCGC 120
QY 139 LysAlaTyrIleArgIleAlaArgLeuArgLysAsnPheGluGlnGluProLeuAlaLys 158
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QY 159 GluValSerLeuGluGlnGlyIleValLeuProCysArgProProGluGlyIleProPro 178
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Db 2152 CAGATTTTCAGCTGCACACCAAGTTGGCC---GAGACGCTCTGGCTCCCTGGATGCT 2208
QY 794 LeuGluSerGluAlaGly-----ValProAlaLeuValGlyProSerAlaPheLysIle 811
Db 2209 CTCTGCTCTGCCCGGCAATGCCATCACCCAGCTGGGACCTTATGCTTCAAGATA 2268
QY 812 ProPheLeuIleArgGlnLysIleIleSerSerLeuAspProProCysArgArgGlyAla 831
Db 2269 CCCCTGTCCATCCGCCAAAAGATCTGCAGCAGCTGGACGCCCCCAACTCCCGGGGCAAC 2328
QY 832 AspTrpArgThrLeuAlaGlnLysLeuHisLeuAspSerHisLeuSerPheAlaSer 851
Db 2329 GACTGGAGGTGTGGCGCAGAAAGCTGTCCATGGACCGGTACCTAACTACTTTCGCCACC 2388
QY 852 LysProSerProThrAlaMetIleLeuAsnLeuTrpGluAlaArgHisPheProAsnGly 871
Db 2389 AAGCTAGTCCACAGGTGTCTATCTTTAGACCTCTCGGAAAGCTCGGCAACAGGATGACGG 2448
QY 872 AsnLeuSerGlnLeuAlaAlaValAlaGlyLeuGlyGlnProAspAlaGlyLeuPhe 891
Db 2449 GACCTCAACAGCCTGGCCAGTGTCTTGGAGGAGATGGCAAGAGTGGATGCTGGTACC 2508
QY 892 ThrValSerGluAlaGluCys 898
Db 2509 ATGCCACAGATGGCGATTGC 2529

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RESULT 6

AY411747

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

2532 bp DNA linear GSS 12-DEC-2003
 Homo sapiens HCM4327 gene, VIRTUAL TRANSCRIPT, partial sequence,
 genomic survey sequence.
 AY411747 GI:39767715
 GSS.
 Homo sapiens (human)

ORGANISM Homo sapiens
REFERENCE Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Perrieria,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 2532)
AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Perrieria,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.
FEATURES
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/organism="Homo sapiens"
/mol_type="genomic DNA"
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gene
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Alignment Scores:
Pred. No.: 1.34e-196 Length: 2532
Score: 2326.50 Matches: 451
Percent Similarity: 69.22% Conservative: 136
Best Local Similarity: 53.18% Mismatches: 208
Query Match: 48.56% Indels: 53
DB: 9 Gaps: 13
US-10-624-932C-2 (1-898) x AV411747 (1-2532)


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Qy 164 GlnGlyIleValLeuProCysArgProGluGlyIleProAlaGluValGluTrp 183
Db 550 CAGGAAGTCTTACTCCAGTGTCCGACCTCGAAGGATCCAGTGGCTGAGNNNNNNN 609
Qy 184 LeuArgAsnGluAspLeuValAspProSerLeuAspProAsnValTyrIleThrArgGlu 203
Db 610 NNGAANAATGAAGACATAATTTGATCCCTGTTGAAGATCGAATTTTATTTACTATTGAT 669
Qy 204 HisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysValAla 223
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Qy 224 LysAsnIleValAlaArgArgSerAlaSerAlaAlaValIleValTyrValAsnGly 243
Db 730 AAAAACATTTGTGCCAAGAGGAAAGTACAACCTGCCACTGTCAATAGTCTATGTCAACGGT 789
Qy 244 GlyTrpSerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGln 263
Db 790 GGCTGTCTCCACTGGACGGAGTGTCTGTGTGAACAGCCGCTGTGGACGAGGTATCAG 849
Qy 264 LysArgSerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGly 283
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Qy 284 GlnAsnValGlnLysThrAlaCysAlaThrLeuCysProValAspGlySerTrpSerPro 303
Db 910 CAGAGTGTGCAGAAATAGCCTGTACTACGTATTATGCCAGTGGATGGCAGTGCAGGCCA 969
Qy 304 TrpSerLysTrpSerAlaCysGlyLeuAspCysThrHisTrpArgSerArgGluCysSer 323
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Qy 324 AspProAlaProArgAsnGlyGlyGluCysGlnGlyThrAspLeuAspThrArgAsn 343
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Qy 403 GlyPheGlnProValSerIleLysProSerLysAlaAspAsnProHisLeuLeuThrIle 422
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Qy 479 ValSerArgLeuSer-----ThrGlnAsnTyrPhe----- 498
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Qy 525 AlaIleProArgGlyLysIleTyrGluIleTyrGluIleTyrLeuHisLysProGluAspVal 544
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Qy 545 ArgLeuProLeuAlaGlyCysGlnThrLeuLeuSerProIleValSerCysGlyProPro 564
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Qy 565 GlyValLeuLeuThrArgProValIleLeuAlaMetAspHisCysGlyGluProSerPro 584
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Qy 605 HisLeuGlyGluGluAlaProSerHisLeuTyrTyrCysGlnLeuGluAlaSerAlaCys 624
Db 1918 GTGTGCGGGGAGGAAACTTCACCCACCCCTGTCTACATTTCAGCTGGATGCAGAGCCTGC 1977
Qy 625 TyrValPheThrGluGlnLeuGlyArgPheAlaLeuValGlyGluAlaLeuSerValAla 644
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Qy 645 AlaAlaLysArgLeuLysLeuLeuLeuPheAlaProValAlaCysThrSerLeuGluTyr 664
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Qy 665 AsnIleArgValTyrCysLeuHisAspThrHisAspAlaLeuLysGluValValGlnLeu 684
Db 2098 AGCATCCGAGTCTACTGTCTGGATGACACCCAGGATGCCCTGAAGGAATTTTACATCTT 2157
Qy 685 GluLysGlnLeuGlyGlnLeuIleGlnProArgValLeuHisPheLysAspSer 704
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Db 2578 GCCCCCAAGCAGAGAGGCCATGACTGGAGGATCTGGCCCATTAAGCNCNNNNNNNNNN 2637
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RESULT 8
LOCUS   AY401471
DEFINITION Mus musculus HCM0901 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION AY401471
VERSION   AY401471.1
KEYWORDS GSS.
SOURCE   Mus musculus (house mouse)
ORGANISM Mus musculus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 2775)
AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
          Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
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          Adams,M.D. and Cargill,M.
          Adams,M.D. and Cargill,M.
TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
          gene tricos
JOURNAL   Science 302 (5652), 1960-1963 (2003)
PUBMED   14671302
REFERENCE 2 (bases 1 to 2775)
AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
          Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
          Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
          Adams,M.D. and Cargill,M.
          Adams,M.D. and Cargill,M.
TITLE     Direct Submission
JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
          Rockville, MD 20850, USA
COMMENT   This sequence was made by sequencing genomic exons and ordering
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Alignment Scores:
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Score: 2111.00 Matches: 413
Percent Similarity: 61.73% Conservative: 150
Best Local Similarity: 45.29% Mismatches: 293
Query Match: 44.06% Indels: 56
DB: 9 Gaps: 12

US-10-624-932C-2 (1-898) x AY401471 (1-2775)

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Db      49 GGAGCCGATGGCAGTGAATTCCTCCGACTCTATCCCATCTGCC---CCTGGAACGCTG 105
Qy      44 ProHisPheLeuValGlnProGluAspValTyrIleValIysAsnLysProValLeuLeu 63
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Db      106 CCTCATTTTCATCGAGGAGCCGAGAGTGCATCATCAAGAGCAACCCGATTGCACATC 165
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Qy      84 GlnValAspHisValIleGluArgSerThrAspGlySerSerGlyLeuProThrMetGlu 103
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Db      226 CAGATGAACATGTGTCGAGGAGAGCCCTGGATGAGAGCTCAGGCTTGAAGGTCGCGGAA 285
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Qy      104 ValArgIleAsnValSerArgGlnGlnValGluLysValPheGlyLeuGluGluTyrTrp 123
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Qy      124 CysGlnCysValAlaTrpSerSerSerGlyThrThrIysSerGlnIysAlaTyrIleArg 143
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Qy      164 GlnGlyIleValLeuProCysArgProProGluGlyIleProProAlaGluValGluTrp 183
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
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      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Qy      244 GlyTrpSerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGln 263
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db      706 GGTCTGTCTCTCTCGGACAGAGTGTGAGCTTGCATTTGCTGTGTGTAGAGATGGCAG 765
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Qy      264 LysArgSerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGly 283
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db      766 AAACGTTCCGGACCTGCACCAACCCGCTCTCTCAATGGTGGGCGCTTTTGTGAGGGA 825
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Qy      284 GlnAsnValGlnLysThrAlaCysAlaThrLeuCysProValAspGlySerTrpSerPro 303
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Qy      304 TrpSerLysTrpSerAlaCysGlyLeuAspCysThrHisTrpArgSerArgGluCysSer 323
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Db      886 TGGAGTGAATGGTCACTCTGCAGCCAGAGTGTGAACATCTTCGTATCCGTGAGTGACCA 945
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      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Qy      344 CysThrSerAspLeuCysValHisSerAlaSerGlyProGluAspValAlaLeuTyrVal 363
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db      1006 TGCACAGATGGTCTCTGCATTTCTAGGCAATGAGAAATGCCAGCGACATTTGTTGTACTCC 1065
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Qy      364 GlyLeuIleAlaValAlaValCysLeuValLeuLeuValLeuIleLeuValTyr 383
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Qy      384 CysArgLysLysGluGlyLeuAspSerAspValAlaAspSerSerIleLeuThrSerGly 403
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      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db      1183 TTCAGACCTTCAACTTCAAAACAGTTCTGTCAGGAAATTCCTACTACTGAATCTCTGCC 1242
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Qy      422 IleGlnProAspLeuSerThrThrThrThrThrThrThrThrThrThrThrThrThrThr 441
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Qy      442 AspGlyProSerProLysPheGlnLeuThrAsnGlyHisLeuLeuSerProLeuGly--- 460
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Db 1297 GAT---CCGCTCGACAAGAGCTCATGACAGAGTCTCACTCTTCAATCTTTATCTGAC 1353
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Qy 461 -----GlyArgHis-----Thr 465
Db 1414 TACCATGGCAAGATCACTCGGGGACTTTCCCCCATGGAACAACCGGGATTTCAGTACA 1473
Qy 466 LeuHisHisSerSerProThrSerGluAlaGluPheValSerArgLeuSerThrGln 485
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Qy 486 AsnTyrPheArgSerLeuProArgGlyThrSerAsnMetThrTyrGlyThrPheAsnPhe 505
Db 1516 -----TACTGCCGACAGGACAGCTGAGGACACTGTGTCTTTGGCCAT 1563
Qy 506 LeuGlyArgLeuMetIleProAsnThrGlyIleSerLeuLeuIleProProAspAla 525
Db 1564 TTAGGGGACGCTTAGTAATGCCAAATACAGNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1620
Qy 526 IleProArgGlyLysIleTyrGluIleTyrLeuThrLeuHisLysProGluAspValArg 545
Db 1621 NNN 1680
Qy 546 LeuProLeuAlaGlyCysGlnThrLeuLeuSerProIleValSerCysGlyProProGly 565
Db 1681 CTGCAGTCAAGTGTGAGTCTCTGAGTCTCTGAAGTCACTGTGGGCTCCAGAT 1740
Qy 566 ValLeuLeuThrArgProValIleLeuAlaMetAspHisCysGlyGluProSerProAsp 585
Db 1741 ATGCTTGTCACACTCCCTTTCGCTGACCATCCTCACTGTGCAGACGTCAGTTCAGAG 1800
Qy 586 SerTrpSerLeuArgLeuLysLysGlnSerCysGlySerTrpGluAspValLeuHis 605
Db 1801 CACTGGAACTTACCTCGAAGAGAGGACCCAGCGGGAGTGGGAGGAGTATGATCA 1860
Qy 606 LeuGlyGluAlaProSerHisLeuTyrTyrCysGlnLeuGluAlaSerAlaCysTyr 625
Db 1861 GTGGAGATGATGCCATCC-----TGTTACTGCTCTTGATCTCTTGGCTGTGCAC 1914
Qy 626 ValPheThrGlnLeuLeuGlyArgPheAlaLeuValGlyGluAlaLeuSerValAlaAla 645
Db 1915 GTGCTGCTGATAGCTTTGGAAAGCTATGCTCCACAGAGAGCCCAATCACAGACTGTGCC 1974
Qy 646 AlalysArgLeuLysLeuLeuPheAlaProValAlaCysThrSerLeuGluTyrAsn 665
Db 1975 GTAAAGCAGCTCAAGTGGCTGTGTGGCTGTGCATGTCTGTAACCTCTTGGATTACAAC 2034
Qy 666 IleArgValTyrCysLeuHisAspThrHisAspAlaLeuLysGluValValGlnLeuGlu 685
Db 2035 CTGAGATTACTGTGTGGACAATACCTCTGTGTCATTTCCAGGAAGATTTCTGACGAA 2094
Qy 686 LysGlnLeuGlyGlnLeuIleGlnGluProArgValLeuHisPheLysAspSerTyr 705
Db 2095 CGGCACCAAGCGCGCAGCTCTCTGGAAGAACCAAGCTGTGCATTTCAAAGGGAATACA 2154
Qy 706 HisAsnLeuArgLeuSerIleHisAspValProSerSerLeuTrpLysSerLysLeuLeu 725
Db 2155 TTCAGTCTCAGGCTCTGCTGCTGATACCTCCCTCCCTCTCTGGAGGATCAAAACCGTTC 2214
Qy 726 ValSerTyrGlnGluIleProPheTyrHisIleTrpAsnGlyThrGlnArgTyrLeuHis 745
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Qy 746 CysThrPheThrLeuGluArgValSerProSerThrSerAspLeuAlaCysLysLeuTrp 765
Db 2275 TGTGCTTCTCCCTGGAGCGCTACACGCCCCACCAACCCAGCTGTCTCTCAAAATCTGC 2334
Qy 766 ValTrpGlnValGluGlyAspGlyGlnSerPheSerIleAsnPheAsnIleThrLysAsp 785
Db 2335 ATTGGCGCAGCTCAAGGCCATGAACAGATCCTCAAGTGCAGACATCCATCTCTAGAGAT 2394

Qy 786 ThrArgPheAlaGluLeuLeuAlaLeuGluSerGluAlaGlyValProAlaLeuValGly 805
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Qy 806 ProSerAlaPheLysIleProPheLeuIleArgGlnLysIleSerSerLeuAspPro 825
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Qy 826 ProCysArgArgGlyAlaAspTrpArgThrLeuAlaGlnLysLeuHisLeuAspSerHis 845
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Qy 846 LeuSerPhePheAlaSerLysProSerProThrAlaMetIleLeuAsnLeuTrpGluAla 865
Db 2575 TTATCATATTTCCGTCCCAAGACGCTTCCCTGTCTATTTGAACCTCTGGAAGCT 2634
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Qy 886 ProAspAlaGlyLeuPheThrValSerGluAlaGlu 897
Db 2695 ACACACAGAAACTATCCAAATCATCACAGACCCACAG 2730

RESULT 9
AY401469
LOCUS
DEFINITION Homo sapiens HCM0901 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION AY401469
VERSION AY401469.1 GI:39757458
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2775)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Perriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 2775)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Perriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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/db_xref="taxon:9606"
gene <1..>2775
/locus_tag="HCM0901"
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Pred. No.: 1.3e-176 Length: 2775
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Percent Similarity: 61.78% Conservative: 157
Best Local Similarity: 44.73% Mismatches: 302
Query Match: 43.92% Indels: 51
DB: 9 Gaps: 11

Qy 697 ArgValLeuHisPheLeuAspSerTyrHisAsnLeuArgLeuSerIleHisAspValPro 716
 Db 2128 AAATTCCTGCTGCTTCAAGAGGAATACCTTTAGTCTTCAGATTTCTGCTTGTATATCCC 2187
 Qy 717 SerSerLeuTyrPheLeuSerLeuValSerTyrGlnGluIleProPheTyrHisIle 736
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 Qy 737 TrpAsnGlyThrGlnArgTyrLeuHisCysThrPheThrLeuGluArgValSerProSer 756
 Db 2248 TGGTGCAGTAACCGGAGCCCTGCATCTGCTCCCTTCCCTGGAGCGTTATACGCCCATC 2307
 Qy 757 ThrSerAspLeuAlaCysLeuLeuTyrValTrpGlnValGluGlyAspGlyGlnSerPhe 776
 Db 2308 ACCACCCAGCTGTCTCTGCAAAATCTGCATTCGGCAGCTCAAAGGCCATGAACAGCTCCTC 2367
 Qy 777 SerIleAsnPheAsnIleThrLysAspThrArgPheAlaGluLeuLeuAlaLeuGluSer 796
 Db 2368 CAAGTGCAGACATCAATCTCTAGAGAGTGAACGAGAAACCATCACTTTCTTGGCACAAGAG 2427
 Qy 797 GluAlaGlyValProAlaLeuValGlyProSerAlaPheLysIleProPheLeuIleArg 816
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 Qy 817 GlnLysIleLeuSerSerLeuAspProProCysArgArgGlyAlaAspTrpArgThrLeu 836
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 Db 2608 GCTGTCTATTGAACTGTGGGAAGCTGCTCAGCATGATGTGATCTTGATCTCCCTG 2667
 Qy 877 AlaAlaAlaValAlaGlyLeuGlyGlnProAspAlaGlyLeuPheThrValSerGluAla 896
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 Db 2728 CAG 2730

RESULT 10
 LOCUS AY411748
 DEFINITION Pan troglodytes HCM4327 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
 ACCESSION AY411748
 VERSION AY411748.1 GI:39767716
 KEYWORDS GSS.
 SOURCE Pan troglodytes (chimpanzee)
 ORGANISM Pan troglodytes
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 1 (bases 1 to 2532)
 Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferrera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
 Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
 Science 302 (5652), 1960-1963 (2003)
 14671302
 2 (bases 1 to 2532)
 Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferrera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
 Direct Submission
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES
 source Location/Qualifiers
 1..2532 /organism="Pan troglodytes"
 /mol_type="genomic DNA"
 /db_xref="taxon:9598"
 <1..>2532
 gene /locus_tag="HCM4327"

ORIGIN

Alignment Scores:
 Pred. No.: 5,59e-160 Length: 2532
 Score: 1917.50 Matches: 391
 Percent Similarity: 60.85% Conservative: 125
 Best Local Similarity: 46.11% Mismatches: 279
 Query Match: 40.02% Indels: 53
 DB: 9 Gaps: 13

US-10-624-932C-2 (1-898) x AY411748 (1-2532)

Qy 99 LeuProThrMetGluValArgIleAsnValSerArgGlnValGluLysValPheGly 118
 Db 1 CTGCGGTGCGCGAGGTGCAGATCGAGTGTGCGGCGAGGTGAGGAGCTCTTTGGG 60
 Qy 119 LeuGluGluTyrTrpCysGlnCysValAlaTrpSerSerGlyThrLysSerGln 138
 Db 61 CTGAGGATTTACTGTGTGCCAGTGGCTGTGAGCTCTGCGGCGACCAAGAGTTCG 120
 Qy 139 LysAlaTyrIleArgIleAlaArgLeuArgLysAsnPheGluGlnGluProLeuAlaLys 158
 Db 121 CGAGCTTACGTCCGCATCGCTTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 180
 Qy 159 GluValSerLeuGluGlnGlyIleValLeuProCysArgProGluGlyIleProPro 178
 Db 181 NNN 240
 Qy 179 AlaGluValGluTrpLeuArgAsnGluAspLeuValAspProSerLeuAspProAsnVal 198
 Db 241 NNNNNNGTGAATGGCTCAAGAATGAGGATGTCATCGACCCCGGAGGACCACTTC 300
 Qy 199 TyrIleThrArgGluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsn 218
 Db 301 CTGCTCACCATCGACCAACCTCATCATCGCGAGCGCCGCTGTCGGACACTGCCAAC 360
 Qy 219 TyrThrCysValAlaLysAsnIleValAlaArgArgSerAlaSerAlaValIle 238
 Db 361 TATACCTCGTGGCCAGAAACATCGTGGCCAAACGCGGAGCACCACCTGCCACGTCATC 420
 Qy 239 ValTyrValAsnGlyTyrTrpSerThrTrpThrGluTrpSerValCysSerAlaSerCys 258
 Db 421 GTCTAGTGAATGGCGCTGTGTCCAGCTGGGAGAGTGGTCCGCTCTCAACCGCTGT 480
 Qy 259 GlyArgGlyTrpGlnLysArgSerArgSerCysThrAsnProAlaProLeuAsnGlyGly 278
 Db 481 GGNNGANNCTGGCAGAAGCGCACCGGACCTGCACCAACCCCGCCCTCAACGGAGGG 540
 Qy 279 AlaPheCysGluGlyGlnAsnValGlnLysThrAlaCysAlaThrLeuCysProValAsp 298
 Db 541 NNNNTCTGCGAGGCGCCANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNTCCAT 600
 Qy 299 GlySerTrpSerProTrpSerLysTrpSerAlaCysGlyLeuAspCysThrHisTrpArg 318
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 Qy 319 SerArgGluCysSerAspProAlaProArgAsnGlyGlyGluCysGlnGlyThrAsp 338
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 Qy 339 LeuAspThrArgAsnCysThrSerAspLeuCysValHisSer----- 352
 Db 721 CTGCACTTAAGAACTGCACAGATGGGTGTGTGATGCATAAATAAGAAAACTCTAAGCGAC 780

Qy	353	-----AlaSerGlyProGluAspValAlaLeuTyrValGlyLeu	365
Db	781	CCCAACAGCACCTGCTGGAGGGCTTCAGGG-----CATGGCGCTGTATGGGGGCTC	834
Qy	366	---IleAlaValAlaValCysLeuValLeuLeuLeuValLeuLeuValTyrCys	384
Db	835	GTGGTGCCCGTCTTCNTGTCNTGGCAATCCTCATGGCGGTGGGGGTGGGTGTACCCG	894
Qy	385	ArgLysLysGluGlyLeuAspSerAspValAlaAspSerSer---IleLeuThrSerGly	403
Db	895	CGCAACTCCCGTGACTTCGACACAGACATCACTGACTCATCTGCTGCCCTGACTGTGGT	954
Qy	404	PheGlnProValSerIleLysProSerLysAlaAspAsnProHisLeuLeu-----Thr	421
Db	955	TTCCACCCCGTCAACTTTAAGAGCGGCAAGGCCACCAACCCGAGCTCTCTACACCCCTCT	1014
Qy	422	IleGlnProAspLeuSerThrThrThrThrThrThrThrThrThrThrThrThrThrThr	441
Db	1015	GTGCGCTCTGACCTGACGCGCGCGGCATCTACCGCGGACCGGTGATGCCCTGCAG	1074
Qy	442	AspGlyProSerProLysPheGlnLeuThrAsnGlyHisLeuLeuSerProLeuGlyGly	461
Db	1075	GACTCC---ACCGACAATAATCCCATGACCACTCTCTCTGTGGACCCCTTACCCAGC	1131
Qy	462	GlyArgHisThrLeuHisHisSerSerProThr-----SerGluAla	475
Db	1132	CTTAAGGTCAAGGTCTACAGCTCCAGCACTACGGGCTCTGGCGCAGCGCTGGCAGATGG	1191
Qy	476	GluGluPheValSerArgLeuSerThrGlnAsnTyr-----	487
Db	1192	GCTGACTGTGGGAGTCTTGCCGCGCTGGCACATACCTTAGCGATTTCGCCCGGGACACC	1251
Qy	488	-----PheArgSer-----LeuProArg	493
Db	1252	CAC TTCCTGCACCTGCCGACGGCAGCGCTGGTTCAGCAGAGCTCTTGGGCGCTGCCCGGA	1311
Qy	494	GlyThrSerAsnMetThrThrThrGlyThrPheAsnPheLeuGlyGlyArgLeuMetIlePro	513
Db	1312	GACCCAGNAGCAGCGTCAGCGGCACCTTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	1371
Qy	514	AsnThrGlyIleSerLeuLeuIleProProAspAlaIleProArgGlyLysIleTyrGlu	533
Db	1372	NNNNNNNGGTGACTTGCTGGTGCCCAATGGAGCCATTCCCCAGGCGCAAGTCTACGAG	1431
Qy	534	IleTyrThrLeuThrLeuHisLysProGluAspValArgLeuLeuAla---GlyCysGln	552
Db	1432	ATGTATCTACTATCAACAAGCGCAAGATACC---CTCCCGCTTTCGAAGGAGACCCAG	1488
Qy	553	ThrLeuLeuSerProIleValSerCysGlyProProGlyValLeuLeuThrArgProVal	572
Db	1489	ACAGATTGAGCCCTCAGTGACCTGTGGACCCACAGAGCCTCTCTGCTGTGCCACCCGTC	1548
Qy	573	IleLeuAlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArgLeuLys	592
Db	1549	ATCCTACCATGCCCCACTGTGCCGAAGTCAGTGCCCGTCGACTCGATCTTTCAGCTCAAG	1608
Qy	593	LysGlnSerCysGluGlySerTrpGluAspValLeuHisLeuGlyGluGluAlaProSer	612
Db	1609	ACCCAGCCCAACAGGGCCACTGGAGGAGGTGGTACCTCGATGAGGAGACCCCTGAAC	1668
Qy	613	HisLeuTyrTyrCysGlnLeuGluAlaSerAlaCysTyrValPheThrGluGlnLeuGly	632
Db	1669	ACACCTGTCTACTGCCAGCTGGAGCCCGGCGCTGTACATCTCTGTGGACAGCTGGGC	1728
Qy	633	ArgPheAlaLeuValGlyGluAlaLeuSerValAlaAlaLysArgLeuLysLeuLeu	652
Db	1729	ACCTACGTGTTCAGCGGCGAGTCTATTCCNNNNNNNCCAGTCNNNNNGCTCCNCGTGGCC	1788
Qy	653	LeuPheAlaProValAlaCysThrSerLeuGluTyrAsnIleArgValTyrCysLeuHis	672
Db	1789	GTCTTNGCCCTGCGCTCTGCACCTCCCTGGANNNGGCTCCGGGCTACTGCTCGTGGNN	1848
Qy	673	AspThrHisAspAlaLeuLysGluValIleGlnLeuGluLysGlnLeuGlyGlyGlnLeu	692

Db	1849	NNNNNNNNNNNNNNNNNNNNNNNGAGTGTGGAGCTGGACGCGACTCTGGGCGGATACTTG	1908
Qy	693	IleGlnGluProArgValLeuHisPheLysAspSerTyrHisAsnLeuArgLeuSerIle	712
Db	1909	GTCGAGGACCCGAACCGCTAATGTTCAAGGACAGATTACACAACCTGGCCCTCTCCTC	1968
Qy	713	HisAspValProSerSerLeuTyrLysSerLysLeuLeuValserTyrGlnGluIlePro	732
Db	1969	CATGACCTCCCCCATGCCATGCCATGGAGGACGAGCTCTGGCCAATACCAGGAGATCCCC	2028
Qy	733	PheTyrHisIleTrpAsnglyThrGlnArgTyrLeuHisCysThrPheThrLeuGluArg	752
Db	2029	TTCCTGTCAATTTGGAGTGCAGCCAGAAGGCCCTCCACTGCACATTTCACCTCGGAGAGG	2088
Qy	753	ValSerProSerThrSerAspLeuAlaCyLSylsLeuTirpValTrpGlnValGluGlyAsp	772
Db	2089	CACAGCTTGCTGCCCTCCACAGAGCTCACCTCAAGATCTGCTGCGGCAAGTGGAAAGGGAG	2148
Qy	773	GlyGlnSerPheSerIleAsnPheAsnIleThrLysAspThrArgPheAlaGluLeuLeu	792
Db	2149	GGCCAGATATTCAGCTGCATACCACCTCTGGCA--GAGACACCTGCTGGCTCCCTGGAC	2205
Qy	793	AlaLeuGluSerGluAlaGly-----ValProAlaLeuValGlyProSerAlaPheLys	810
Db	2206	ACTCTCTGCTCTGCCCTCGCAGCACTGTCCACCACCAGCTGGAGACTTATGCTTCAAG	2265
Qy	811	IleProPheLeuIleArgGlnLysIlelleSerSerLeuAspProProCybArgArgGly	830
Db	2266	ATCCCAGCTGCCATCCGACAGAAGATGCAACAGCTTAGATGCCCCCACTCACCGGGC	2325
Qy	831	AlaAspTrpArgThrLeuAlaGlnLysLeuHisLeuAspSerHisLeuSerPhePheAla	850
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Qy	851	SerLysProSerProThrAlaMetIleLeuAsnLeuTirpGluAlaArghisPheProAsn	870
Db	2386	ACCAAAGCAGGCCCCACGCGTGTGATCCTGGAGCTCTGGGAGCTCTGCAGCAGGACGAT	2445
Qy	871	GlyAsnLeuSerGlnLeuAlaAlaValAlaGlyLeuGlyGlnProAspAlaGlyLeu	890
Db	2446	GGGGAGCTCAACAGCTGGCGAGTGCTTGGAGGAGATGGCAAGAGTGAGATGCTGGTG	2505
Qy	891	PheThrValSerGluAlaGluCys	898
Db	2506	GCTGTGGCCACCGACGGGAGCTGC	2529
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BC033727			
LOCUS			
DEFINITION		1532 bp mRNA linear HTC 25-MAR-2004	
ACCESSION		Homo sapiens unc-5 homolog A (C. elegans), mRNA (cdna clone	
VERSION		IMAGE:5166762), containing frame-shift errors.	
KEYWORDS		BC033727 GI:21707230	
SOURCE		HTC	
ORGANISM		Homo sapiens (human)	
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS		Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.	
		1 (bases 1 to 1532)	
		Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,	
		Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,	
		Altshul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,	
		Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,P.,	
		Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,	
		Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,	
		Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,	
		Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,	
		Abramson,R.D., Mullaby,S.J., Bosak,S.A., McEwan,P.J.,	
		McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,	
		Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,	
		Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,	
		Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodrigues,S.,	

Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
 Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
 Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
 Butterfield, Y.S., Krzywinski, M.I., Skalek, U., Smalios, D.E.,
 Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.
 Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 12477932
 2 (bases 1 to 1532)
 Strausberg, R.
 Direct Submission
 Submitted (02-JUL-2002) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgaps-re@mail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: National Institutes of Health Intramural
 Sequencing Center (NISC),
 Gaithersburg, Maryland;
 Web site: <http://www.nisc.nih.gov/>
 Contact: nisc_mgc@nhgri.nih.gov
 Akhter, N., Ayale, K., Becketrom-Sternberg, S.M., Benjamin, B.,
 Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
 Dietrich, N.L., Granito, S., Guan, X., Gupta, J., Haghighi, P.,
 Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,
 Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
 McDowell, J., Pearson, R., Stantropop, S., Thomas, P.J., Touchman, J.W.,
 Turgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
 Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAK Plate: 68 Row: i Column: 2
 This clone was selected for full length sequencing because it
 passed the following selection criteria: Genomescan gene prediction
 This clone has the following problem: frame shifted.

FEATURES

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 /note="Vector: pCMV-SPORT6"

ORIGIN

Alignment Scores:
 Pred. No.: 2,21e-157 Length: 1532
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 Percent Similarity: 67.55% Conservative: 2
 Best Local Similarity: 67.20% Mismatches: 1
 Query Match: 39.33% Indels: 182
 DB: 3 Gaps: 2

US-10-624-932C-2 (1-898) x BC033727 (1-1532)

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 Db 11 GCAGGTCCCGCAGCAGAGTCCCGCGCCAAACCCAGTGCCTGGTGCACCCGCGACTG 70
 Qy 43 LeuProHisPheLeuValGluProGluAspValTrileValLysAsnLysProValLeu 62
 Db 71 CTTCCCACTCTCTGGTGGAGCCGAGATGTACATCGTCAGAACAGCCAGTGTCTG 130
 Qy 63 LeuValCysLysAlaValProAlaThrGlnIlePhePheLysCysAsnGlyGluTrpVal 82

Db 131 CTTGTGTGCAAGGCGCGCGCCAGCAGCATCTTCTTCAAGTGCACGCGGAGTGGGTG 190
 Qy 83 ArgGlnValAspHisValIleGluAArgSerThrAspGlySerSer----- 97
 Db 191 CGCCAGGTGGACCAACGCGTATCGAGCGCAGCAGCAGCGGAGCAGTGTAGGGAGATAGAGAG 250
 Qy 97 ----- 97
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 Db 371 TCTTGTGGAGGGTCTGCGAGAGAACCGCAGGGTCTCTTCTGCCCCGAGCATCCGACT 430
 Qy 97 ----- 97
 Db 431 CCAGCCTCCCATGGCCGGAACATCTGNAACGTTCAATGATCTCATCGATTTCTCAACCCAA 490
 Qy 97 ----- 97
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 Qy 97 ----- 97
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 Qy 98 -GlyLeuProThrMetGluValArgIleAsnValSerArgGlnValGlnValGluLysValPh 117
 Db 611 AGGGCTGCCACCATGGAGGTCCGCAATTAATGTCCTCAGGACGACGAGTCCAGAGAGGTGT 670
 Qy 117 eGlyLeuGluGluTrpCysGlnCysValAlaTrpSerSerSerGlyThrThrLysSe 137
 Db 671 CGGGCTGGAGGAATACTGGTGGCGAGTGGCGATCGAGCTCTCTCGGCGCACCCCAAGAG 730
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 Qy 157 aLysGluValSerLeuGluGlnGlyLeValLeuProCysArgProGluGlyLlePr 177
 Db 791 CAAGGAGGTGCTCTGAGCAGCGGCAATCGTGTGCCCTGCCGTCCACCGAGGCGATCCC 850
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 Qy 257 rCysGlyArgGlyTrpGlnLysArgSerArgSerCysThrAsnProAlaProLeuAsnGl 277
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 Qy 277 yGlyAlaPheCysGluGlyGlnAsnValGlnLysThrAlaCysAlaThrLeuCysProVa 297
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Db      1043 GGACGGCAGCTGGAGCCGCTGGAGCAAGTGGTGGGCTGTGGGCTGGAGCTGCACCCACTG 1102
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Qy      357 uAspValAlaLeuTyValGlyLeuLeuAlaValAlaValCysLeuValLeuLeuLeuLe 377
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Qy      377 uValLeuLeuLeuValTyCysArglystysGluGlyLeuAspSerAspValAlaAspSe 397
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Qy      397 rSerIleLeuThrSerGlyPheGlnProValSerIleLeuProSerIleValAlaAspAsnPr 417
Db      1343 GTCCATCTCACCCTCAGGCTTCAGCCCGCTCAGCATCAAGCCCGAGCAACCAACCC 1402
Qy      417 oHisLeuLeuThrIleGlnProAspLeuSerThrThrThrThrThrThrThrThrThr 437
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Qy      437 uCysProArgGlnAspGlyProSerProlyspheGlnLeuThrAsnGlyHisLeuLeuSe 457
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Qy      457 rProLeuGly 460
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LOCUS   AY401470
DEFINITION Pan troglodytes HCM0901 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION AY401470
VERSION   AY401470.1 GI:39757459
KEYWORDS GSS.
SOURCE   Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
REFERENCE 1 (bases 1 to 2507)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE    Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL  Science 302 (5652), 1960-1963 (2003)
PUBMED  14671302
REFERENCE 2 (bases 1 to 2507)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE    Direct Submission
JOURNAL  Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT  This sequence was made by sequencing genomic exons and ordering them based on alignment.
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Alignment Scores:

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Pred. No.:      8.5e-131      Length:      2507
Score:          1591.50      Matches:    332
Percent Similarity: 55.76%    Conservative: 133
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Query Match:     33.22%      Indels:      49
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US-10-624-932C-2 (1-898) x AY401470 (1-2507)

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Db      3 TTGAAGGTCCGCGAAGTGTTCATCAATGTTACAGGCAACAGGTGAGGACTTCCATGGG 62
Qy      119 LeuGluGluTyTrpCysGlnCysValAlaTTPSerSerSerGlyThrThrLysSerGln 138
Db      63 CCCGAGGACTATTTGGTGGCGTGTGGGCTGGAGCCACCTGGGTACTTCCAGAGCAGG 122
Qy      139 LysAlaTyIleArgIleAlaArgLeuArgLysAsnPheGlnGlnGluProLeuAlaLys 158
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Qy      159 GluValSerLeuGluGlnGlyIleValLeuProCysArgProGluGlyIleProPro 178
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Db      243 GCNNNGTGGATGGCTGAAATAATGAAGAGCCCATTTGACTCTGAACAAGACGAGACATT 302
Qy      199 TyrIleThrArgGluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsn 218
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Qy      219 TyrTrpCysValAlaLysIleValAlaArgArgSerAlaSerAlaAlaValIle 238
Db      363 TACACCTGATGGCAGCCCAACATCGTGGCTAGAGGAGGAAGCTGTGCGCCACTGTGTGG 422
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Qy      259 GlyArgGlyTrpGlnLysArgSerArgSerCysThrAsnProAlaProLeuAsnGlyGly 278
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Qy      279 AlaPheCysGluGlyGlnAsnValGlnLysThrAlaCysAlaThrLeuCysProValAsp 298
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Qy      319 SerArgGluCysSerAspProAlaProArgAsnGlyGlyGluGluCysGlnGlyThrAsp 338
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Db      840 GTGTGCACCCCTTACAGACGCGGACGAGTACTATGGCGTGGACGCTATTGACTCTTCT 899
Qy      399 IleLeuThrSerGlyPheGlnProValSerIleLysProSerLysAlaAspAsnProHis 418

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603029876F1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5200171 5', mRNA sequence.									
BI758231									
BI758231.1 GI:15749809									
EST.									
Homo sapiens (human)									
Homo sapiens									
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.									
NIH-MGC http://mgc.nci.nih.gov/.									
National Institutes of Health, Mammalian Gene Collection (MGC)									
Unpublished (1999)									
Contact: Robert Strausberg, Ph.D.									
Email: cgapbs@mail.nih.gov									
Tissue Procurement: Life Technologies, Inc.									
cDNA Library Preparation: Life Technologies, Inc.									
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)									
DNA Sequencing by: Incyte Genomics, Inc.									
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov									
Plate: LLAM11501 row: g column: 20									
High quality sequence stop: 793.									
Location/Qualifiers									
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ORIGIN									
Alignment Scores:									
Pred. No.: 1.85e-114 Length: 1034									
Score: 1402.00 Matches: 296									
Percent Similarity: 89.68% Conservative: 8									
Best Local Similarity: 87.32% Mismatches: 26									
Query Match: 29.26% Indels: 13									
DB: 4 Gaps: 2									
US-10-624-932C-2 (1-898) x BI758231 (1-1034)									
QY 36 ProGlyAlaAsnProAspLeuProHisPheLeuValGluProGluAspValTyrIle 55									
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QY 56 ValLysAsnLysProValLeuValCysLysAlaValProAlaThrGlnIlePhePhe 75									
DB 62 GTCAAGAACAGCCAGTCTGCTTGTGTGCAAGCCGTCGCCGCCAGCATCTTCTTC 121									
QY 76 LysCysAsnGlyGluTrpValArgGlnValAspHisValIleGluArgSerThrAspGly 95									
DB 122 AAGTGCACCGGGAGTGGGTGGCCAGGTGGACACCGTGTATCGAGCCGAGCAGACGG 181									
QY 96 SerSerGlyLeuProThrMetGluValArgIleAsnValSerArgGlnValGluLys 115									
DB 182 ACCAGTGGGCTGCCACCATGGAGGTCCGCATTAATGTCTCAAGCCAGCAGGTCTCAGAAG 241									
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DEFINITION		603029876F1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5200171 5', mRNA sequence.	
ACCESSION		BI758231	
VERSION		BI758231.1 GI:15749809	
KEYWORDS		EST.	
SOURCE		Homo sapiens (human)	
ORGANISM		Homo sapiens	
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
AUTHORS		NIH-MGC http://mgc.nci.nih.gov/ .	
TITLE		National Institutes of Health, Mammalian Gene Collection (MGC)	
JOURNAL		Unpublished (1999)	
COMMENT		Contact: Robert Strausberg, Ph.D. Email: cgabbs-remail.nih.gov Tissue Procurement: Life Technologies, Inc. cDNA library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM11501 row: g column: 20 High quality sequence stop: 793.	
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ORIGIN			
Alignment Scores:			
Pred. No.:	1.85e-114	Length:	1034
Score:	1402.00	Matches:	296
Percent Similarity:	89.68%	Conservative:	8
Best Local Similarity:	87.32%	Mismatches:	26
Query Match:	29.26%	Indels:	13
DB:	4	Gaps:	2
US-10-624-932C-2 (1-898) x BI758231 (1-1034)			
QY	36	ProGlyAlaAsnProAspLeuLeuProHisPheLeuValGluProGluAspValTyrIle	55
DB	2	CTGTGTCCCAACCCGACCTGCTTCCCCTCTCTGGTGGAGCCCGAGGATGTATCATC	61
QY	56	ValLysAsnLysProValLeuLeuValCysLysAlaValProAlaThrGlnIlePhePhe	75
DB	62	GTCAAGAACCAAGCAGTGTGCTTGTGTGCAAGCGCTGCCGCCACGACGATCTTCTTC	121
QY	76	LysCysAsnGlyGluTyrValArgGlnValAspHisValIleGluArgSerThrAspGly	95
DB	122	AAATGCAACGGGGAGTGGGTGGCCAGGTGGACCCACGTATCGAGCGCAGCAGCGGG	181
QY	96	SerSerGlyLeuProThrMetGluValArgIleAsnValSerArgGlnGlnValGluLys	115
DB	182	AGCAGTGGGCTGCCACCATGGAGGTCCGATTAATGTCTCAAGCGACGAGTGCAGAAG	241
QY	116	ValPheGlyLeuGluGluTyrTrpCysGlnCysValAlaTrpSerSerSerGlyThrThr	135
DB	242	GTGTTCCGGCTGGAGGAATACTGGTGCCAGTGTGGCATGGAGCTCCTCGGCGCACACC	301

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Qy 136 LysSerGlnLysAlaTyrIleArgIleAlaArgLeuArgLysAenPheGluGlnGluPro 155
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Qy 156 LeuAlaLysGluValSerLeuGlnGlnGlyIleValLeuProCysArgProProGluGly 175
Db 362 CTGGCCCAAGAGGAGTCCCTGGAGCAGGCGCATCGTCTGCCCTCCGCTCCACCGGAGGC 421
Qy 176 IleProProAlaGluValGluTyrLeuArgAenGluAspLeuValAspProSerLeuAsp 195
Db 422 ATCCCTCCAGCGAGGTGGAGTGGCTCCGGACAGAGACTGGTGGACCGCTCCCTGGAC 481
Qy 196 ProAsnValTyrIleThrArgGluHisSerLeuValValArgGlnAlaArgLeuAlaAsp 215
Db 482 CCCAATATACATCACCGCGGAGCACAGCTGGTGGTGGACAGCGCCGCTTGTCTGAC 541
Qy 216 ThrAlaAsnTyrThrCysValAlaLysAenIleValAlaArgArgSerAlaSerAla 235
Db 542 ACGGACAACTACACCTCGTGGCCCAAGAACATCGTGGCAGCTCGCCGAGCGCTCCGCT 601
Qy 236 AlaValIleValTyrValAsnGlyTyrTrpSerThr-TripThrGluTrpSerValCysE 255
Db 602 GCTGTCTATCTCTACGTGACGGTGGTGGTGGACCGAGTGGTGGCTGGCTGGC 661
Qy 255 rAlaSerCysGlyArgGlyTrpGlnLys-ArgSerArgSerCysThrAsnProAlaProL 275
Db 662 -GCCAGCTGTGGCGCGCTGGCAGAAACCGAGCGGAGCTGCAC-AACCCGGTGGCTC 719
Qy 275 euAsnGlyGlyAlaPheCysGlu-GlyGlnAsnValGlnLysThrAlaCysAlaThrLeu 294
Db 720 TCAACGGGGCGCTTCTGTGAGGGGCGAGATGCCAGAAA---GCAGCTGGCGCCACCT 776
Qy 295 CysProValAspGlySerTrpSerProTyrTrpSerLysTrpSerAlaCys--GlyLeuAspC 314
Db 777 GTGCCAGTGAAGCGCACTGTAGCAGTGGAGCGGCTGGTGGCTCTTGGGCTTGGCTT 836
Qy 314 YThrHis-TripArgSerArgGluCysSerAsp-ProAlaProArgAsnGlyGlyGluG 333
Db 837 GCACCACTTGGCGGAGCGGAGTGTCTGAAACCCAGCAGCCCGGACCGGAGGGGAG 896
Qy 333 uCys---GlnGlyThrAspLeuAspThrArgAsnCysThrSerAspLeuCysValHisE 352
Db 897 GTGTGCCAGGTCACTGGACCTGGCACCCGGGATGG-TCCAGTGAAGTCTGTGTGCC-AC 954
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DEFINITION
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mRNA sequence.
ACCESSION
VERSION
BI818609.1 GI:15929902
KEYWORDS
SOURCE
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ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 818)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-x@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov

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oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 Kb,
insert size range 1-3 Kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."

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Query Match: 28.16% Indels: 58
DB: 4 Gaps: 1

US-10-624-932C-2 (1-898) x BI818609 (1-818)

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Qy 41 AspLeuLeuProHisPheLeuValGluProGluAspValTyrIleValLysAenLysPro 60
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Qy 61 ValLeuLeuValCysLysAlaValProAlaThrGlnIlePhePheLysCysAenGlyGlu 80
Db 184 GTGCTGCTTGTGTGCAAGGCGGTCGCCGCCACGATCTTCTCAAGTGCACCGGGAG 243
Qy 81 TrpValArgGlnValAspHisValIleGluArgSerThrAspGlySerSerGlyLeuPro 100
Db 244 TGGGTGGCCAGGTGGACCACTGATCGAGCGGACGACGAGCGGAGCAGTGGGCTGCC 303
Qy 101 ThrMetGluValArgIleAenValSerArgGlnGlnValGluLysValPheGlyLeuGlu 120
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Qy 121 GluTyrTrpCysGlnCysValAlaIleTrpSerSerSerGlyThrThrLysSerGlnLysAla 140
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Qy 141 TyrIleArgIleAlaArgLeuArgLysAenPheGluGlnGluProLeuAlaLysGluVal 160
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Qy 161 SerLeuGluGlnGlyIleValLeuProCysArgProProGluGlyIleProProAlaGlu 180
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Db      |||||||
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Qy      |||||||
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Db      |||||||
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Qy      |||||||
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Job time : 10108 secs